

**FIGURE 1**

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCGCTCTCCGCTTCTGCATCGCGGCTTCGGCG  
GCTTCCACCTAGACACCTAACAGTTCGCGGAGCCGGCCGGTCTGTCGAGGGGGTCCGACACGGGAGTTCGGCGGCTCT  
TGTGCATCTTTGGCTACCTGTGGGTGGAAGATGTCGGACATCGAGACTGGTTCAGGACATCCCGCGCATCAGCG  
GCTATTGGTTCCCGCCACCGTGCCTGGTGGTTCGGTTCGGCAAACCTCGCCCTCATCAGCCCGGCTACCTCTTCC  
TCTGGCCCGAAGCCTCTCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGGTG  
CAGGAACCTGGATTCTCTTTATTTGGTCAATTAIATTTCTTATACGATTTCTACGGCACTTGAAACAGGAGCTT  
TTGATGGGAGCCAGCAGACTATTATTATCATGCTCCTCTTTAACTGGATTTCATCGTGATTACTGGCTTAAGCAA  
TGGATATGTCAGTTGGCTGATGATTCCTCTGATCATGTTCAGTACTTTATGCTGGGGCCAGCTGAACAGAGACATGA  
TTGATATCATTTTGGTTTGGAAACACGATTAAAGGCTTGCATTTTACCCTGGGTATCCTTGGATTCAACTATATCA  
TCCGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTCCTAATGTTTCAGATACC  
CAATGGAGTTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTGTGACCCTGGCTGCCAGTAGGAGAGGAG  
GAGTATCAGGATTTGGTGTGCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGAGGCGGGAGACACA  
ACTGGGGCCAGGGCTTTGCACTTGGAGACCACTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTT  
CCTCCAGTGTGGGTGCACCTTAACAACTGCGTTCGGCTAACACTGTTGGACCTGACCCACACTGAATGTGATC  
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAGTTTCACGATTTCTATTCA  
AGTCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAAACTGACTACATTTTGTGGTGTCTTCTCT  
TCTCCCTTTCCGCTCGAATAATGGGTTTAGCGGGTCTCAATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAA  
ACCCTTCCCAAAAGGACCTTATCTCTTTCTTGACACATGCCTCTCTCCACTTTTCCCAACCCCCACATTTGCA  
ACTAGAAAAAGTTGCCCATAAATTTGCTCTGCGCTTGACAGGTTCTGTATTATTATGACTTTTGCAAGGCTGGT  
CACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAGACAGCCAG  
GATGAAGGCTTTCTCAGCTTTTGAATTTGCTTCGACTGACATCCGTTGTTAACCGTTTGCCACTCTTCAGATATT  
TTTTATAAAAAAGTACCCTGAGTTTCATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGGTTGGTGTCTGG  
GTGTTTGTCTTCTGAGCTAAGTGATCAAGACTGTAGTGGAGTTGAGCTAACATGGGTAGGTTAAACCATGGG  
GGATGCACCCCTTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA  
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCTATTTTCAATC  
TCAATCTGGATATGTGTTCAATGATTAAGGAGGAGAGACCTCATACGCTATTAAATGTCACTTTTTCGGCTTA  
TCCCCCGTTTTTGTGTATGTTTCAATTAATTTGAGGAGGCGCAGCTCCTCTCTGACAGTAGATCATTTTTTTA  
AAGCTAATGTAAAGCACATTAAGGGAATAACATGATTTAAGGTTGAATGGCTTAGAATCATTTTGGGTTGAGG  
GTGTGTTATTTGAGTCATGAATGTACAACTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTCGTA  
GGTGGGCTTTTCTATCAGAGCTGGGCTCATAAACCAATAAAGTTTTTGAAGGCCATGGCTTTTCACACAGTTA  
TTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGTATTGAGTGGCTGTCACTTTGAGGCAACTA  
AAAAGGCTTCAAAGCTTTTGATCACTTTCTTTTCAGGAAACATTGTGCTCAACAGTATGACTATCTTCTCCCTC  
ACTCTTAAACAGTGTGATGTGTGTTATCTTAGGAAATGAGAGTTGCAAAACACTTCTCATTTTGAATGAGGTTT  
GTGTGATCTTCTCATATTAAATTTATGATATAAATAGGTGGGAGAGTCTGAACCTTAACCTGTATGTTTGT  
TGTTCACTGTGGCCCAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACTCCAATATGTTGCACTGACAC  
TCATTGTACAGCTGGAGACTCATTGTATGTATAAAGATTTTCTGACAGTGAAGTACCCGAGTCTCTGGTGT  
ACCTCTTACCAAGTCTGCTGCTCGGAGCAGTCATTTTCTTAAAGGTTTACAAGATTTAGAACTTTCAGGTT  
CAGGGCAAAATGTTTCATGAAGTTATCTCTTAAACATGGTTAGGAAGCTGATGAGCTTATTGATTTTGTCTGGA  
TTATGTTTCTGGAATATTTTAAACAAACAGCTATTGGAGTTTGTGACTTGGAGGCAAAACATGACAGTGGAT  
TCTCTTTACAAATGGAATAAAAAATCCTTATTTGTATAAAGGACTCCCTTTTGTAAACATATCTTTTAT  
TGTGAAAAATTTGAATTAATAATGTGCAACTTG

2/615

## **FIGURE 2**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGILSPAYLFLWPEAFLYRFQIWRPITATFYFVVGEGTGFLYLVN  
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF  
KACYLPFWILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSRGGVSGFGVPPA  
SMRRAADQNGGGGRHNWQGQFRLGDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

10052586.011502

**FIGURE 3**

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACTGGGGTCAAATGCACGGATT  
 CTCACCTCGTACAGTTACGCTCTCCGCGGCACGTCCGCGAGGACTTGAAGTCTTGAGCGCTCAAGTTTGTCCGT  
 AGGTGCGAGAGAGGCC**CATGG**AGGTGCCGCCACCGGCACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCATTATTC  
 CCGAGTCTTTGCTGCCGAAGCTGTGACTGCCGATTCCGAAGTCTTGAGGAGCGTCCAGAAGCGGCTTCCCTACGT  
 CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAT  
 TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAATACC  
 AGCTTTTATTTCATGCTAAACAACAATACATGAGCAGAGCCAGGCAGAAATTATCATAAACCGTTTGATGCTGT  
 GCAATCTGCACATCGTGCTGCCACACAGAGCTTCATTCTGTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTT  
 TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCTTAAGCCATTTTGTAAAT  
 TGCAGGAGCTGTACGCGGAAGTCTTTTAGGATAAACGTAGGCCTGCGTGGCTGGTGGCTGGTGGCATAATTGG  
 AGCCTTGCTGGGCACTCCTGTAGGAGGCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTCAGGAAG  
 AAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAAGAGTGGAAAGGCAGACTACAAGTTACTGAGCA  
 CCTCCCTGAGAAAAATTGAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAAATTGAAGCACTGCT  
 AAACCTTCTAGAAAACCTTCAGTAATAGATAAAACAAGACAAGGACT**GGA**AGTGCTCTGAACTTGAACTCACTG  
 GAGAGCTGAAGGGAGCTGCCATGTCGATGAATGCCAACAGACAGGCACCTCTTTGGTCAGCCTGCTGACAAATT  
 TAAGTGCTGGTACCTGTGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTTCTTTTAACTAAGAATGGGGCTGTT  
 GTACTCTCACTTTACTTATCCTTAAATTAAATACATACTTATGTTTGTATTAACTCTATCAATATATGCATACAT  
 GGATATATCCACCACCTAGATTTTAAAGCAGTAAATAAAACATTTCGCAAAAGATTAAAGTTGAATTTACAGTTT

4/615

## **FIGURE 4**

```
></usr/seqdb2/set/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEIYHNRFDAVQSAHRAATRGFIRYGWRNGWRTAVFVTIFN
TVNTSLNVYRNKDALSHFVIAGAVTGSILFRINVGLRGLVAGGIIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRIQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
```

**Important Features:**

**Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and 171-195

**N-glycosylation site:**

amino acids 153-156

1002586-011502



**FIGURE 5**

CGGACGCGTGGGCGCGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCTCTGCGCGCGCCCTGAAGTCGGC  
 GTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGCTTAAAGAAATGAGGACAGGCTTCC  
 TAGATAAATTTTCGTGGCCAGAAATGTAATGTAATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCG  
 CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAAGCTGTGGTGATCTCTAAGCCAGAACAGTTGA  
 ACCATGCTCTTTCACACATGTGGTGTAATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAAATGCTCAGG  
 TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT  
 TGATGTTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC  
 CGGGACTAGCTGTGTTTTTCAAATGCACTTATATTTTTAGCACTCTGATCTCAAAATTTGGAAGAACCAGGAA  
 AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCCTTTGTTATATTCTGTTTGTAGATAGGTTTTTTATC  
 TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT  
 TTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTATATAATACAGACTATATG  
 AATTGGATAATGAGTATCAGTTTTTTATCTCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGGTTACATCA  
 TCTTGTCATTTTAGAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCAGCTT  
 TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAGGTGTTTGAGACCAAGCTGGCCAAATGGCGAAACCCCATC  
 TACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCCTGTAATCCAGCTACCTGGGAGGCTGAGGCAGG  
 AGAATCGCTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCCCACTGCACCTAGCCTGGGGAGAA  
 AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTCTGAAGATGTACAAAAAATATAGCTT  
 CATATATCTGGAATGAGCACTGAGCCATAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCATAAATGAGGT  
 TTTTTTGGTAAAGAAAAATATTGTTCTTATGTATGAAGAAGTGACTTTTATATATGATTTTTTAAATGCC  
 CAAAGGACTAGTTTGAAAGCTCTTTTAAAAAGAAATTCCTCTAATATGACTTTATGTGAGAA

1052536.01502

6/615

## **FIGURE 6**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILEFTGWWIMIDAADVYPKPEQLNHAFHTCGVFSTLAFFMINAV  
SNAQVRGDSYESGCLGRTGARVNLFIGFMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF  
GRTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

105586-0133  
202310-082200

**FIGURE 7**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCCTATACCTACTGTAGCTTCTCCAG  
 TATGACCCATAAAGGCTACTGCTGCTACTACGCGGCTAGACAGTTACTGTTCCAGCTCTAGGATGTGCGTTCCTC  
 CACTAGAACCTCTCTGAGGGAGGTAATTAATAAACAGTGGAAATGGAATAAACAGTGTCTGTAGTCACTCTGTAAATA  
 TGTCTCCTGTCAACAATGTATACATTTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCACTTACTA  
 GTGAAGTATTTCTGCCAATAGAGAAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACGTGTG  
 AAGCTAGTTTTCTGTGTGCTTGTGTCTATTCTGTGTATATAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT  
 TCTGGAAGGAATTTCTCTGATTTTCATGAAGTGTGCCATTTCTGCTTTCTTTATTTCTCGGATAACTTGATTGTCT  
 TTCTATGTCTGTCTCTATCTTCAACCAGCCATGGCTGTATCTTCTCAAATTTTAGCATTTATAACAACAGCTCTT  
 CTATTAGGATAGTGTCAAGAGGGCGCTAAACTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTGTCTATT  
 GTGGCCTTGACTGCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCTTTTTC  
 AGCCCTTCCAATTTCTGCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTTGACAGCAAAAGGAATGGACT  
 TTTCTGAAAGCTAAATGGAAACCAACAGCCAGAGTTTTTCAGTCACTCCGCTCTGGCATGGGCCATGTTCTTATT  
 ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAAGATACTGAAGAGGGGAAACAGCTCACT  
 GAAAGCATCTTCATACAGAACAGCAAACTCTATTTCTTGGCATCTGTTTAATGGGCTGACTCTGGGCCCTTCAG  
 AGGAGTAAACCGTGATCAGATTAAAGAACTGTGGATTTTATGGCCACAGTGCAATTTTCAGTAGCCCTTATTTTT  
 GTAATGCACTCCAGGGCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAACATGTTCCATGTCTGTATGGCC  
 CAGGTTACCACTGTCTATTATCAACAACAGTGTCTGTCTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTG  
 GAAGCCCATCAGTCTTCTCTCTATATTTATTAATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGG  
 CAAGAAGGATCCGAGATCTAAGTGCCAACTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTT  
 ACCAAACCCAGAGTGATGAGTCAGATGAAGATACCTTTCTAACTGGTACCCACATAGTTTTCAGCTCTCTTGAAC  
 CTTATTTTCACTTTTCAGTGTGTGAATATTTATCTTTCACTTTGATAAACACAGAAATGTTTCTAAATCCTAA  
 TATCTTTGCTATATCTAGCTACTCCCTAAATGGTTCCTCAACAGGCTTAGAGTACCCAAAGGCTAAGAAATTC  
 TAAAGAACTGATACAGGAGTAAACAATATGAAGAAATTCATTAATCTCAGTACTGTGAATAACAGAAAGTTATAT  
 GTCCAGATTATTTTCTTGGCTTCAAGCTTCCAAAAAAGCTGTGAATAATCATGTTAGCTATAGCTTGTATATAC  
 ACATAGAGATCAATTTGGCAAATATTCACAATCATGTAGTTCTAGTTTACATGGCCAAAGTCTTCCCTTTTAAACA  
 TTTAAAGCTAGGTTGTCTCTTGAATTTTGGAGCCCTAGAGATAGTCAATTTGCAAGTAAAGAGCAACGGGACC  
 CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTPAA  
 ATATTTTGTCTGAAGAAGCAGTTTCTTCAGACACAACATCTCAGAAATTTTAAATTTTAGAAATCTAGGGAAATGG  
 ATTTTGTGAATAATCTTTTGTAGTTTAAACATTTGGTTCCTAGTCACCATAGTTTACCCTGTATTTTAAAGTCA  
 TTTAAACAAGCCACGTTGGGGCTTTTCTCTCAGTTTGGAGAGAAAATCTGTATGTCATTACTCTCGAATTA  
 TTACATTTTGGAGATAAGAGGGCAATTTATTTTATTAGTTACTAATTCAAAGCTGTGACTATTGTATATCTTTC  
 CATGAGGCGAGTTAACTCTGCTAGATAGAGAAGTCAGGTGATAGATGATATTAATAATTTAGCAAAACAAAGTGAC  
 TTGCTCAGGCTCAGCTGGGTTGATAGATAAGAGAGTGGGCTTAACTGGCAGCCCTGTATGTTTACAGACTAC  
 CATACTGTAAATATGAGCTTTATGTGTCTATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCTAAGTTTC  
 ATGCAAGTGAATATAAGGTAATATACTATTATATAATTCATTTGTGATATCCAAATAATATGACTGGCAAGAAAT  
 TGTGTGAAATTTGTAATTAATAATATTTATAAACCCT

**FIGURE 8**

MEKQCCSHPVICSLSTMYTFLLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSSELVKLVFCVLVSFCVIK  
 KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFSNFSIITALLFRIVLKKRLNMIQ  
 WASLLTLFLSLIVALTAGTKTLQHNLAGRGFHDAFFSPNSCLLFRSECPKDNCTAKEWTFPEAKWNNTTARVFS  
 HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY  
 CHSAFVALIFVTAFQGLSVAFILKFLDNMFEHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFIYNA  
 SKPQVPEYAPRQERIRDLSCNLWERSGDEELERLTTPKPSDESEDLTF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,  
 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

9/615

## FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCG  
AAGACTAACATTTTGTGAAGTTGTAAACAGAAAACTGTGTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTC  
CTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT  
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTACTCCAGAAAAATGCTTATTTGGGGCAATGCTA  
AATATTGCCGSCAGTTTTATGCATTGTCTACCATTTATGTTTCGTTATAGCAAGTTCATGCTCTGAGTCCTGAAGAG  
AACGTTATCATCAAATTAACAAGGCTGGCCTGTACTTGGAACTCTGAGTTGTTTAGGACTTTCTATTGTGGCA  
AACTTCCAGAAAAACAACCTTTTGTCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT  
ATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAATCCATGGCAAAACAAGTCTTCTGGATCAGACTG  
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGTGACTTGTCTCATCAGTTTTCGACAGTGGCAATTTT  
GGGACTGATTTAGAACAGAACTCCATTGGAAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA  
GCAGAATGGTCTATGTCTATTTCCCTTCTTTGGTTTTTCTGACTTACATTCTGATTTTCAGAAAAATTTCTTTA  
CGGGTGGAAAGCCAATTTACATGGATTAAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG  
CTACTTTCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTTCTCAGGGATTGGGGAAAGG  
TTACAGAAAGTTGCTTATTCTTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACA CTGATGAATGCT  
GATAATCAGGAAACATGAAGAAGCCATTGTATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA  
CCTATGCCATATCTTTTATCTCAGAAAAATAAAGTCAAAGACTATG

1052556.01507

10/615

**FIGURE 10**

MWWFQQGLSFLPSALVIWTSAAFI PSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIVVRY  
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLPAAHVSGAVLTFMGSLYMFVQTILSYQM QPKI  
HGKQVFWIRLLLVICGVSALSMLTCSSVLHSCNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT  
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

2025-05-26 01:50

11/615

## FIGURE 11

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGGCCGGGGTGCGGAG  
CCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCCGCCGCTGCACCTTCGCTTGTACTTGTCTGTCGACGC  
GACTGCCCGCGCGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTGCTGTGGTTCCTCCGACCTGG  
CAGAGCTGCGGAGCTCTCTGAGGTCCCTTCSAGAGTACCGGAAGGAGCACAGGCTTACGTGTTCTGCTCTTCT  
GCGGCGCCTACCTCTACAAACAGGGCTTGCCATCCCGGCTCCAGCTTCTGAATGTTTGTAGCTGGTGCTTGT  
TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA  
GTATTTTGGCAACAGTTGGTGGTGTCTACTTTCTGTATAAAGTGGCCTGCTGCAGAGAAAGTGGAGGAGA  
ACAGAAACAGCTGTGTTTTTCTTATTGTTTTTGAGACTTTTCCCCATGACACAAACTGGTTCCTGAACCTCT  
CGGCCCAATTCTGAACATTCCTATCGTGCAGTTCTTCTTCTCAGTCTTATCGGTTTGATCCCATAAATTTCA  
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCTAACCTCTCTGGATGCTCTTTCTCTCTGGGACATGCTCTTTA  
AGCTGTTGGCCATTGCCATGGTGGCATTAAATCTCGGAACCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT  
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATGACTCTGGATTTTCTGTTTGGCCATCC  
CTGGACTCAGTTGCTTATTGTGTAATGGATGTGGTCTCTAAAGCCCTCATTGTTTTTGATTGCCTTCTATAG  
GTGATGTGGACACTGTGCATCAATGTGAGTGTCTTTTCAGAAAAGGACACTCTGCTCTTGAAGGTGATTATCATC  
AGGTTTTCAAACCGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCTAGAAAAATGCTGTTTGTGGCCGGGCG  
CGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGTGATTCAAGGTCAGGAGTTCAAGACC  
AGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT  
AATCCAGCTACTCGGAGGCTGAGGCAGGAGAAATTGCTTGAACCAAGTTGCAGAGGTGTCAGTAAGCCAAGAT  
CACACCATGCACCTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

1052536.011502

12/615

## **FIGURE 12**

MRPLLGLLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYRKEHQAYVFLFCG  
AYLYKQCFAIPGSSFLNVLGALFGFWLGLLLCCVLTSVGATCCYLLSSIFGKQLVVSFYFPDKVALLQRKVEENR  
NSLFFFLFLRLFPMTENWFLNLSAPILNIPVQFFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL  
LAIAMVALIPGTLIKKFSQKHLQLNETSTANHIHSRKDT

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

20250301 09:55:01



**FIGURE 13**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG  
 GGGGCGTGTGGGCCCAGCGTGTGTGGCCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA  
**TG**AGTTTCTCATCGACTCCAGCATCATGATTAACCTCCAGATACTATTTTGGATTGGGTGGCTTTCTCTCA  
 TGGCCCAATTGTTTAAAGACTATGAGATACGTCACTAGTATGTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT  
 CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGGA  
 AATATCGGACTACTGCATAAACCAACGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA  
 AACTAGGAGATCCCTTCCCATTTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTG  
 GTGTGATTGGAGTGACTCTCATGGCTCTTCTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTT  
 ACTTCTCAGGAAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAAACCATGGATATGATCA  
 TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGGAAGTGATACAAACCATCAG  
 GTTCTGGGGAATGATAAAAAGTGTACCACTTCAGCATCAGGAAGTGAAATCTTACTCTTATTCAACAGGAAG  
 TGGATGCTTTGGAAGAATTAAGCAGGCCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAAATAG  
 AATACTCCAAAACCTTCAAGGGGAAATATTTAAATTTCTTGGTTACTTTTTCTCTATTACTGTGTTTGGAAAA  
 TTTTCATGGCTACCATCAATATTGTTTTGTATCGAGTTGGGAAAAAGGATCCTGTCAAGAGGCATGTAGATCA  
 CTGTGAATTATCTGGGAATCCAATTGTATGTGAAGTTTGGTCCCAACACATTTCCCTCATTTCTGTGGAAATA  
 TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTATGCCCCTCTAGCAGTAAGTCTCT  
 CCAATGTCATTGTCTGCTATTAGCACAGATAAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGA  
 GTATGCTCTTTAGAATACCGCACCATTAATCACTGAAGTCTTGGAGAACTGCGAGTTCAACTCTATCACCGTTGGT  
 TTGATGTGATCTTCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTGGCTCACAAACAGGCACACAGAGA  
 AGCAAAATGGCACCT**TGA**ACTTAAAGCTACTACAGACTGTAGAGGCCAGTGSTTTTCAAAATTTAGATATAAGAGG  
 GGGGAAAAATGGAACCGGGCTGACATTTATAAAACAAACAAATGCTATGGTAGCATTTTTCACCTTCATAGC  
 ATACTCTTCCCGTCAGGTGATACATATGACCATGAGTAACATCAGCAGAAACATGAGAGGGAGAACTAACTCAA  
 GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGGCGAGAGGAGCAAGAACTAAAG  
 GTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTTA  
 AGGTTACATGGAAAAGGTTATAGCTTTGCTTGAAGTTGACTCATTAATACAGAGACTGTAAACAAAAA  
 AAAAAAAGAGCGCGCGGACTCTAGAGTCGACCTGCAGAAGCTTGGCGCCATGGCCCACTTGTTTATTG  
 CAGCTTATAATG

14/615

## **FIGURE 14**

MSFLIDSSIMITSQILFFGFGWLFFMROLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVINSSSRYPHW  
KMNLGVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFFWKLGDPPILSPKHGILSIEQLISRV  
GVIGVTLMAILSGFGAVNCPYTYMSYPLRNVTDLDLALERRLLQTMDMIISKKKRMAMARRMTMFQKGEVHNKPS  
GFWGMIKSVTTSASGSENLTLIQOEVDLEELSROLPLETADLYATKRIEYSKTFPGKYFNFGLGYFFSIYCVWK  
IFMATINIVFDRVGKTDPTVRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFYFAISSSKS  
SNVIVLLLAQIMGMYPVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVLSALSSILFLYLAKHQAPE  
KQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

1052536-01502

CAGGAGGAACACGACGCTCTCAGAGCCGCGGAGGAGGCGCTGTCAGAGAGGACACGCGCGGCTCGCGCCGGACATCTGCGCCGCC  
 CAGGAGCTCCCGACGCTCGCGTCTCCGCTGGCTGCTGTCTGTCTGTCTGCTCGCCGCGCGCCGCTCGCTCCGCC  
 CACAGCGCCACGCGCTCTCGACCCCACTCGGAGAGTCCGTGACGCGCCGACAGCTGCCCGCGCTGGTGTGGACAGGCC  
 AAGTTCGGCATCTTCATCACTCGGAGGATGTTTTCGTCGCCACAGTTCGGTAGCGAGTGGTTCGTGTGGTATATGG  
 CAAAGAGGAAAAATACCGAAGTATCTGGAAATTTATGAAAGATAATTCCTCCTCAGTTTCAAATATGGAATTTG  
 GACCACATATTTACACGAAATTTTAAATGCCAACGCTGGGGCAGATATTTTCGAGCCCTCTGGTGCCAAATAT  
 ATTGTCTTAACCTCCAAACATCATGAGGCTCTTACCTGTGGGGGGTCAGAATAATCTGTGGAACTCGGAATGCATAT  
 GATGAGGGGGCCCAAGGAGCAATTCGAAAGAACTTAGGATGCGCATTAGGAAACAGAACTGACCTCGCTGTGTGGA  
 CTGTACATATCTCCCTTTTGAATGGTTTCTACCTGCTCTCCCTTAGAGGATGAATTCAGTTTCCATTAAGCGGCAAA  
 TTTTCAGTTTCTAAGACATTCGCCAGAGCTCTATGATGTATGTAACAACATCAGCTCGAGTTCTGTGGTCGAT  
 GGTGACGGAGAGACCCCGATCAATATGGAAGACACAGAGCTCTTTCGGCTGGTTATATATGAAGACCGAAT  
 CGGGGCAACAGTATGACCAATGATCTTGTGGGAGCGTGTGATCATCTGTATGACATGTGTGGCTCTATACCTGCAAT  
 GATCGTTATATACCCAGCAATCTTTGCGACATARAATGGGAAACTGTCATGACATACAGCAAACTCTCTGGGGG  
 TATAGGAGGGAGCTGGAAATCTCTGCATATCTTCAACAATTGAGAATATGGTAGAAGCACTGTATGAGACAGTTTCA  
 TGTGAGGAATATCTTTTGTAGTAATTTGGGCCCCACAGTATGGCCACTTTCTGTAGTTTGTGAGGNGGAGCT  
 AGCGAGTGTGGGTCTGTGCTAAAGTCAATGGAGAACTATTATTAAGAACTTACCTGGCGATCCCGAATGAC  
 ACTGTCACCCCAAGTCTGTGTGTAACATCAACGAGCTAAGGAAAAATAGTCTATGCACTTTTCTTAATGGGCC  
 ACATCAGGACAGCTGTCTCTGGCCATCCCAAGTATTCTGGGGGACACAGAGCTGAAACTCTGGGCACTGGGA  
 CAGGCACATCTCGATTTCTTTTGGAGCAAAATGGCAATTTGTGGAGAAGCTGCACAGCTAACCACTCATCAGATG  
 CGGTGTAACTGGGGCTGGGCTCTAGCCCTAACTAATTTGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT  
 ATGTCTAAGGCTAGGAAATATCAGGTGTCTATATGTTAGCAGCATGGAGAAGCACTGTGAACCTGGTAAGGAAAA  
 TTATTTTGGCAGTTCAGCCCTCTCCCTTTCCCACTAAATTTTCTTAAATACCCATGTAACTTTTAACTCT  
 CAGTGCATCTTGGCAATTAAGTCTCTTCACTGATTTGTTTCTCATGTGTGATCTCAGAGGTGAGAATTTTTCAT  
 CATTTATGTAGCAAGAAATGTGGTGTATATGAGCGCAACTGAAATTTTATGTGAGCCGATATCCCCCGAT  
 TATATATGTATGCATCACTTAATATGGGATATTTCTTGGGAAATGCACTGCTAGTCAATTTTTTTTGTGGCCAA  
 CATCATAGAGTGATTTACAAATCTCTAGATGGCATAGCTCATCTACACCAATATGTATGTGATAGATGCTGTG  
 CTCTTAGGCTACAGACATATACAGCATGTATCTGAATACCTGTAGGCAATATGAACAGTGGTATTTGTATATCGAA  
 ACATATGAAACATAGAGAAGTACAGTGAATAAATCTGTAAATAAATTTGGTGACCTGTATAGGCGCATTCACCA  
 GAATGGCTCTACAGAGCTGGAAGTGCTCTGGTGGTATCAGTGAAGTGAATGTGAAGGCGCTAGGACATTTATGGA  
 CACTCGCAGCGTTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTCCTCTCAATT  
 ATAAATTAACATAAGTGTACTGTAACTTTTCAACCAAGTTTAAATTTTAAAACTTTTGGCTCTTTGTGTAATAC  
 ACTTAGCTTAAAACTAAACATCTGTGGCAATTGAA

## FIGURE 16

MRPQKELPLRAPFLMLLLLLLMLPPPCPAHSAFTDFDPTWESLDARQLPAWFDAQKGIFIHGWGVFSVPSFGSEWF  
 NYWQCEKPIKYFVEKLEWNPYPSFKYEDFGPLFTAKFFNANQAWIDPQASQAYIVLTSKHGEGFTLWGSYSEWN  
 NAIDEGPKRDI VKELEIVARNRTLPLGLYLSFWFLPELEDESSPHKRQFPVKTLPELYELVYNQOYPEL  
 WSDGGDGAQYQWNSTGFLAWLYNESVPRGTVTNDRNGAGSCIKHGEGFTCDSRYPNGHLLPKHWCNKMTIDL  
 SWGYRERAGISDYLTIELBLQVLVBTSYCGGNLLNIGTDLGTISVVEERLQRQVSGVLKVNGBAIYETTYSR  
 QNDTVTPDVWVTSKPKELGVYAI FLKWPTSGQLFLGHGPKAILGATEVKLLHGQPLNWI SLENGIMVLEPQITI  
 HOMPCKQWGAALATNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

**FIGURE 17**

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAAAAAAAAAAAAACACA  
 CCAAAACGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTCCTGCTTCTCCGTTACTGATCGTCTG  
 CTCCTTAGAGTCTCTTCGTGAAGCTTTTTATTCCTAAGAGGAGAAAATCAGTCACCGCGAAATCGTGCTGATTAC  
 AGGAGCTGGGCATGGAATTTGGAGACTGATGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCCTCGGGA  
 TATAAATAAGCATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCAACCTTTGTGGT  
 AGACTCGACCAACCGAGAAGATATTACAGCTCTGCAAGGAAGGTGAAGGCAGAAATTGGAGATGTTAGTATTTT  
 AGTAAATATGCTGGTGTAGTCTATACATCAGATTGTTTGTCTACACAAGATCCTCAGATTGAAAAGACTTTTGA  
 AGTTAATGTACTTGCACATTTCTGGACTACAAAGGCA1TTCCTCCTGCAATGACGAAGAATAACCATGGCCATAT  
 TGTCACTGTGGCTTCGGCAGCTGGACATGTCCTGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTG  
 TGTGGATTTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACCAACATGCTCTGTG  
 TCCTAATTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCACTCTGGAACCTGAGGAAGT  
 GGTAAACAGGCTGATGTCATGGGATTCTGACTGAGCAGAAGATGATTTTATTTCCATCTTCTATAGCTTTTTTAAC  
 AACATTGGAAGGATCCTTCTCGAGCGTTTCTGCGAGTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCACT  
 TATTGGATATAAAATGAAAGCGCAATGAACACCTAGTTTCTGAAAACTGATTTA CCAGGTTTAGGTTGATGTC  
 TCTAATAGTGCAGAAATTTAATGTTTGAACCTCTGTTTTTCTAATTAATCCCACTTTCTCAATATCATTTTGTG  
 AGGCTTTGGCAGTCTTCATTACTACCACTTGTCTTTAGCCAAAAGCTGATTACATATGATATAACAGAGAAAA  
 TACCTTTAGAGGTGACTTTAAGGAAAAAGAAAAAGAACCAAAATGAC1TTATTAATAATTAATTTCCAAGATTA  
 TTTTGGCTCACCTGGAAGGCTTTGCAAAATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTATG  
 CACTTAATTTTGTATAATTTGTGTTCTTTCTCTGTTCTACATAAAATCAGAACTCTCAAGCTCTCTAAATAAA  
 ATGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACCTCAATGGGTAGGTTTCATCCTTACCCATT  
 GCACTCTGTTTCTGAGAGATACCTCATTCCAATGCCAACATTTCTGCACAGGGAAGCTAGAGCTGGATAC  
 ACGTGTGCAAGTATAAAAGCATCACTGGGATTTAAGGAGAATTGAGAGAATGTACCCACAAATGGCGCAATAA  
 TAAATGGATCACACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**THE**

## FIGURE 18

MKFLLDIILLLLPLLIIVCSLESFVKLFIPIKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL  
 VLWDINKHGLEETAACKGLGAKVHTFVVDSCNREDIYSSAKVKVAEIGDVSILVNNAGVYVT  
 SDFLATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAGHVSVFPFLLAYCSSK  
 FAAGFHKTLDELAALQITGVKTTCLCPNFVNTGFIKPNPSTLGPTLEPEEVVNRMLHGILT  
 EQKMIFIPSSIAITLTLERILPERFLAVLKRKISVKFDVAIVGYKMKAO

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

**FIGURE 19**

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGGTGGCCTAGAGAT  
 GCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCGCGCAGCCCGCTCCACGCGGTAG  
 CGCCCGAGTGTGCGGGGGCGCACCCGAGTCTGGGCC**ATG**AGGCGGGAAACCGCGCTACAGGCCG  
 TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCCGCAGCGGTCGCCTGCTGAGTGCCTCGG  
 ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTATAAAG  
 TCATTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA  
 GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACGAAACTGATAGAAAAGTTCA  
 TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC  
 AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATATCACAATTTA  
 GGAACCTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCGCGTGGTCATGTACCATCAGC  
 CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGAATGATGACCCGTGCAACA  
 TGAAGAACAATTTCAATTTGCAAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG  
 AAGGTGAGGAAACAGAGCTGACAAACACCTGTACTTCAGAAAGAACACAGGAAGAAGATGCCA  
 AAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA  
 TTCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA  
 GAAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAAGCAACACCATCTGGCCCTCTCCTCACC  
 AGGGAACAGCCCGGACCTAGAGGTCTACAATGTCTAAGAAAAACAAGCGAAGCTGACTTAG  
 CTGAGACCCGGCCAGACCTGAAGAATATTTCAATTCGAGTGTGTTTCGGGAGAAGCCACTCCCG  
 ATGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC  
 TGGTGAGCGTGGAGAGTGGATTGTTGACCAATGACATTTATGAGTTCTCCCAGACCAAATGG  
 GGAGGAGTAAGGAGTCTGGATGGGTGAAAAATGAAATATATGGTTATT**AGG**ACATATAAAAAA  
 CTGAAACTGACAACAATGGAAGAAATGATAAGCAAAATCCTCTTATTTCTATAAGGAAAA  
 TACACAGAAGGCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA  
 CCTCCTGTTGGACCCACAGTTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC  
 TTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGTCACTTGGTT  
 GGTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC  
 TTGAAAAACCACTCTGTTTTCTTGCTCTATACAGCAGCACATATTATCATACAGACAGAAA  
 ATCCAGAATCTTTTCAAAGCCACATATGGTAGCAGGTTGGCCTGTGCATCGGCAATTCTC  
 ATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAA

## FIGURE 20

MRPGTALQAVLLAVLVLGLRAATGRLLSLENDLGGQPCVRCGGTQRCQKVYVLFHDTSSRRLN  
FEEAKEACRRDRGGQLVSESEDEVCQKLEKFIENLPLSGDFWIGLRRBEKQKSNSTACQDLYA  
WTDGSISQFNNYVDEBSCSEGEVCMVYHQPSAPAGIGGYPQWQNDRCNMKNNFICYSDS  
KPAVPSRAEAGEETELTPVLPEETQEEADAKTTFKSERAALNAYILTSLPLLLLLVVTV  
VCVVYICRKRKEQPPDSTKKQHTWPSHQGNSPDLEVYNVIRKQSLADELATRPDLKNTSF  
RVCSGEATPDDMSCDYDNMAVNPSESGFTVLVSVESGEFVTNDIYFSPDQMGRSKESGWVENE  
TYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

## Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152



## FIGURE 21

AGGCTCCCGCGCGCGGCTCTGCTGGCACTGGAGTGGGAACCCGGGCTCCCGCGGCTTAGAGAACACCGCATGAACCA  
CTGGAGCTCTCCGCGAGGCCGCGCCGACCTGGAGCTCTGCTGCTGCTGCTTGTGGGCTCTTCTGCTGCTCT  
CGAGGCTGGACCTGGAGCACCGCTGCTCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTCGAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTCTGGGGGGTCCATCCCATATTTCGTGTGCGCAGGGAGTACT  
GGAGGGAGCCGCTCTGAAAGTGAAGGCTCTGGGCTTGAAACACCTCACCACCTATTGCTCGGTGAAACCTGCATG  
AGCCGAAGAGAGGCAAAATTGACTCTCTCTGGGAAGACTGGACCTGGAGGGCTCTGCTCTGATGGCGCAGAGATCG  
GGCTCTGGGTGATTCTGCTGTCAGGCCCTCATCTCTGAGTGAAGTGAAGCTCTGGGGGCTTGGCCAGCTTGCTAT  
TCCAGACCGCTTGGCATGGGCTGAGGACATTAAGAAGGCTTCAACGAAGCATGGAGCTGAGCTTTATTTGAACCA  
TGAGTGTCCAGGGTGTGGCTCACTGACAGCTGAGGCTGGGGGACTATCATTTGCCGTGTCGAGGAATGAATATG  
GTTCTCTATAAATAAGACCGGCATACATGCCCTATGCTCAAGGAAGCACTGGAGAGCATGGCATGTTATGGAACCTG  
TCTCGATTTCGACAAACAAGATGGGCTGAGCAAGGGGATTGTCAGGGAATCTTGGCAGCATCAACTGCATGCT  
CAACACAGAGCTTGGCTACTGACCACTTCTCTTCAACAAGTCCAGGGGACTCAGGCCAAGATGGTGAAGTGGAT  
ACTGACGGGTGGTGTGACTCTGTGGGGAGGCCCTCAAAATCTGAGGATCTTCAGGTTTGAAGAACCGTGT  
TGCCTATGTGGACCGCGGCTCCCTCATCAACCTTCATGTTCCACGAGGAGCAACCAATTTGGCTCTCATGAATG  
GAGCCATGCATCTCATGACTACAGCTCAGATGTCCAGCATGAGCTGATGCTGTGTCAGAGAACCGCGCG  
ATTACAACGCGCAAGTACATGAAGCTTCGAGATCTTCTGGCTTCATCTCAGGCATCCTCTCCCTCCCCACCTG  
ACCTCTTCCCAAGTGGCGTATGAGCCCTTAAGCCCTTAACTGGCTTGTACTCTGTCTGTGGAGGCCCTCAAGTAC  
TGGGGAGGCCAATCAAGTCTGAAGAACGCCATCAAGTGGAGAACCTTCAGTCAAGTGGGGAATGGACATGCTCT  
TCGGGTGATCTTCTATGAGACAGCATACCTCTGCTGTCGACTCTTCAGTGAGCCATGTCATGATCTGGGGGACG  
TGTTTGTGAACACAGTATCCATAGGATCTTGGGACTACAGAACAGGAAGTGTCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTTGTGTGAAGATCTGTGCGAGTCAACTATGGGAGGAATATTGATGACCAACCGAA  
CTCTTAATTGGAATCTCTATCTGAATGATTCCGCTGAAAACCTCAGAATCTATAGCTTGATATGAAGGA  
GCTTCTTTCAGAGGTTCCGCTGTGAACATTTGNNGTTCCTCCAGAAACACCCATCACTGCTTCTTCTGG  
GTAGTCTTGCCATCACTCCAGCGCTTGTGACACCTTTCTCAGACTGGAGGGCTGGAGAAAGGGGTTGATTCG  
CTAATGGCCAAACCTTGAACCTTACTGAGACATGGACCCAGAAAGCTCTTACCTCCAGGCTCCCTGGTTGA  
CGACGGAATCAACCAAGTTCATCGTTTTTGGAGGAGAGTGGCGGCCCTGTCATCTACAGTTACAGGAAACCCCC  
ACCTGGGCGAGGAACCGATGATTAAGTGAACGGCTGGACACCCCTCTGCTGTGTGCGAGTGGGAGCTCGGCCTCT  
CTCTTGACCTGAAGCTGTGGTGTGCTGCCCCACCCCTCACTGCAAAAGGCTCTCTTAAGTAGCAACCTCAGG  
ACTTGGGGCTCAGTCTGCCGCTCTCTCAGCTCAAAACCTCAGGCTCGAGGAAAGTGGGATGGCTCTGGGCC  
TGCTTTGTGATGATGGCTTTCTTACAGCCCTGCTCTGTGGCGAGGCTGTGGGCTGTCTAGGTTGGTGGAGC  
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAGTGTGAAACGCTGCCCTTGACCCGAGCTCAGACGCC  
TGCAGACTCTGTGGAATCAGGCGTCTTTTGTGCTGTCTGGAGGCTTGGCCACATCTCTACGGGCCCAT  
TTTATCCCCGAATCTCGGGTGTGTCACCAAGTGAAGGGTGGGGAAGGGGTGCTCACTGAGCTGACTTTTGT  
CTTCTCTCAAAACCTTCTGGAGCTTTCTTGGGATTTGGGAAGGAATCGGCTGGAGAAATGATGACTTCCCC  
CTGCTTCCCCTCGCTGCTTCCCAAGGGTGAAGGCTGGGCTGGAGAAACAGAAATCTCCACCTCGCTCTCTCA  
CAAGTTACGAGGTTGCTCTGTGTTCTCAGTGAGGAGAGCTGATGAGTCTGCGCAAGGCAATGGCCATGTCTGCA  
CTCAGGAGGAGGAGAGCAAGAGAGGCCCATCTCATGTGAGTCTGCGCAAGGCAATGGCCCATGTCTGCATCTCC  
AGGGAGGAGGACAGAGAGGCCCATCTCATGTGAGTCTGCGCAAGGCAATGGCCCATGTCTGCATCTCAGGGA  
GAGAGACAGAGAGCCGAGCTCATGTGAGTCTGCGCAAGGCAATGGCCCATGTCTGCATCTCAGGAGGAGG  
CAGAAAGGCCGAGCTCAGTGGCCCGGCTCCCCCCCCCAGCCGCAACCTGGCCAGAGACGAGCAGCTTCTTC  
GAAGTGTGCTCAAGTCCGCAATGAGCTTTGAGCTTTGTCTGGGGCCAGCCCAACCTGGCTTGGGCTCATGTTCTGA  
GTGTGAGTAAAGCTATAACCTTGAATCAAA

## FIGURE 22

MTTWSLRRRPARTLGLGLLLVVLGFLVLRRLDWSLTVLPLRLHRQLRQGLQAGWNFMLEDSTFWI  
FGGSIHYFRVPREYWRDRLKMKACGLNLTLTYYVWNLHEPERGKFDGNSGLDEAFVLMMAE  
IGLWVLRPPGYICSEMDLGLPSWLLQDPMGRLLTYKGFTEADVLYFDHLSMRVYVQPKYR  
GGPIIAVQVENYESYGNKDPAIMPYMVKKALDEDRGIVELLTSDNKGDLGSKGIVQGVLATINLQ  
STHELQTLTLFLFNQVQTPQKPMVMEYTWGFDWSWGGPHNILDSEVLTKTVSAIVDAGSSINLY  
MFHGNDNPGFMNAGMHFDYKSDVTSYDYDAVLTEAGDYTAQYMKRLDVSAGISGLPLPPPD  
LLPKMYPBPLTPVLYLSLWDALKYLGEPIKSEKPINQENLPVNGNGQSGFYLYTETSITSSG  
ILSGHVHDDRQVFNVTYSIGFALDYKTTKIAVLPIQNTYTVLRLVBNRGVNVYGENIDQRKGL  
IGNLYLNDSPKLNFRISYLDMMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLISSTPCDFTLK  
LEGNEKGVVFINQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG  
RNQYIK

Signal sequence:

amino acids 1-27

## Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

**FIGURE 23**

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAGA  
 AAAAGAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAAATTCATCTAAATCATCT  
 GAAACACAATGCACAGAGAGAGGATGCTTCTCTCCCAAATGTTCTTATGGACTGTTGCTGGG  
 ATCCCCATCCTATTTCTCAGTGCCCTGTTTCATCACAGATGTGTTGTGACATTTTCGCATCTTT  
 CAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAAATTCACAGAGCTCTCCTGCTACAAT  
 TATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCCAGCTGC  
 TACTTCTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGG  
 GCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTCTACAAGAAACCTAAA  
 ATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAATGGGTGGAC  
 GGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAACATAGCTACC  
 CTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATGGAATGATGTAACC  
 TGTTTCTCAATTATTTTCGATTGTGAAATGGTAGGAATAAATCCTTTGAACAAAGGAAAA  
 TCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCAAGAACATGGCCAC  
 ACCCACCGCCCCACAGAGAAATTTGTGCGCTGAACCTCAAAGGACTTCATAAGTATTTGTTA  
 CTCTGATACAAATAAAAAATAAGTAGTTTAAATGTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

10  
 20  
 30  
 40  
 50  
 60  
 70  
 80  
 90  
 100  
 110  
 120  
 130  
 140  
 150  
 160  
 170  
 180  
 190  
 200  
 210  
 220  
 230  
 240  
 250  
 260  
 270  
 280  
 290  
 300  
 310  
 320  
 330  
 340  
 350  
 360  
 370  
 380  
 390  
 400  
 410  
 420  
 430  
 440  
 450  
 460  
 470  
 480  
 490  
 500  
 510  
 520  
 530  
 540  
 550  
 560  
 570  
 580  
 590  
 600  
 610  
 620  
 630  
 640  
 650  
 660  
 670  
 680  
 690  
 700  
 710  
 720  
 730  
 740  
 750  
 760  
 770  
 780  
 790  
 800  
 810  
 820  
 830  
 840  
 850  
 860  
 870  
 880  
 890  
 900  
 910  
 920  
 930  
 940  
 950  
 960  
 970  
 980  
 990  
 1000

**FIGURE 24**

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF  
TELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQEF  
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTP LTKSLSFWDVGEPNNIATLED CATMRDSSNPR  
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

24/615

**FIGURE 25**

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC  
 TGGTGAGGGTTCTTACTTTGGCCTTCGGTGGGGGTCAAGACGCGAGGCACCTACGCCAAAGGGG  
 AGCAAAGCCGGGCTCGGCCGAGGCCCGCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA  
 CACGTGACGGTCTGTCCGCGCTCTCAGACTAGAGGAGCGCTGTAACGCCATGGCTCCCAGA  
 AGCTGTCTGCGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG  
 ACACTCGGTTCGTTTCGTAGTGGATAGGGGTCTGACCGGTTTCTCCTAGACGGGGCCCCGTTCC  
 GCTATGTGTCTGGCAGCCTGCACACTTTTCGGGTACCGCGGGTGCTTTGGGCCGACCGGCTTT  
 TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTACCACGAGC  
 CACAGCCTGGGGTCTATACTTTAATGGCAGCCGGGACCTCATTGCCCTTTCTGAATGAGGCAG  
 CTCTAGCGAACCTGTTGGTCATCTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG  
 GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATTAAGAACCTCAGATCCAGACT  
 TCCTTGCCGCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC  
 ACAATGGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG  
 ACTTCAGCTACATGAGGCACCTTGCTGGGCTCTCCGTGCACCTGCTAGGAGAAAGATCTTGC  
 TCTTCCACACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG  
 TAGATTTTGGCCAGCTGACAACATGACCAAAATCTTTACCTGCTTCGGAAGTATGAACCCC  
 ATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT  
 CCACACGGTCTGTGTGAGCTGTAAACCAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG  
 TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG  
 GACGCTTCCTTCGATTACTACCAAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC  
 CCACACCTAAGCTTTTTGCTCTTCGAGATGTATCAGCAAGTTCAGGAAGTTCCTTTGGGAC  
 CTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTGACTCTGCACTGGTTGGGCATT  
 TACTGGCTTTCTAGACTTGCTTTGCCCGCCGTGGGCCATTCAATCAATCTTGCCAATGACCT  
 TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATACCATTT  
 TTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCCTATGTGATGGTGG  
 ATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAGAGACAACTATTTTGAAGGGGAAAC  
 TGGGTCCAAACCTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA  
 GTGACTTCAAGGGCCTGTTGAAGCCCAATCTGGGGCAACAACTCTTACCCAGTGATGA  
 TGTTCCCTCTGAAAATTTGATAACCTTGTGAAGTGGTGGTTTCCCTCCAGTTGCCAAATGGC  
 CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG  
 TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAAGTCTGGATCAATGGGTTTA  
 TTTGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCTCTACGTGCCAAGATTCTCTGC  
 TGTTTCTTAGGGGAGCCCTCAACAAAATTACATTGCTGGAACTAGAAGATGTACCTCTCCAGC  
 CCCAAGTCCAATTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA  
 TCAATTCCTTTCACTGATACACTGAGTGCTCTGAACCAATGGAGTTAAGTGGGCATCTGA  
 AGGTAGGCGGGCATGGTGCTCATGCCTGTAAATCCAGCACCTTTGGGAGGCTGAGACGGGTG  
 GATTACCTGAGGTGAGGACTTCAAGACAGCTGGCCAACTGGTGAACCCCGTCTCCACTA  
 AAAATACAAAATAGCCGGGCGTGATGGTGGGCACTTAATCCAGCTACTTGGGAGGCTG  
 AGGCGAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTG  
 CACTCCAGCTGGCTGACAGTGAGACACTCCATCTCAAAAAA

**FIGURE 26**

MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVLW  
 ADRLMKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA  
 EWEMGGPLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS  
 YRACDFSVMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIFTLLR  
 KYEPHGPIVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGLASVNMVFMFHGGTNFGYWNG  
 ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKQFQEVPLGPLPPSPKMMGLGPVTLH  
 LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPNNGVHDRA  
 YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSDDFKLLKPPILGQTIL  
 TQWMMFPLKIDNLVKWFFPLQLPKWVPYQAPSGPTFYSKTFPILGSVGDTPFLYLPGWTKGQVW  
 INGPNLGRYWTQGGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL  
 HRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
 603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
 231-237, 274-280, 296-300, 307-313, 447-453, 484-490

**FIGURE 27**

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTGG  
 GGCCCCAGCCTGGCCCGGGTCACCTTGGCATGAGGAGATGGGGCCTGTTGCTCCTGGTCCCAT  
 GCTCCTGTGCGCCGGTCTCTACGGAAGTCCCTTCTACAACGGCTTCTACTACTCCAACAGCGC  
 CAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGGTGGT  
 GGAGACACCCGAGGAGACCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGCGGCTA  
 CCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCTGTGCGGA  
 GAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCAACGCTCCTTTGGGGA  
 CTACCAAGGCCGCGTGACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAGATCCAGGA  
 TCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGAGGATGAAAG  
 CGGTCTGGTGGAGCTGGAGCTGCGGGTGTGGTCTTTCCTTACAGTCCCCCAACGGGCGCTA  
 CCAGTTCAACTTCCACGAGGGCCAGCAGGTCGTGCGAGAGCAGGCTGCGGTGGTGGCCTCCTT  
 TGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGGCTGCGTGCAGGA  
 TGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCCAGGCTGGCACC  
 TGGCGTGCAGAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGATGTATTCTGCTTCGC  
 TACTGCCCTCAAGGGCGGGTGTACTACTTGGAGCACCCCTGAGAAGCTGACGCTGACAGAGGC  
 AAGGGAGCGCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGACAGCTCTTTGCCGCGCTG  
 GAAGTTCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGATGGCAGCGTCCGCTACCC  
 TGTGGTTACCCGCACTCCTAACTGTGGGCCCCAGAGCCTGGGGTCCGAAGCTTTGGCTTCCC  
 CGACCCGAGAGCCGCTTGATCGGTGTTTACTGCTACCGCCAGCACTAGGACCTGGGGCCCTC  
 CCCTGCCGCATTCCCTCACTGGCTGTGTATTATTAGTGGTTTCGTTTTCCCTGTGGGTGG  
 AGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCTTTAAACATTTTTTTACTATT  
 TTTGTAAAGCAAACAGAACCCCAATGCCTCCCTTGTCTCCTGGATGCCCACTCCAGGAATCAT  
 GCTTGTCTCCCTGGGGCATTGTGCGTTTTGTGGGCTTCTGGAGGGTTCCCCGCCATCCAGGCT  
 GGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGCGGTGGCCTGTCTAGAATGCCGCGG  
 GGAGTCCGGGCATGGTGGGCACAGTCTCCCTGCCCTCAGCCTGGGGGAAGAAGAGGGCCCTC  
 GGGGGCCTCCGAGCTGGGCTTTGGGCTCTCCTGCCACCTCTACTTCTCTGTGAAGCCGCT  
 GACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAAGCCAGTTCTAGGCTTCCAGGCGAATC  
 TGAGGGAAGGAAGAACTCCCTCCCCGTTCCCTTCCCTCTCGGTTCCAAGAAATCTGTTT  
 TGTGTCACTTTGTTCTCCTGTTTCCCTGTGTGGGGAGGGGCCCTCAGGTGTGTACTTTGG  
 ACAATAATGGTGCTATGATGCCTTCGCCAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 28**

MGLLLLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHKDLLNGVKLVVETPEETLFTYQG  
ASVILPCRYYEPALVSPRRVRVKWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQDKE  
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESLVELELRGVVFPYQSPNGRYQFNHFGQQVCA  
EQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGFGLAPGVRSYGPRHRL  
HRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW  
LADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303,  
307-313

1052586-01502



**FIGURE 29**

GCAAGCGGCGAAAATGGCGCCCTCCGGGAGTCTTGCAAGTTCCTCTGGCAGTCTCTGGTGCTGTTG  
 CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGAAC  
 TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGGTGGTGCCTGCTTGT  
 CAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTAAATATT  
 GCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT  
 ACTATTTTATCATTTGATAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC  
 TTCATAAACTTTATAAGTGATAAAGAGTGGAAAGATATTGAGCCCGTTTTCATCATGGTTTGGT  
 CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG  
 TGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT  
 TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGCAGATTGCCTT  
 TGTCTTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAATTATTATCAGAA  
 TCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA  
 GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAGACTTTCCACAGAATGCCATAAGACAACGC  
 TCTCTGGGTCCTCATTTGGCCACAGATAAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA  
 TGATTTTGATAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTGAACCTGTGACTTTTT  
 GAATATTGCAGGTTTCAGTCTAGATTGTCATTAAATGAAGAGTCTACATTTCAGAACATAAAA  
 GCCTAGGTATACAAAGTTTGAAAATGATTTTAAGCACAGTATGATGGTTTAAATAGTCTCTTA  
 ATTTTGAAAAATCGTGCCAAAGCAATAAGATTATGTATATTTGTTTAAATAAACCTATTTTC  
 AAGTCTGAGTTTTTGAATAATTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT  
 ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTGTTTCACTGTGTGAAAAAAG  
 AAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGCTCAAGAAATGTGATATTTCAAGTACAA  
 TTTCTGGTCTTTTTAGAGGTATATTTCCAAAATTTCCCTTGATTTTATAGGTTATGCAACTAAT  
 AAAAAGTCACTTACATTAATTAATACAGTTTCTACACATGGTAATACAGGATATGCTACTG  
 ATTTAGGAAGTTTTTAAAGTTCATGGTATTTCTCTGATTCCAACAAAGTTTGATTTTCTCTGTG  
 ATTTTTCTTACTTACTATGGGTTACATTTTTTATTTTCAAATTGGATGATAATTTCTTGGAA  
 ACATTTTTTATGTTTTAGTAAACAGTATTTTTTGTGTTTCAAAGTGAAGTTTACTGAGAGA  
 TCCATCAAATTGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTCAGATTTTACATC  
 ATTCTTGCTGAACCTTCAACTTGAAATGTTTTTTTTTCTTTTTGGATGTGAAGGTGAACATT  
 CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAATAATCAAAGAAGCTT  
 AATATAAAGTTTGCATTTCTACTCAGGAAAAAGCATCTTCTGTATATGTCTTAAATGTATTT  
 TTGTCCTCATATACAGAAAGTTCTTAATTTGATTTTACAGTCTGTAATGCTTGATGTTTTAAAA  
 TAATAACATTTTTTATATTTTAAAAAGCAAACTTCATATTATCGTGTGTTCTTCTCGTACTG  
 GTAATATTGTGTGGGATTTTCACAGGTAAAGTCAGTAGGATGGAACATTTTGTGATTTTAA  
 CTCCTTAAAGAGCTAGAATACATAGTTTTTACCTTAAAGAGGGGAAAAATCATAAATACAA  
 TGAATCAACTGACCAATTACGTAGTAGACAATTTCTGTAATGTCCTCTCTTTCTAGGCTCTGT  
 TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTCTTTAAAGCCCTCTCC  
 TTTAGAATTTAAATATTGTACCATTAAAGGTTTGGATGTGTGAAGTGTGATGCTTACAGAA  
 AATATCCTAAGCACAAAATAAACCTTTCTAACCACTTCATTAAAGCTGAAAAA

30/615

### **FIGURE 30**

MAPSGSLAVPLAVLVLLLVGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLQ  
PEWESFAEWGEDLEVNIQKVDVTEQPGLSGRFIIITALPTIYHCKDGEFRRYQGPRTKKDFINF  
ISDKEWKSIIEPVSSWFGPGSVLSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL  
FSGLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEADDEEDVSEEEAE  
SKEGTNKDFPQNAIRQRSGLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

2025 RELEASE UNDER E.O. 14176

**FIGURE 31**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGGC  
 TCGCCCAACCTTACTACCTTCTGTGGCCCTGCTCTCTGCTGCTTCTACTCGTGAGGAAAC  
 TGCCGCCGCTCTGCCACGGTCTGCCACCCAAACGCGAAGACGGTAACCCGTGTGACTTTGACT  
 GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCCGAGATCCA  
 TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAAACACAATTCCTT  
 TCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCTTGATGA  
 CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATG  
 ATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTA  
 ATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAACGTACAGGGC  
 TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA  
 CATACCCCTCACCAAGCAACTCCCTACCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC  
 GCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA  
 TCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA  
 ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCAAGTGTGAGATGGGGAAAAACAAGA  
 AGGATAAAATAGATCCTCACTTTGGCAGTGCTTCCCTCTCCTGTCAATTCCAGGCTCTTTCCAT  
 AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTCCCTTGGCTGNGACTGGNTGGGG  
 CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATGTGAGGCACCTACAGGAAGGC  
 CTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGAGGGGGGA  
 AATGGTTTCCCTCAAAGCTTGGGTGAGTGTGTTAACTGCTTATCAGCTATTGAGACATCTCCA  
 TGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTT  
 AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAAG  
 GACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAGTATAAGCCTAA  
 CTTTGTGCTAGTCTTAAGGAGAAACCTTTAAACCAAAAGTTTTATCATTGAAGACAATATT  
 GAACAACCCCTATTTTGTGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT  
 GTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCACTAACCTCTGACATACTCCCAACAC  
 CCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATTTCTTTTG

**FIGURE 32**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAFLLVRKLPPLCHGLPTQREDGNPCDFDW  
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT  
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNCTGL  
NFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENVI  
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

**FIGURE 33**

CGGACGCGTGCGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCAGTGTGCGGCG  
GCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCGCGGCA  
CTGATCCCCACAGGTGATGGGCAGAACTGTGTTACGAAAGACGTGACAGTGATCGAGGGAGAG  
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGAGTACTGAATCCC  
AACAGGCAGACCATTATTTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGTTGCTG  
AATTTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGCTCAATTTCTGATGAAGGAAGA  
TACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGTCCTGGTCC  
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA  
GTCAACTGCACGTCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA  
GAGCTAAAAGGCAAATCCGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG  
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCAGTGATCTGCCAGGTGGAGCACCTGCG  
GTCAGTGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT  
CAGATGACTTATCCTCTACAAGGCTTAAACCGGGAAGGGGACGCGCTTGAGTTAACATGTGAA  
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTTGGGTGAGAGTCGATGATGAAATGCCTCAA  
CACGCGCTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGTTACA  
TACCCTGTGAAGCTTCAAACATAGTGGGGAAGCTCACTCGGATTATGCTGTATGTATAC  
GATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACC  
ACCATCCTTACCATCATCAGATTCCCAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT  
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGTCTCATCATT  
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT  
GAGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACCTCCGAAGAA  
AAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAATGAGGTGTCCAACCTGGCCCTATT  
TAGATGATAAAGAGACAGTGATATTGG

1052536.01502

**FIGURE 34**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSSGSQCAAAAAAAPPGLRLLLLLFSAALIPTGDGQNLFTKDVTVIEGEVATISQ
VNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNTELKGKSE
VEEWSDMYTTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTORYLEVQYKQVHIQMTYPLQ
GLTREGDALELTCEAIGKPQPMVMTWVRVDDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAIVGGV
VAVVVFAMLCLLIILGRYFARHKGTFTHEAKGADDAADADTAIINAEQQNNSEEKKEYFI

```

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310, 430-434

**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408, 411-417, 427-433, 428-432

**FIGURE 35**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCCTAGGGGGCCCTTGTCAGGAGGAGACAGCCTCCCGCCCCGGGGAG  
 GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCGGTTTCTGCGGTGACGTGCCGGCCG  
 AGTTGGGTCTCCGGTGGTTTCCAGCCGGCTCCCTCTTCTGGTCTCCCTTCTCCGCTGGGCGGTTTATCGGGAGG  
 AGATTGCTCTCCAGGGCTAGCAATTTGGACTTTTGATGATGTTGACCCAGCCGGCAGGAATAGCAGGCCAACCGTAT  
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCGAATCA  
TGTCTGTGATGGTGGTGAGAAAGAGTGACACGGAAATGGGAGAAATCCCAGGCAGGAACACCTTTTGTCTGTG  
 ATGGCCGCTCATGATGGCCGGCAAAAGGGCATTTTCTACCTGACCTTTTCTCTATCTCTGGGACATGTACAC  
 TCTTCTTCCGCTTTGAGTGCCGCTACCTGGCTGTTGAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT  
 TCCTTTTCTCCATGGCTACACTGTTGAGGACAGCTTCAGTGACCTGGAGTGATTCTCCGGGCGCTACCAGATG  
 AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCGAGGGCCAGCGACCAACCGCTCGTA  
 TCAAGAATTTCCAGATAAAACAACAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCTCCCC  
 GGGCTCCCATTCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTTGGGTGGGAATTGTG  
 TTGGAAGAGGAATACCGCTACTTCTACTCTTCTACTCTTCTCTCTCCCTCTCACAATCTATGCTTCGCT  
 TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGAGACATTTGAAAGAACTCTCTGGAACCTG  
 TTCTAGAAGTCTCATTTGCTCTTTTACACTCTGGTTCGTGGGACTGACTGGATTTTCACTATTTCTCTCGTGG  
 CTCTCAACAGACAACCAATGAAGACATCAAAGGATCATGGACAGGAAGAATCGCTCCAGAACTCCTACAGCC  
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGGCCCTTTGCCCCCACTGTGCTGGATCGAAGGGGTA  
 TTTTGCCTAGGGAAAGTGAAGTGACCTCCAGTACTCAAGAGACAGTAGCAGCCTCTGGCCACAGAGCC  
 CAGCCCCACAGAACACTGAACTCAAATGAGATGCCGAGGACAGCAGCATCCCGAAGAGATGCCACCTCCAG  
 AGCCCCACAGCCACACAGGGGCGAGCTGAAGCTCAGAAGTAGCCCTATCTATGGAAGAGACTTTTGTGTGTT  
 TAATTAGGCTATCAGAGATTTTCAAGTGAGAAGTTAAACCTCAGACAGAGCAAGTAAGCTGTCCCTTTTAAT  
 GTTTTCTTTGGTCTTTAGTCAACAGTTGCACTGGCATTTTCTTCTGCTCAAGCTTTTTTAAATTTCTGAAC  
 CAGGACAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAATAGGGTCTCTTGGGCTCTGGCAGCTGTTCT  
 CAGTGGCTCAGCCACAGGGTCCCTTTGGACCCCTCTCTTCCCTCCAGATCCCAGCCCTCTGCTTGGGGTCA  
 TGGTCTCATCTCGGGCTAAAAGTTTGTGAGACTGGCTCAAATCTTCCCAAGCTGTGCACGTGCTGAGTCCAGA  
 GGCAGTCACAGAGACTCTGGCCAGGGGATCTAACTGGGTCTTGGGGTCTCAGGACTGAAGAGAGGGAGAG  
 TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTTGCCCAAAATCTTTTAGGAATGGGACAGGTACCT  
 TCCACTTTGTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTCCTTTTGACTCCTGCTCCCATTAGGAG  
 CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
 ACTATCCCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
 GCTCTCCTCTCCTCTCTCCCCGATGTACCTCAAAAAAAAAAAAAATGCTAACAGTTCTTCCATTAAAGCT  
 CGGCTGAGTGAGGGAAGGCCAGCACTGTGCCCTCTCGGTAACTCACCTTAAGGCTCGGCCCACTCTCGGCT  
 ATGTTAACCACTGGGGCTTCTCCAAGCCCGCTCTTCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT  
 CACCTCGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTCAGGGAAGAAGATTATGT  
 ATTATATGTGGCTATATTTCTAGCAGCACTGTGTTTCTCTTTCTAAGCCAGGCTCTGCTGTGATGACTTAT  
 GCGGTGGGGGATGAATCCGGAATTTTCATCTATTGAAGGCGATTAACCTGTGCTATATGCA

**FIGURE 36**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFECRYLAVQ  
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI  
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYLFIL  
SLSLLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI CFFTLWSVVGLTG FHTFLVAL  
NQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSRPPSTQ  
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEA AAEAK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245



[illegible]

**FIGURE 38**

><subunit 1 of 1, 737 aa, 1 stop  
 ><MW: 78475, pI: 5.09, NX(S/T): 11  
 MQPRRAQAPGAQLLPALALLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP  
 EPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSDGYLCICNEG  
 YEGPNCEQALPSLPATGWTESMAPRQLQFPVPATQEPDKILPRSQATVTLPTWQPKTGQKVEM  
 KWDQVEVIPDIAACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFGQCSSL  
 IDGRSVTPLQASGGGLVLLLEMLALGNNHFIGFVNDVSTKSIVALRLTLVVKVSTCVPGESHAN  
 DLECSGKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQDGSNFTC  
 VCLPGYTGELCQSKIDYCIIDPCRNGATCISLSGFTCQCPEGYFGSACEEKVDPCASSPCQN  
 NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRVTGTSYKCLCDPGYHGLYCEE  
 EYNELCLAPCLNAATCRDLVNGYECVCLAELYKGTCHCELYKDPCANVSCNLNGATCSDGLNGTC  
 ICAPGFTGEECDIDINECDSNPCHGGSCLDQPNGYNCHCPHWVGANCEIHLQWKSGHMAES  
 LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSRRPAYEEFYNCRSIDSEFSNA  
 IASIRHARFGKKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

**FIGURE 39**

GAGCCGCCGCCGCCGCCGCCGCCGCCGCTGCAGCCCCAGGCCCCGGCCCCCCCCACCCACGTCCTG  
 CGTTGCTGCCCCGCCCTGGGCCAGGCCCCAAAGGCCAAGGACAAAGCAGCTGTCAGGGAACTCC  
 GCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCAACAGGTTTCCAAGATGGTTTGCCGGGGCT  
 TCGCGTGTTCACGAAGCTGCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTGCTGC  
 TAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGTCCGGC  
 TGGTCATTGCAGTGGGCATCTTCTGTTCCCTGATTGCTTTAGTGGGCTGATTGGAGCTGTAA  
 AACATCATTAGGTGTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATTGTTTCA  
 TTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGACACACAGGTCAGCTTCTGGAGGTTG  
 GTTGAACAATACGGCAAGTGTCTGAAATGACATCCAGAGAAATCTAAACTGCTGTGGGTTCC  
 GAAGTGTAAACCAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCACTCGTGTCTCG  
 CATGTGCTCCAATCATAGGAGAAATATGCTGGAGAGGTTTTGAGATTTGTTGGTGGCATTGGCC  
 TGTTCCTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACAGGAACAGAAAG  
 ACCCCCGCGCGAATCCTAGTGCATTCCTTTGATGAGAAAACAAGGAAGATTTCTTTTCGTATT  
 ATGATCTTGTTCACTTTCTGTAATTTCTGTTAAGCTCCATTGGCCAGTTTAAAGGAAGGAAAC  
 ACTATCTGGAAGTACCTTATTGATAGTGGAAATATATATTTTTTACTCTATGTTTCTCTACA  
 TGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTCTGAAGCTCGGTGGC  
 CTGGAATTTACTGTATTCATTGTGCGGGCAGTGTCCACTGTGGCTTTCTTAGCATTTTTACCT  
 GCAGAAAACTTTGTATGTGTAACCACTGTGTTGGTTATATGGTGAATCTGAACGTACATCTCAC  
 TGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCCTACTGAAAAAGAGTGGAAAT  
 TATTAATATCAGAAAGTATGAGATCCGTTATGTTAAGGAAATCCAATTTCCAATTTTTTT  
 TGGTCTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTAGTATAAAAAATGATAATTTACTTGT  
 AGTCTTTTATGATTACCAATGTATTCTAGAAATAGTTATGCTTAGGAAATTGTGGTTAA  
 TTTTGTACTTTTACAGGTAAGTCAAAGGAGAAGTGGTTTCATGAAATGTTCTAATGTATAAT  
 AACATTTTACCTTCAGCCTCCATCAGAAATGGAACGAGTTTTGAGTAATCAGGAAGTATATCTAT  
 ATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAAAGACTGCATTTTAAACAAGTTAG  
 TATTAATGCGTTGGCCCACTAGCAAAAAGATATTGATTATCTTAAAAATTTGTTAAATACCG  
 TTTTCATGAAATTTCTCAGTATTGTAAACAGCAACTTGTCAAACCTAAGCATATTTGAAATGA  
 TCTCCATAATTTGAAATGAAATCGTATTGTGTGGCTCTGTATATTCTGTTAAAAAATTA  
 GGACAGAAACCTTTCTTTGTGTATGCATGTTTGAATTAAGAAAGTAATGGAAG

Figure 1. The structure of the proposed model.

## FIGURE 40

```
>>/usr/seqdb2/sst/DNA/Dnaseqg.min/ss.DNA39979
>>subunit 1 of 1, 204 aa, 1 stop
>>MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACVSKNCLCALNLLYTLVSLLLTIGIAWGGIGFLGLISSLRVGVVIGLFLFLALVGL
LIGAVKHQVLLFFMYMILLVLTVQFVSACALALNQEQQGLLEVGNNTASARNDIQRNL
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTEILGVWLTYR
YRNCKDPRANPFLAFL
```

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

**FIGURE 41**

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCCTGGGCCCTCTACCTTTCCCTTGGTGTGC  
 TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGTCT  
 GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGTGGCTTCC  
 AGGTCAAGGCCCTACACTTTTCAGTGAACCTTCCACCTGATTGTGTCTATGACTGGCTGATCC  
 TCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCCTGGC  
 AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCGGGGC  
 CTAACAGGGAATTTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCATTACCACTGCAGTG  
 GCATCTTCCAGAGCCCTGGTCTCGGGATCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC  
 AAGAAGCTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAGCAGGAAGCC  
 CCAAGACCTGAGTTGTGACACAAAGTGGCCCTGCAGAGGTGAGCTGCCCGCCTCTCTTCT  
 CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCAGATCCCCA  
 CAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT  
 GGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGTCTCCAGCTCTGCTGCACCTCCCCA  
 CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACCTGCTCCTGAGGAGGGCCCTGGGC  
 CTCGCTCCGCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTCTCTCTGCGGATGC  
 CAGATCCTCATCTGTATCACCAGATGGGCCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC  
 TCTCGGTCACTGTCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA  
 AGGCTACTGTGAATAGAAGTAACAGTTTCACTCCATGATCTCACTTAACACCCCAATAAATC  
 TGATTCCTTATTTTCTCTTCTGTCTGTCACATATGCATAAGTACTTTTACAAGTTGTCCAG  
 TGTTTTGTAGATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG  
 TTTAGCTATAATTGTGATTCTCTCTTAACACAACAGAAATTCGTGCTGTAGATCAGGAATTT  
 CTATCTGTTATATCGACCAGAATGTTGTGATTAAAGAGAACTAATGGAAGTGGATTGAATAC  
 AGCAGTCTCAACTGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT  
 TGGTCATTATACTTGGGGGTTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA  
 GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCCAACGAAAAATAA  
 TCTGGCCCCAAATGTGAGTTGTACTGAGTTTGAGAAACCCAGCCCTAATGAACCCTAGGTGT  
 TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTCAGCTAT  
 TCTTACTGACATACCAGTCTTTAGCTGGTGTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC  
 CCTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTT  
 GGGAAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTAAAAA  
 GGCCCCAGAGAGCTAACTCACCTTCCACCATATGAGGACGTGGCAGAAGATGACATGTATG  
 AGAACCAAAAAACAGCTGTGCGCAAAACACCGACTCTGTGCTTGCCTTGATCTTGAACCTCCAG  
 CCTCCAGAACTATGAGAAATAAAATCTGGTTGTTTGTAGCCTAA

42/615

## **FIGURE 42**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAPKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFOIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLLKHMQDVRVLLGHLLMELRELSGHRQKPGTTKATAE
```

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 43**

GCGAGTGTCCAGCTGCGGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTTC  
 TGTGTGCCAGAAACCGCAAGCAGTTGTCTAACCCAGTGGGACAGCGCGGATTGGAAGAGCGGGAA  
 GGTCTTGCCCGAGAGCAGTGTGACACTTCCTCTGTGACC**ATG**AAACTCTGGGTGTCTGCATT  
 GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTTCTACCTCTATTGGGCA  
 CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT  
 GGAGGAAGCCAAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAATGGAAGCCTTGACTAGCAA  
 GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG  
 GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTCTCCTGCAGGACTCAGCTGCAGGTTTTAT  
 CGCCAACTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA  
 AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAAATTTCCAGAGGGGAAC  
 TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC  
 CTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA  
 TGCCGGGGAGGAGGCCACCACAACCAAGTACAGGTGCTGGACTACCTCAGCTATGCTGTCTT  
 CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAAG  
 CCACGAACGAGCTGGAGGGGAATCTGCGGTACTTTGAGCAGTTATTTGGAGGAAGAGAGAGAAAA  
 AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCATCTATGAGAGGCCTGT  
 GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGGAGGGTGTCAAAGTGAC  
 ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACACCATGGCAACAGGGCCCCCAGCTGCT  
 CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT  
 CATGCTGTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCAC  
 CGTTCGTGATCCCAAGACAGGAGTCTCACTGTGCGCAGCTACCGGGTTTCCAAAAGCTCCTG  
 GCTAGAGGAAGATGATGACCTGTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG  
 GTTAACAGTAAAGATGCGAGAATTGTTACAGGTTGCAAAATTATGGAGTGGGAGGACAGTATGA  
 ACCGCACCTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAACAGAGGGGAATAGGTT  
 AGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTGGTGGTCCACCGTCTTCCCTGATCT  
 GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACTCTTTCGGGAGCGG  
 GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGCTGCAAGTGGGTCTC  
 CAATAAGTGGTTCATGAACGAGGACAGGAGTCTTGTAGACCTTGTGGATCAACAGAAGTTGA  
**CTGAC**ATCCTTTCTGTCTTCCCTTCTGGTCTCTCAGCCCATGTCAACGTGACAGACACC  
 TTTGTATGTTCCCTTGTATGTTTCCATACAGGCTGATTTTGGAGAAATGAATGTTTGTCTGGA  
 GCAGAGGAGAGCCATACTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTAGCC  
 TGTGCCATCCCTGGCCCAAAGCTAGGATCAAAGTGGCTGCAGCAGATTAGCTGTCTAGCGC  
 CTAGCAAAGTGCCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTTAGTGAACCAAAGTTC  
 TGATACCTTGTTTACATGTTTGTTTTATGGCATTTCTATCTATTGGGCTTTACCAAAAAAT  
 AAAATGTCCTTACCAGAAAAA

10652586.011507  
 205110.9852501

**FIGURE 44**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN  
 KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDELVLQDSAAAGFIANLSVQRQFFPTD  
 EDEIGAALKALMRLQDTPYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTVLWM  
 EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLRYFEQ  
 LLEEREKTLTNTQTEAELATPEGIYERPVDYLPERDVYESLCRGEQVGLTPRRQKRLFCRYHH  
 GNRAPELLIAPFKEEDEWDSPHIVRYDVMSDEETERIKEIAKPKLARATVRDPKTVLTVAS  
 YRVSKSSWLEEDDDPVVARVNRMMQHITGLTVKTAELLQVANYGVGGQYEPHDFFSRRPFDG  
 LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYRTRHAACP  
 LVGCKWVSNKWPFHERGQEFRLPCGSTVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235



**FIGURE 45**

GGGGCGCTTGCCCTTCGCGACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG  
 CGGCGGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCGTCCCAGCC  
 TGTCTGTGCTGCTTTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTGCAACCCGATCCTGGGC  
 TTCGCTCGATTGCGCCCGAGGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGG  
 TCGTCTGTGTCTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA  
 GGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATTCTCCCTCTCTCCAGGTGTGA  
 GCAGCCTATCAGTCACCATGTCCGCGAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTGTGTCTGC  
 TGCTGCTGCGGGGCGCGCGGCGAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTACCA  
 GAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCCCTCTTGAGG  
 AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC  
 ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA  
 ACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT  
 TCACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC  
 ATCCACCAACAGGTAACCGACTAAAGAAAACACCCGAGAGAAAACCTGGCAATAAAGATTGTA  
 AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCGGATTTAATTAC  
 AGAAGAATTTTGTGTGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCAATGTGG  
 GCCTTGTTCAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAAACTTTACATCAGCCA  
 AAGATGTTTGTGTGCCATAAAGGAAGTAGGTTTCAAGAGGGGTAAATCCAAATACAGGAAAAG  
 TCTTGAAGCATACTGCTCAGAAATTTCTCACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA  
 AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTTGTGG  
 CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCAAGCCATCCCTGAAGAACTGG  
 GGAATGTTTCAGGATGTACATTTTGTGTGCAAGGCTGTCTGTGCGAATAATGGCTTCTTCTCTT  
 ACCACATGCCCCAAGTGGTTTGGCACCACAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA  
 CTCATGAACAAATGATGTGCGAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG  
 ATGGCTCCAGCAGTGTGTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG  
 CCAAGACTTTTGAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC  
 AGGCGACGGAGTTTCAGTTTCACTGACTATAGCACCAAGAGAAATGTCTAGCTGTATCAGAA  
 ACATCCGCTATATAGTGGTGGAAACAGCTACTGTTGATGCCATTTCTCTTCACTGTTAGAAATG  
 TGTTTGGCCCTATAAGGGGAGGCCCCAACAGAATCTCTAGTAATTGTACAGATGGGCGAGT  
 CCTATGATGATGTCCAAGGCCCTGCGAGCTGCTGCACATGATGAGGAATCACTATCTTCTCTGT  
 TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC  
 ACGCTTTCTTCAACAAGAGAGTTTCAAGGATTAGAACCATTGTTTCTGATGTCTATCAGAGGCA  
 TTTGTAGAGATTTCTTAGAATCCAGCAATTAATTGGTAACATTTTGACAACTGAAAGAAAAGT  
 ACAAGGGGATCCAGTGTGTAATTTGTATTCTCATAATCTGAAATGCTTTAGCATACTAGAAT  
 CAGATACAAAATCTAAGTATGTCAACAGCCATTAGGCAAAATAGCACTCCCTTAAAGCCG  
 CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT  
 GGCTCTTAGAAACTCAGGAAGAGGAGATAATGTGGATTAAAACTTAAAGAGTTCTAACCATG  
 CCTACTAAATGTACAGATATGCAAAATTCATAGCTCAATAAAGAAATCTGATACTTAGACCAA  
 AAAAAAAAAA

**FIGURE 46**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVYVG  
 NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTGK  
 KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKNFVG  
 KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFATKEVGFRRGNSNTGKALKHTA  
 QKFFTVDAGVRKGIPKVVVVVIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV  
 TFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCKTCYNSVNI AFLIDGSSSV  
 GDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQTEFSFTDYSTKENVLAVIRNIRYMS  
 GGTATGDAISFTVRNVFGPIRESPNKNFLVITDGGQSYDDVQGPAAAAHADAGITIFSVGVAWA  
 PLDDLKDMASKPKESHAFPTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
 425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
 239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 47**

GCCCGCGCCCGCGCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAG  
 CCTGCTCCCTGCTCAGCTGCGCGTCTCGCTCTGCGGCTCTGCCCTCTGCATCCTGTGACGCT  
 GCTGCCCGCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTACAGTTCTTCCTCTTCTG  
 GGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT  
 GGGTGTGTGAGGAGGGGGCCGGATCCCCACCGTCTGCGAGGGCCACATCGACTGTGGCTCCC  
 TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTTT  
 TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGCTGCCATCCAGAATGGGT  
 TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCTTCTACATCCCTGACG  
 GCTCCTTACCAACATCTGGTTCTACTTCGGCGTCTGTGGGTCTTCTCTTCTATCCTCATCC  
 AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGTGGCTGGGCAAGGCCGAGG  
 AGTGCATTCCCGTGCTGGTACGAGGCTCTTCTTCTTCACTCTCTCTTCTACTTGCTGT  
 CGATCGCGGCGCTGGCGCTGATGTTATGTACTACACTGAGCCAGCGGCTGCCACGAGGGCA  
 AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGCTGCCCA  
 AGGTCCAGGACGCCAGCCCACTCGGGTCTGCTGCAGGCTCGGTTCATACCTCTACACCA  
 TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA  
 CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAGACCAAGTGGTGGGATG  
 CCCCAGCATTGTGGGCTCATCATCTTCTCTCTGTGCACCTCTTTCATCAGTCTGCGCTCCT  
 CAGACCACCGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA  
 CACAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCTTTGACAAACGAGCAGGACG  
 GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCTGGTGTGGCCTCACTGCACGTCATGA  
 TGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCAGTGGACCGCCG  
 TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGCTGCTCCTCTACCTGTGGACCTTGGTAGCCC  
 CACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCAGAGCTGCCATCTGGTGCCTC  
 CTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC  
 AGGTGAGCCCCACCCCTGCCCCAGCTCCAGGACTGCCCCTGAGCCGGGCCTTCTAGTCGT  
 AGTGCTTTCAGGCTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC  
 ACGGTGGAGCTGCCTCTTCTTCCCTCCTCCTGTGGCCATACTCAGCATCTCGGATGAAA  
 GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGCTGCTGGAGAGAGCGGGGAACTCCCCACC  
 ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTCTTCTGTCACGTCCCCCAGGGGACCTGCCC  
 CCCTTCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTTAATAAACAGCCAGTGGC  
 TGTAATAAAAAA

**FIGURE 48**

MGACLGACSLLSASCCLGSA PCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVES  
QLYKLPWVCEEAGAGIPTVLQGHIDCGSLG YRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR  
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQR  
WLGKAEBCDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFI SLNLTFCVCVS  
IAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY  
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAAACEGRA  
FDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLY  
LWTLVAPLLLRNRDFS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

GC CGCGCGCTCTCTCCCGGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGGCCGGGGCG  
GGCTCTCGCGCGCGGAACAGTGCTCGGATGCGAGGAGATCCAGGGCTCCTCTCTCTCTCTCT  
CTTTCTGCTCTGTGCTGTGGGCAAGTAGACCCCTTACAGTGCCCTGGAAACCACCTATGGCC  
TGCATACCGCCTCCTGTCTGCTTGTGCCCAGTCTACCTCAATTTAGCCAAGCCAGACTTTGG  
AGCCGGAAGCCAAATTAGAAGATATCTTCTTCATGTGGACCCAGCTGTCTAAGGAAATCCCACT  
GCCCATCTACGAAGAGCGCAACATATCTGTCTTATGAAACGCTCTATGCCAATGGCAGCGC  
CACAGAGACGCGAGGTGGGCATCTACATCTCTCAGCAGTAGTGGAGATGGGGCCCAACCCGAGA  
CTCAGGGTCTCTCAGGAAGTCTCAAGGAAGCGGCAGATTTATGCGTATGACAGCAGGTTACAG  
CATTTTGGGAAGGACTCTCTGCTCAAGTACCTCTTTCTCAACATCAGTGAAGTATGCTACGGG  
CTGCACCGGCGCAAGGTGTGGCAGAGAAGCATGTCTCAGCTGCGCCACTGCATACGATGG  
AAAAACCTATGTGTAAGGAACCCAGAAGCTTCGATGGGCTCTTAAAGCCCAAGTTTAAAGA  
TGGTGTCTGAGGGGCCAACAGCTCCACTTCAGCATGCGCGAGCAGATGAAATTTCACTGATG  
CCGGGTGAAACGCGACCATATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGCATCGCAT  
GGATTATGATTATGCCCTCTCGGAAGTCAAAAAGCCCCACAGAGAAATTTATGAAGATTGG  
GGTAGCCCTCTGCTAAGCAGCTGCGAGGGGGCAGAATTCATCTCTGTTTATGCAATGA  
CCGACCGAGCAATTTGGTGATCGCTCTCTGTGACGTCAAAGACAGAGACTGATGACTCTCTA  
CCGACATGCGATGCGCAGCGGGGCCAGGGGCCAGGGGTCTGATGAGGATGTGGAAGAG  
ACAGCAGCAGAAGTGGGAGCGAAAAATTTAGCATTTTGTTCAGGCACCAAGTGGGTGGACAT  
GAATGGTTTCCCAAGGATTTCAACGTGTGCTGTGTCAGAACTCTCTCAAAATGCGCCAGAT  
TTGCTATTGGATTAAAGGAAACTACTGGATTGATGGGAGGGGTGAACACAGTGTTCCTCCTG  
GCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCCAAATGTTTTTTGTCAATTGGC  
TTGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTAAGGTCTCTTATATCTTTACCATTTTC  
GTACCACTGTGCAAGATGACTGGCTTTACTATTTGAAAACTGGTTTGTGTATCATATCATATATC  
ATTTAAGCAGTTTGAAGGCATACCTTTGTCATAGAAAATAAAAAAATACTGATTTGGGGCAATG  
AGGAATATTGACAAATTAAGTATATCTTCACGTTTTTGCACAACTTGATTTTATTTATCTCTG  
AAGTTGTTTCAAGAGATTATATTAATATTTGGCATAACAGAGATATGAAAAAATAAAAAA

**FIGURE 50**

MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS  
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSSGKSRR  
KRQIYGYSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAAHCIHDGKTYVKGTK  
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL  
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA  
SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNLY  
DREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

**FIGURE 51**

GGGAGGGGGCTCCGGGCGCGCGCAGACCTGCTCCGGCCGCGCCCTCGCGCTGTCTCTCCGGGAGCGCGCAG  
 CAGTAGCCCGGGCGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCATCGGCGCCACCACCC  
 CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCGAGACCCGCTGCCAAAC**ATGG**ATTTTCTCTCGGCGCTGGT  
 GCTGGTATCTCTCGCTCTACTCTCGAGGCGGCGCGGAGTTCGACGGGAGGTGGCCCGAGGCAAAATAGTGTATCGAT  
 TGGCGCTATGTGCTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTGCGCAGTCTTGGGACAGTGTGACCGC  
 TGTGTGCGCAACACGATGCAAAATGTTGAATGTATCGGGCCAAACAAGTGTCAAGTGTATCTGTTTATGTCTGG  
 AAAAACTGTAATCAAGATCTAAATGAGTGTGGCCTGAAAGCCCGGCTGTAAAGCAGAGGTGCATGAACACTTA  
 CGGCAGCTACAAAGTGTCTGTCTCAACGGATATATGCTCATGCCGATGGTTCCTGCTCAAGTGCCTGACCTG  
 CTCCATGGCAAACTGTCAAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGCCT  
 GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGACCTCCTGGCCCTAGATT  
 TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG  
 CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAA  
 CGTACGTGGGTCTTACAAGTGCAAAATGTAAGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCCAAA  
 AGTTATGATTGAACCTTCAGGTCCAATTATGTATCAAAAGGGAATGGTACCATTTTAAAGGGTGACACAGGAAA  
 TAATAATTGGATTCTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATCTCTCTATCATTACCAA  
 CAGGCTACTTCTAAGCCAAACAAAGACCTACACCAAAGCCAAACCAATTTCTACTCCACCACCACCACCACC  
 CTTGCCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCAGGACTGACAACTATAGC  
 ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACCAACAGGGTACAGACAGACCTCAGAAAAACAGAGG  
 AGATGTGTTTCAAGTCTTCTGTTACAGTGTGTAATTTTGACCATGGACTTGTGGATGGATCAGGAGAAAGACAA  
 TGACTTGCACTGGGAACCAATCAGGAGCCAGCAGGTGGACAAATATCTGACAGTGTGCGGAGCCAAAGCCCCAGG  
 GGGAAAAGCTGACGCTGTTGCTACTCTCGGCGCCTCATGCATTACGGGACCTGTGCGCTGTCACTCAGGCA  
 CAAAGTGCAGGGGCTGCACTCTGGACACATCCAGGTGTTTGTGAGAAAAACGGTGCACCGAGCAGCCTGTG  
 GGGAAAGAAATGGTGGCATGGCTGGAGCAAAACAGATCACCTTCGAGGGGCTGACATCAAGAGCAATCAACA  
 AAGAT**GTG**TTAAAGGGTTGGAAAAAAGATCTATAGTGGAATAATAAAGAACTGGGATTATTAGAGCTGGAGAA  
 AGAAGCTGAGGGGCAACCACTTATGAGGTTTCAAGTATATGAAGGTTGGCACAAGAGGGTGGCAGCAGCTG  
 TTCCTCATATGCATTAAGATAGAACAAGAGGAACTGGCTTAGACTAGAGATAAAGGAGCATTCTTGGCAGG  
 GGCCATTGTAGAATACTCTTATAAAAAAAGAACTGTGAATACTCAGTATCTCTCTCTTCTAAAAAATTAGA  
 TAAAAATTGTCTATTAAAGTGTAAAGATGTTCTTACCAAGGAAAAGTAACAAATATAGAATTTCCCAAA  
 AGATGTTTTGATCTACTAGTAGTATGCAGTGAAAACTTTAGAACTAAATAATTTGGACAAAGCTTAATTTAGG  
 CATTTCCTCTTGACCTCTAATGGAGAGGGATTGAAAGGGGAAAGAGCCCAAAATGCTGAGCTCACTGAAATA  
 TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC  
 AGATATTTTAGTATCTCAGTATAGTTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAGAGAG  
 ATTTTCATCGGGTGCACTTCTCTGCTCGTGTGTGACAAAGTTATCTTGGCTGCTGAGAAAGAGTGGCCCTGCC  
 ACACCGGCAGAGCTTCTCTTCACTCTCAGTATGATTTCAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
 AGAACAGTAATATTTTTTGAACAATAGGTACAAATAGAAGTCTTCTGTCAITTAACCTGGTAAAGGACAGGCTGG  
 AGGGGGAAAAATAAATCATTAAAGCTTTAGTAAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCATT  
 TCTTTTATGTTTAACTGCACAGCTGAAGATGAAGGGGAAAAATAAATGAATAATTTTACCTTTTGATGCCAA  
 TGATACATTGCATTAACATGATGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTTAATGTTTT  
 CTAATAAATAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTTTGTATAAATAAACACTGTATGTAAT

1052536.01502

**FIGURE 52**

MDFLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPCQPR  
 CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS  
 CSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQCVNT  
 FGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRSYKCKCKEGYQGDGLT  
 CVYIPKVMIEPSGPIHVPKNGTILKGDITGNNNWIPIVGVSTWWPPKTPYIPIIITNRPTSKPT  
 TRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDNRVQTD  
 QKPRGDVFSVLVHSCNFDHGLCGWIREDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL  
 PLGRMLHSGDLCLSFRRKVTGLHSGTLQVFRVKHGAHGAALWGRNGGHGWRQTQITLRGADIK  
 SESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87



GGGGCCGCCCCCGGC GCCCATTCGGGCCGGGCCCTCGCTCGCGCGGCGACTGAGCCAGGCTGGG  
CCCGCTCCCTGAGTCCCAAGATCGCGCGCGGGCGAGGGGCGACCTTCCACACACGGGGAGCC  
CAGCTGTGACGGCCCTCAGAGAAATGCTGCTGCTGCGCGGGCAGCCCTTGGCATGGGTGTGCA  
TGTGGGTGACAGCCCTGGGAGACATGTGTGTTCTGCCTCAGAGGACCCCTGGAGTTCACAGTCCC  
TGAAGACCCAGCTGTGGACATGGTGGGACCCGATGCCACCTGTGCTCTCTCTCCCTGAT  
GCCTGGCTTACAGCTTGSCACAGCTCAACCTATCTGGCAGCTGACAGATACCAAACACAGCTGG  
GCACAGCTTTGCTGAGGGGCAAGCCAGGGCAGCGCCTATCTGCACCAACCGACGCCCTCTTCCC  
GGACCTGTGGTGACAGGGCAGACCATCTCTAGGCTGCAGCGCTGCTGTGTGGCGACAGGG  
CAGCTTCACTGCTTCTGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGCAGCTGCAGGTGGC  
CGCTCCCTATCGAAGCCCGAGCATGACCTTGGAGGCCCAACAGGAGCATCTGCGGCCAGGGGACG  
GTGATCACTACGTGCTCTCCAGCTACAGGGCTACCTTGAGGCTGAGGTGTTCTTGGCAGGATGG  
TGAGGGTGTGCCCTGACTGSCAACGTCAGCAGCTCGCAGATGGCCAAACAGCAGGCGCTGTT  
TGATGTGACACGCGTCTGTGGGTGGTGTCTGGTGTGCAATGGCACCTACAGCTGCTGGTGGC  
CAACCCCGTGTGTCGACAGGATGGCGARGCTCTGTACCATCAGCAGGGCAGCCTATGACATT  
CCCCCGCAGAGGGCGCTGGGGTGCAGCTGGGGCTGTCTGTCTTCAATTGCATCTGCTGGTGCG  
CTGGCTTTCTGTGTGCTGTGGAGAAAGTCAACACAGCTGTGTGAGGAGGAATGCAGAGCTGCA  
GGACACAGGATGGGGAGGGAGAAGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG  
CAAGAGAAGATGATGGACAGAAATAGCTGAACATGAGGACACAGGGAGCTGTAACCCCTCCCT  
ACAGCTCTACCTCTGCTGTGCAATGGGGCTGCATCTGTAGCCCTGCCCCACAGATGCATC  
CTGCTCTGACAGAGTGGGCTCCTTCTCAAAGATGCGATACACAGACCACTGTGACAGCTTAT  
TTCTCCAATTGGACATGATCCCAAGTCACTCTGCTGCCTTTTTTCTATAGACACAACTGAACA  
GACACCCACAACCTTAGTTCTTAAGTCATCTGCTGCTGCTGCTTATTTCACAGTACATACA  
TTTTCTAGGAGACAGATACATCAGCACATCACCAACCTCTTCTTCCAGTGTGCTGTGGTGA  
TCTGGCTGCGCTTTTCTTCCAAAAGATGCAATATTACAGTACTGACACCCCTGCTGCTTATTTC  
ACCAAAGACACCGATGCATAGTACCCCGGCCCTGTGTTCTCCAATGGCCGTGATACACTAGTGA  
TCATGTTCCAGCCGTCTTCCACTGCATAGAATCTTTTCTTCTCAGACAGGAGCATGTGCGGCC  
TCAACATCTCTTGGAGTCTAGAAGCTGTTTCTTCTCCCTCCTTCTCCCTGCCCAAGTGAA  
GACAGGGCAGGGCCAGGAATGCTTTGGGACAGCGGGGAATGCCCCACACCCCACTATGT  
TGCTATTTCTGGGCTGGGCGAGTCTTTTCTGACCTTGCCTCTGCCCAGCTCTGTGGCTCTG  
AGAGTGAGACTTCAGACGTTCTGATGCTTCCGATGTGATCTCTCCCTGCCCAGGAATGGA  
AGATGTGAGGACTCTTAATTAAATGTGGGACCTCGAGGGATTTTGTAACCTGGGGGTATATT  
TTGGGAAAAATAAATGCTTTTGTAAAAAAAAAAAAAAAAAAAAAAAAA

54/615

## **FIGURE 54**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALVQVPEDPVVALVGTDLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHVSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVVRVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGGGVPLTGN
VTTSCMANEQGLFDVHSLRVVLGANGTYSCLVNPNVLPVQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVWCWRKIKQSCEENAGAEDQDGEGEKSKTALQPLKHSKEDDGGQEIA
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

2025.03.25.07.00.00

AGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGTG  
GCTATATGTCCTCGTGCCGATTTCCGCAAGAGATTCTACGAGGTGGTCCAGAGCCAGAGGGCTCCT  
CTCTCGTGCGCTCGGACGTGGATCTCTGTGGTGGTCGAAGATCTTTAGGCTCTTCAAGCCTTTGTCACG  
TGTGACACAGTGTCCAATATACGCTGTGGTCCAGTTTCTGGGTGCGACGAACCTTGAACATGTGCAITTT  
CTTGAGCATATAAAGACAGTTTCAATTTATTTATTCTCATAAACTGTGGAGTCATATGTAGACCTT  
TTGGATATTTCTTCAACCTGATGAAGACCATATATCTTTGTGTGTGACTCCCATAGGCCAGTCA  
AATGTCGTCAATGTATACAACGATACCGAATCAAAATTAATCTATTAACCAAGATGATGACCTT  
GAAGTTCGCCGCTATGAAGACATCTTCAGGAGTGAAGAGGAGGATGAAGAGCATTGAGAAAT  
GACAGTGTATGGGTGACAGCCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA  
ACCATTCGGAGAGGAGGACGCGCGAGAGTGGGAGGCGCGGAGAAGAGACATCTCTTTTGATCTAC  
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGTGGATGTTTGTAGCTGGCTTGATGTGTG  
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTTGGACTAACAGACCAGTGGGTGCAA  
CACAAAGATCACTCAAATGAATAACGTGACTGATGTGGTGTCTCTGACGCGCCACGTTTCCCGC  
GACACCAACCGGAAGCAGGATGAGGAGACACACTCTCCGTGGACTGCAACCGGATCTCTTTT  
GAGTATGACCTCCGCTGTGGTCTCTACCAAGCATGGTCCCTCCATGACAGCTTGTGCAACACC  
AGCTATACCCGACCGAGTTCAAGTCTGGTCTGTGTCATGGACAGAAGCGGCTCCGAGGATTC  
CTTGACAGATGGGTCTCTCCCTGAAGCAGGTTGAAGCAGAAGTTCCAGGCATGTGACATCTCT  
TTGAAGGAGAATTTGCGGGAAATGATTGAAGATGTGCAAAATAAATTTGGGATGAAGGACATG  
CGGTGTGCAGACTTTTCAGCATTTCAITTTGGGTTCAAGACAAGTTTCTGCGACGACCTGGTCT  
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC  
CAGGCTCTGGAACGCTCTCCAGGAGTAACCTGGAACAAGTGTACCATGGCTTGGAACTGCCC  
AAGAAGCAGCTGCGAGCCAGCCAGCAGACCATTTGCAGACTGCCTTTGCACCAACTCTGTCATC  
TCCCAGGGGGCTCTTCTGTACTGCTCTCTCATGTAGGAGGACCTCAGATGTGATGCTGTTCTCT  
AGGCCGGCATCTTCAAGCTGTCTGACCAAAACCTGCTCAAGTCTTTGTGTGTTTCGACAAAG  
AACCGGCGCTGCAAACTGCTGCCCTGTGTGATGGTGTGCCCCCTGAGCATGGAGCATGGCACA  
GTGACCGTGTGGGGCATCCCCAGAGACCAGCATCGTCCGACAGGAAGAACTTTTGGGAGG  
CGGTTTGAAGAAGCAGCGGAAGACCAAGCTCCCGATGTGTCACAACCAATTTTGACCTTCA  
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCATTTATTTCCCTCTGTCC  
TTGAAATTTGATTTCTTCCGAATGACCTTTATTTATTGTAAGTGGCTTCATTTAGATGTGA  
AGTTATGGACATGATTTAGATGTAGAAGCAATTTTATTATTAATAAATGCTTTATTTAGGAA

**FIGURE 56**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAFLEHKEQFHYFILINCGANVDLLDILQPDIEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDDDLEVPAYEDI FRDEEEDEEHSGNDSGSEPSSEKRTLRLEEIVEQTMRRRRORREWEARRRDILFDYEQYEHGTSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRHVSRRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKRLQEFLEADMGLPLKQVKQKFQAMDISLKENLREMI EESANKFPGMKDMRVQTFSIHFGFKHKFLASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCLCTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLPLVMAAPLSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAEESTSSRMLHNFDLSVIELKAEDRSKFLDALISLLS

**FIGURE 57**

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC  
 CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCCGCTTGCTGACGGCGTCGAG  
 CCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG  
 GCCGCCGGCGGGGACCAGCACAGGCGGCGTTTCTCCTTCGGAACGGGGAACGTCTAGCAACCCCT  
 TCTGTGGGGCTCAATTTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTGCTCCCT  
 TCAAGTGGTTTTGGAACCGGGCTCTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA  
 ACAAATACAGGTGCCTTGACACCAAGAGGCCCTCAAGTGGTCAACAAATATGGAACCCCTGCAA  
 GGAAACACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCTTCTCCAGA  
 CCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA  
 GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAGTGCAGTGGCA  
 CGATCTCGGCTCACTGCAACCTCCGCCCTCCCGGTTCAAGCGAGTCTCCTGCCTCAGCCCTCTG  
 AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGGCTCGATGTACGTCAGC  
 ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACTGAACGTGTACGCG  
 CCGGCGCGCGCCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCGCGGAGGCGCCCTTC  
 ATCTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCGCCCGGAGGAAGTGGTGCTG  
 GTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGCACGGACGACGCCACGCGCGC  
 GGGAACTGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC  
 TTCGGGGGAGACCAGGAAATGTGACCCCTGTTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA  
 GGACTGATGATGTACCCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCAGAGTGGCACC  
 GCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGTTGCCACCTG  
 CTGGATGCAACCAACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC  
 AAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAACCTGAACTTCCAGAGAGACCCGGAA  
 GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTTGGTG  
 CTCCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC  
 AATTGGCTCTTGCCCTATAATATCACCAAGGAGCAGGTACCCTTGTGGTGGAGGAGTACCTG  
 GACAAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT  
 GCCACTTTCGTGTATGCCCACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA  
 ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAGTACCTGCAGCTGGATTTCACCAA  
 GAGTGGGCTGTAGACTCAAGGACAAGAAGATGGCTTTTGGATGAGTCTGTACCACTCTCAAGA  
 GACCTGAGAAGCAGAGGCAATTTCAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC  
 CCCCACTCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGAACAAGAGTCTACCCA  
 CCCAGTTTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTG  
 TGTGTGGGACCTGCAGCTGCCCTTCCAGCCCTGACATCCCATGATGCCCTCTACTTCACTGTT  
 GACATCAGTTAGGCCAGGCCCTGTCAACACCACTGTGCTCAGCTCTCCAGCCTCAGGACA  
 ACCTCTTTTTCCTTCTTCAAATCCTCCACCCCTCAATGTCTCCTTGTGACTCCTCTTTA  
 TGGGAGGTCGACCCAGACTGCCACTGCCCTGTCTACTGCACCCAGCTTGGCATTTACCATCCA  
 TCTCTCAACCTGTCTGTGTTTCACTATGGCCTGGAGGCCCTAGGGCAGGTTGTGACAT  
 GGAGCAAACTTTTGGTAGTTTGGGATCTTCTCTCCACCCACACTTATCTCCCCAGGGCCAC  
 TCCAAAGTCTATACACAGGGTGGTCTCTTCAATAAAGAAGTGTGTATTAGAAAAA

## FIGURE 58

```
</usr/seqdb2/ss/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPVGLNFGNLGSTSTPATTSA PSSGF
GTGLFGSPKATPGTFLTGSTTALHTKRPQVVTKYTGTLQGKMHVGTAKPIQVFLGVPPSRPLLG
ILRFAPPEBPWPWKGRDATTYPGWSLALSPGWSAVERSLRTASAKRVQASLLPQLPSLVWG
YRCLQESWGLQASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVVLFLQRLGLFGFLSTDDSHARGNWGLLDQMAALRWQVENATAAFGCD
PGNVTLFGQAGAMSIIGLMSPLASGLFPHRAISQSGTALFLRLFTLSNPLKVAKKVAHLGAGN
HNSTQILVNLRLALSGTKVMRVSNKMRFLQLNFQRPDEEI IWSMSPVVDGVVIPPDDLVLTLQ
GKVSVPVYLGVNNLELWLLPYNIITKQVPLVVEEYLDNVNEHDWKMLNRNRMMDIYQDATFV
YATLOTATHYHRETFPMFGICPAGHATTRMKCSWILPOENA
```

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

**FIGURE 59**

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCGCCGCGGGTCCCCGAGCGTCCCGCGCCCTC  
 GCCCCGCC**ATG**CTCCTGCTGTGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTTCGAGG  
 AAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAGTCA  
 GACTGTTTCAGAGGGCTGAAAACCAAACTTTGATGACAGAATTCTCAGTGAAGTCTACCATCA  
 TTTCCCGTTATGCCTTCACTACGGTTTTCTGCAGAAATGCTGAACAGAGCTTCTGAAGACCAGG  
 ACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCACCTTCACTATGCTTATTG  
 GAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAAG  
 AGAAAAGGAATAAAACCAAGAAAATGGAGAGAAGGGGACTGAAATATTACAGAGCTTCTG  
 CAGTGATTCCCAGCAAGGACAAAGCCGCTTTTTCTGAGTTATGAGGAGCTTCTGCAGAGGC  
 GCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGGAGGCTGAGCG  
 TGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCCGCTTCAACA  
 GCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCCTCCCCATCTACTGTATT  
 ACCAAAAAGAACATTTGCCACATAATTTTTAAACCTACTGTAGTACAAAGCCAGGATTG  
 CCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAAATAGAGAACAGAGCATTG  
 GGGACATCCAGGTTCTAAATGGCTATTTGTGCACTACTTTGCTCCTAAAGACCTTCTCCTT  
 TACCCAAGAATGTGGTATTCTGTCTTGACAGCAGTGCTTCTATGGTGGGAACCAAACTCCGGC  
 AGACCAAGGATGCCCTTTCACAATTCTCCATGACCTCCGACCCAGGACCGTTTCAGTATCA  
 TTGGATTTTCAACCGGATCAAAGTATGGAAGGACCACTTGATATCAGTCACTCCAGACAGCA  
 TCAGGGATGGGAAAGTGATACATTACCATATGTACCCACTGGAGGACAGACATCAACGGGG  
 CCGTGACAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCAAGTGGCATGGAGACCGGA  
 CGGTGTCCTCTCATCTGTTCTCTGACGATGGGAAGCCACGCTCGGGGAGCGCACCTCTCA  
 AGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTCTGCATCTTACCATTGGGCATCG  
 GCAACGAGCTGGACTTCAGGCTGCTGGAGAACTGTGCTGGAGAACTGTGGCCTCACACGGC  
 GCGTGACAGAGGAGGAGGACGCGAGGCTCGCAGCTCATCGGTTCTACGATGAAATCAGGACCC  
 CGTCTCTCTGACATCCGATCGATTATCCCCAGCTCAGTGGTGAGGCCACCAAGACCC  
 TGTTCCCCACTACTTCAACGGCTCGGAGATCATATTGCGGGGAAGCTGGTGGACGGAAGC  
 TGGATCACCTGCACGTGGAGGTCAACCGCAGCAACAGTAAGAAATTCATCATCTTGAAGACAG  
 ATGTGCCGTGTGCGGCTCAGAAGGCAGGGAAGATGTCAAGGAAGCCACAGGCTGGAGGGC  
 ATGGAGAGGGGACCAACCACTCGAGCGTCTCTGGAGCTACTCACCAAAAGGAGCTGC  
 TGAGCTCCTGGCTGCAAAGTGACGATGAACCGGAGAAGGAGCGGCTGCGGCAGCGGGCCAGG  
 CCCTGGCTGTGAGCTACCGCTTCTCACTCCCTTCACTCCATGCAAGCTGAGGGGGCGGGTCC  
 CAGCATGGATGGCTTGGAGGAGGCCACGCGCATGTGCGCTGCAATGGGACCCGAAACCGGTG  
 TGAGAGCGGTGCGAGGAGCTGGCAGCGAGCCAGGACCTTTGCTCAAGAAGCCAACTCCGTCA  
 AAAAAAACAAACAAAAAAGACATGGGAGAGATGGTGTTTTTCTCTCCACCACC  
 TGGGGATACGAT**G**GAAGATGGCCACCTGCAAGCCAGGAAGACGGCCCTCACCAGACCCATG  
 TCTGCTGGCACCTGATCTTGGACCTCCAGCCTCCAGAACTGTGAGAAATAATGTGTTTTG  
 TTTAAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

60/615

## FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192  
<subunit 1 of 1, 694 aa, 1 stop  
<MW: 77400, pI: 9.54, NX(S/T): 6  
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIISR  
YAFTTVSCRMNLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKS GDRVKEKR  
NKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV  
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINONETFANIIFKPTVVQQAARIAQN  
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTKLRQTK  
DALFTILHDLRPQDRFSIIGFSNRIKVVKDHLSVTPDSIRDGKVYIHHMSPTGGTDINGALQ  
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAAARGQVCIFTIGIGND  
VDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP  
NYFNGSEII IAGKLVDRLDHLHVEVTASNSKKFII LKTDVVPVPQKAGKDVTSRPRGGDGE  
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM  
DGLLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHRGRDGVFPLHHLGIR

### Signal sequence.

amino acids 1-14

### N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

### Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

### N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

105536.01502



**FIGURE 61**

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC  
 ACGAAGGGACGATACAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC  
 TGACTTTTGGCTATAGAAAAAGAAAGGAAACGAAAGAGACAGTTTTTTTGGGAAAGCTAAGTC  
 TTCCCTTTATCGAGTCAAGAAACCCCCCTTCTCTGAGCTATTTACAGCTTTTAAACAAATTGAGT  
 AAAATACGCTCCGGTCACTGTGACTCTGAGGAGCCCTGGGTCCCGTCTGGGACGCGCTCTGTCT  
 CTTTCTCTGTATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG  
 CTGCCAACGGTGTGTGACTCTGAGGAGCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC  
 CTCGGCCGCGCCCCCAGCCCTGCTGTAGATCAGACCCTACATTAATATCACCATCCTGAAGGG  
 TGACAAAGGGGACCCAGGCCAATGGGCCCTGCCAGGCTACATGGGCAGGGAGGGTCCCCAAGG  
 GGAGCCTGGCCCTCAGGGCGAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG  
 CCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCGCAAGACGGCCCTGCACAGCGCGAGGACTT  
 CCAGACGCTGTCTTCTGAAAGGGTCTTGTGAACCTTGTATGGGTGTCTTGACATGGCGAGCCG  
 CCAAGTTTGTGTCTCCCTGCGTGGCATCTACTTCTCAGCCTCAATGTGCACAGCTGGAATTA  
 CAAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGGTGTCTATCTGTACGCGCAGCC  
 CAGCGAGCGCAGCATATGCAGAGCCAGAGTGTGATGTCTGGACCTGGCCCTACGGGGACCGGT  
 CTGGTGTGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTCTGCACACCTTA  
 TGTCACTTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCCTCGGGCCACCTCC  
 CGGCTGGAGAGCTCAGGTGTCTGGTCCCGTCCCTGCAGGGCTCAGTTTGCACCTGTGTGAAGC  
 AGGAAGGCGAGGGAGTCCCCGGGGACCTGGCATTCTGGGGAGACCTGCTTCTATCTTGGCT  
 GCCATCATCCCTCCAGCCTATTCTGTCTCTCTCTCTCTCTGTGACCTATTTTAAAGAGCT  
 TGCTAAACCTAAATATTCTAGAACTTCCAGCCTCGTAGCCAGCACTTCTCAAACTTGGAAA  
 TGCTATGCGAATCACC CGGGGTTCGTGTTAAATGTCAGATTCTGACTCAGCAGGTCTGAGTGGGT  
 CCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGTGATGGGGTCTAGCTATGAACCA  
 CTGGAGCAACAGGTTCTAGGACTTCTCAATATTCTAGTACTTCTGAACTATTCTGGAATCC  
 TCCCACATTCTAGAAATCTCCCAACATTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTTGGC  
 CAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTCAACCTCTGCCCTCCCGGGTTCAAGCGA  
 TTTCTCTGCCCTCAGCCTCCTAGTGGCTGGGATTACAGGCGCGTGTACCATGGCTGGCTAAT  
 TTTGTATTTTAGTAGAGATGGGGTTTACCATATTGGCCAGGCTGGTCTTGAACCTCCTGAC  
 TTTCAAGTGAACCCCGCTTCGGCTCTCAAAATCTGGGATTACAGGTGTGAGCCACCGTGC  
 CTGGCAATTTCAACATTTCTAAATTTCTCATCTCTCAGGCTCTCCGCTGTCTATTTCTCT  
 TTACCCCTTCCCGCTCTTCTCTCTCTCAGGCTCTGCACACTGAGCCACGTTCTATTATTCA  
 TTTATTAAACACTGAGCACTCACTCTGTGTGGTTCGGGGAAGGGGTGAGGGGTGAGACACA  
 GGGCTTGCCCTGCCCTCAGTACTTGCACCTCCAGCCAGCGGGGAGAGATGTGTACATAG  
 GTTTTAAAGCAGAACAGAGCTCATGGGGGCTGTGTTCTGGGTGTTTCAAGTGTCTGTGTCTC  
 TCCATTACCCACTGTCTCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCTAGTATCTC  
 TCTCCGTTTCTCATCCACTGCCAGTGTCTATCGTTACAGCAAAACCCAGGGGCTTTGGC  
 CAGGTCAAGGGTTCTGTAGGAGAGGACCCAGGAGTGTGGGGGCTTTTGGGGGGTGAAGTGGC  
 CCCCAGAAATGGAACCAACCATAGCTCTCCCAAGCTGATACGGCTCTCAGGCTCTGAGAGA  
 ACCTGGCCCTCCCTCAGTGGGATCCCTTCTGTCTCTCCAGGGCTCTGCGAGGGCTTGTCTC  
 AGTCCCTTCCACCAAGTCACTGAACTTCCGTTTCCCAAGGCTCAGGCTCTGAGCTCAGACA  
 CTGATGTCTGTCCCCAGGTGTCTCTGTCCCTCATGCCCCCTCACCAGCGCCACGTCGCCCCG  
 TCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGAGCTCTCTGTCTCAGAGCCCTCTC  
 CGGCTGTGTGTCTCTTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTTGA  
 GCGCTCAGAGCTCTGGGAGCTAGAGCAAAAGGAGGACCTCAGGCTTCCGTTTCTCTTCC  
 AGGTGGGGGTGGCCCTGGCTTCCCTTAGCCCTTCCAAACCCAGGTGGGCTGCCCTTCTCCCC  
 AGGAGGGCGGCTCTGCCTATGGTGTCTATGCAGACTCTGGGCTGAGGTGCCCGGGGGGT  
 GATCTCTGTGTCTCAGAGCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCT  
 GACCAAGTGCAGGAAGCTGTGCTATAAACACCCCTGCCTATCTGCCCTGCCCTGCCACCC  
 CGCCACGCCCTGCGCTCAGCATGATTAAAGATGTGTCTCTCTTGGAAAAA

62/615

## **FIGURE 62**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA  
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPGQGSKGDKGEMGSPGAPCQKRFFA  
FSVGRKTALHSGEDFQTLLEFVRFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH  
IMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH  
LIKAEDD

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-75

**Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

62/615

**FIGURE 63**

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTGGGAC  
 TCGGGAAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTGAGAGGTCCTGAAATAGTACCA  
TGGGGGAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTGGCCTTG  
 ATGATTTGAAAAATAAGTCCTGTTGCACCCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC  
 TGTCTGCCATTGAAGTTTTCCTCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG  
 CCATTGGTCTGGGCATCCACTTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCTTTAAGT  
 GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAGACGCGGGAGGACGAGTACC  
 GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTCGTGGAAGA  
 CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCTGTGCCCAACTGGGTTTCC  
 CAAGCTATGTGAGTTAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTCGGGGAGGAGT  
 TTGTGTCCATCGATCACCTCTTGGCCAGATGACAAGGTGACTGCATTACACCCTCAGTATATG  
 TGAGGGAGGGATGTGCTCTGGCCACGTTGCTTACCTTGCAGTGACACGCCTGTGGTCATAGAA  
 GGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG  
 CCAGCCTTCAGTTCAGGGCTACCACTGTGCGGGGCTCTGTGCATCAGCCCCCTGTGGATCA  
 TCACTGCTGCACACTGTGTTATGACTTGTACTCCCCAAGTCATGGACCATCCAGGTGGGTC  
 TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAAGAGATTGTTCTACCCACAGCA  
 AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGCCACTCAGCT  
 TCAATGAAATGATCCAGCCTGTGTGCTGCCCCAACTCTGAAGAGAACTTCCCCGATGGAAG  
 TGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCTGTCTGTAACC  
 ACGGGCCGTCCTTTGATTTCACCAAGATCTGCAACCCACAGGGACGTGTACGGTGGCATCA  
 TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGACAGCTGCCAGGGGGACA  
 CGCGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACACGCTTTG  
 GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTACCTCTTCTGGACT  
 GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAAGAGGAGGGGACAGGTAGCCACCT  
 GAGTTCTTGAGGTGATGAAGACAGCCCCGATCCTCCCTGGACTCCCGTGTAGGAACCTGCACA  
 CGAGCAGACACCTTGGAGCTCTGAGTTCCGGCACCAGTAGCAGGCCCGAAAGAGGCACCTT  
 CCATCTGATTCCAGCAACCTTCAAGCTGCTTTTGTGTTTTTGTGTTTTTGTGAGGTGGAGTCT  
 CGCTCTGTTGCCCGAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGTTCCC  
 TGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA  
 CACCCAACCTAAATTTTGTATTTTGTAGTAGACAGGGTTTACCATTGTGGCCAGGCTGCTCT  
 CAAACCCCTGACCTCAAATGATGTGCCCTGCTTACGCTCCCAAGTGCAGGATTACAGGCAT  
 GGGCCACCACGCCTAGCCTCAGCTCCTTTCTGATCTTCACTAAGAACAAGAGCAGCAAC  
 TTGCAAGGGCGGCCCTTCCCACTGGTCCATCTGGTTCCTCTCCAGGGTCTTGCAAAATTCCT  
 GACGAGATAAGCAGTTATGTGACCTCAGCTGCAGGTCACCAACCAAGCACTCAGAAAGACGC  
 ACCAGCCAGAGTGCAGAACTGCAGTCACTGCAGCTTTTCATCTCTAGGGACCAGAACCAAA  
 CCCACCTTTCTACTTCCAAGACTTATTTTACATGTGGGGAGGTAAATCTAGGAATGACTCG  
 TTTAAGGCCATTTTCTGATTTTCTTTGTAGCATTGGTGCTGTGACGTATTATTGTCCTTTGA  
 TTCCAAATAATATGTTTCTTCCCTCATGTCTGGCGTGTCTGCGTGGAGTGGTGACGTGAAT  
 CAAATCATCCACTGAAA

64/615

## **FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234  
><subunit 1 of 1, 453 aa, 1 stop  
><MW: 49334, pI: 6.32, NX(S/T): 1  
MGENDPPAVEAPFSFRSLFGLDDLKISFPVADADAVAAQILSLLPLKFFPIIVIGIIALILAL  
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVQLQVFTAASWK  
TMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSI DHLLPDDKV TALHHSVY  
VREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHL CGGSVITPLWI  
ITAAHCVDLYLPKSWTIQVGLVSLLDNPPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT  
FNEMIQPVCLPNSEENFPDGKVCWTS GWGATEDGGDAS PVLNHAAPLISNKICNHRDVYGGI  
ISPSMLCAGYLTGGVDS CQGD SGGPLVCQERRLWKLVGATSF GIGCAEVNKP G VYTRVTSFLD  
WIHEQMERDLKT

**Signal Peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 240-284

20570-9555001

**FIGURE 65**

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGT  
 GAGGTTGGAAAAAGACTCCTGTAACCTCCTCCAGGATGAACCACTGCCAGAAAGACATGGAG  
 AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC  
 ACACAACTCATGGCCAGGATTGAGTCCATGAAGGAAGGGAAAAAGGCATATCTGATGTC  
 AGGAGGACTTTCTGTTTGTGTCACTTTGACCTCTTATTCTGTAACATTACTGTGGATAATA  
 GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC  
 TATTCTTCATATTTTGATATATTTCTCTGGCAGTTTTTCGATTAAAGTGTTAATACTTGCA  
 TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC  
 TTTTACTAGCAAAAGTGATCCTTTGGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG  
 CCCATCATTTTCATTATCCTTGCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT  
 CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTT  
 ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAA  
 GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAAGTACTACTTTTGTTA  
 AATGTGAAAAACCTTCACAGAAAGTCATCGAGGCCAAAAGAGGCAGGCAGTGAGTCTCCCTG  
 TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTATTGAACAGCTAATAAGATTT  
 ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG  
 CTGGTAAGGTAATGTATGATTTCCTCTCTTCAGTGAGACTGAGCCTGATGTGTAAACAAA  
 TAGGTGAAGAAAGTCTGTGCTGTATTCTTAATCAAAGACTTAATATATTGAAGTAACACTT  
 TTTTAGTAAGCAAGATACCTTTTATTCAATTACAGAATGGAATTTTTTGTGTTTCATGCTC  
 CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTGTGTTTTTAACTCATGCACA  
 TGTGCTCTTTGTACAGTTTTAAAAAGTGTAATAAATCTGACATGTCAATGTGGCTAGTTTTA  
 TTTTCTGTGTTTGCATTATGTGTATGGCCTGAAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG  
 AATTGCGAATACATGTAATGTCAACAGACATTTGTATTATTTTATCATGAAATCATGTTT  
 TTCTCTGATTGTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC  
 ATTCATATCATGTTTCTTTGCGTTTCAGCCAATTTCAATTAAATGAACTAAATTAATAA

66/615

## **FIGURE 66**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVVRTFCLFVTFDL  
LFVTLIIWIIELNVNGGIENLEKEVMQYDYYSSYPDI FL LAVFRFKVLILAYAVCRLRHWWAI  
ALT TAVTSAFL LAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL PQEAEEENRLLIV  
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

#### **N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 67**

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC  
 CAACCATTCCTCCCTTGTAAGTTCTCGCCCCCTCAAATCACCCCTCTCCGTAGCCCCACCGACT  
 AACATCTCAGTCTCTGAAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC  
 GGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGTC  
 CACCTCAACGTCTCTCAATGGCTCTGACGCCCCCTGCGCTGCACTTCAACTCCTGCTACAC  
 AGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTCTGAGGA  
 GATGTTCTCCAGTTCGCCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGT  
 GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAAACGTGCAGCCGGA  
 GGATGAGGGGATTTAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA  
 GATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGACTCCACGGTGGCCGTGATTGT  
 GGGTGCCCTCCGTGGGGGCTTCCTGGCTGTGGTCATCTTGGTGCTGATGGTGGTCAAGTGTGT  
 GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC  
 GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGT**AGT**GGGTGGCCGCCCTGCAGCCTCCCG  
 TGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCGCTGCTCGCTCTTGGTGTCCT  
 CCCGTGACCTAGGACCCAGGGCCCACTGGGGCTCCTGAACCCCGCACTTCGTATCTCCCA  
 CCCTGCACCAAGAGTGACCCACTCTCTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG  
 GGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACTGCCAGTCCCTGGGGGAGGCGAGGAGGCAC  
 ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGTGTCACC  
 TGCCCAAGTGTCTGCCTGGCAGTGGCTTCAAGAGGACCTGGTGGGAGGGAGGGCTTCTCTGT  
 GCTGACAGCGCTCCCTCAGGAGGGCCTTGGCTGGCACGGCTGTGCTCCTCCCTGCTCCCAG  
 CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGAAACTTGAGGGGCATGTTAAA  
 GGGATGACTGTGCAATCCAGGGCACTGACGGAAGCCAGGGCTGCAGGCAAGCTGGACATGT  
 GCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC  
 TGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG  
 GGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCACTGAGGGGCTG  
 AGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA  
 CCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAATGAGGAGGCCATGCACAGGGTGGGGCAG  
 CTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTTGCCCTTGGTGGGGTTTCCACTGGCTTT  
 TGGCTACAGAGAGGGGAAGGGAAGCCCTGAGGCCGCATAGGGGAGGCCCTTGGAACTGAGCT  
 GCCAATGCCAGCCCTGTCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACCTCCCTTC  
 GTGGGCAAAAAGTGCAATTGTAGGCCAGGCCACAGTGGCTCAGCGCTGTAATCCGACACTT  
 TGGGAGGCCCAAGGGGGTGGATTACCTCCACTGTGTTAGTAGAAATGGGCAAAACCCCATCTC  
 TACTAAAAATACAAGAAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCAGCTATTGGGA  
 GGCTGAGGCAGAGGAATCGCTTGAGCCCGGGAAGCAGAGGTTCAGTGAACTGAGATAGTGAT  
 AGTGCCACTGCAATTAGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAA

105256.0150  
 256.0150

68/615

## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415  
<subunit 1 of 1, 215 aa, 1 stop  
<MW: 24326, pI: 6.32, NX(S/T): 4  
MHRDAWLPRPAPSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQF  
SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLEFNVQPEDEGIYN  
CYIMNPPDRHRGHGKIHLQVLMEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQ  
KLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

2025.09.25.09.00.00



**FIGURE 69**

GGCGCCTGGTTCCTGCGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCGCGCCGCGAGCCTC  
 GTTCGTGTCCTCCGCCCCCTCGCTCTCTGCACTACTGCTCAGAAACGCTGGGGCGCCACCCCTGGCAGACTAACGAA  
 CGAGCTCCCTTCCCAACCCCACTGCAGGTCATAATTTGGACGCTTTGGCTGCCATTTCTTCAGGTTGAGGGAGC  
 CGCAGAGGGCGGAGGCTCGGCTATTCTGCACTGACAGCCACGCTCGCCCCGAGCGCTCGGTGCTCAGGCCCCCTC  
 GCGAGCGGGGCTCTCCGCTCTGCGGCTCCCTTGTGAAGGCTCTGGCGGCTGCGAGGGCCGGCCGCTCGGTTTGGCT  
 CACCTCTCCCAGGAACTTCACTTGGAGAGCCAAAAGGAGTGGAAAGACCTGTCTTGGAGATTTCTCTGGGGAA  
 ATCCTGAGGTCATTCTATTGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAAACCAAGTGTCTCATGGCTAGA  
 GCAATTCAGCCATGTGTGTTCCCAATGCCACTTTATTGGAGAACTTTGGAAAAATACATGGATGAGGATGGT  
 GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCAGAGCAATGACATGCAGAGTATTTTGGACCTTCAT  
 AATAAATACGAAGTCAGGTGTATCCAAACGCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
 TCTGCAGAAATCCTGGGCTGAAAGTGTCTGTGGGAAACATGGACCTGCAAGCTTGTCTCCATCAATGGACAGAA  
 TTGGGAGCACACTGGGGAAAGATATAGGCCCCCGACGTTTCATGTACAAATCGTGGTATGATGAAGTGAAGACITTT  
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTCTGGCCCTGTATGTACACATTATACA  
 CAGGTCGTGTGGGCACTAGTAACAGAAATCGGTGTGCCATTAAATTTGTGTCTAATCAATGAACATCTGGGGGCGAG  
 ATATGGCCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
 CATGGGCGGCCCTGTCTGTCTGCCCACTATGTTTGGAGGGGGCTGTAGAGAAAACTGTGTCTACAAAGAGGG  
 TCGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAATGAACAGACAGCAGTCAAAAGTCCATGACACC  
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAAATGTCCCAATTTGTTTCT  
 TGTGAAGTAAAGATTAAAGATCAGTGCAAAGGAACAACTGCAATAGGTACGAATGTCTGCTGGCTGTTGGAT  
 AGTAAAGCTAAAGTATTGGCAGTGTACATTATGAATGCAATCCAGCATCTGTAGAGCTCAATTCATTATGGT  
 ATAAATAGACAATGATGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTTTCATCAAGTCCAAATAGA  
 AATGTGATTAAACCAATTTGGCAAATTCAGTCTGTCTAATTCCTTTCACAGCTCTCAAAATGAAGCTCAGGCTGTG  
 ACTTGTGTAAACCACTGTGCACTCTGTCCATTTCATAAGCCTGCTTCACATGTGCCAAAGATATATCTGTCT  
 CGTAACTGTATGCACAAATCCACATTTATGCTCTGTATATGGAACTCGAGTTCATGTATGCTGTGACAAAGA  
 TGCAGAGCAGCAGTACATCTGGATGGTTCGAAATCACGGTGGTATGTTGATGTAAATGCTGTGACAAAGA  
 AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTCTCAGAAAGTTTACAGAAATCTCCAGGAGGAAGGCCATTC  
 AGAGTGTTTGCTGTTGTGTGAACCTGAATACTTTGGAAGAGGACATAAAGACTATTCCAAATGCAATATTTCTGA  
 ATTTTGTATATAAATCTGAACATTACTGTACAGAGTACATCACTATTTTCAGCCCAAAAGGTGCCAAATGCATA  
 TAAATCTTGATAAACAAGCTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAAATGAAAATATAATGG  
 TTTTAGAAATCCTGTGTATAAATATGCTATATTTTCTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
 GTTCTACGTTTCAATATATATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
 GCGCTCAGAAAATCTCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC  
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAAATTTTCCACTTAATAACTGTAAAGTTTTTTTC  
 TGTAAATTTAGGCATATAGAAATATTAATTTCTGATATTGCACCTCTTATTTTATATAAAATAAATCTTAAATATC  
 CAAATGAATCTGTATAAATGTTTGTATCTCTGGGAATGGCCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
 ATGAAAACATCTCTAGTGATCTAGTATAGTAAATGTAGGGTTAAGCATGGACAGCAGAGCTTTCTATGTACTGTTA  
 AAAATTGAGGTCACATATTTTCTTTGTATCTCTGGCAAATACCTCTGCAGGGCAGGAAGTATAATAGCAAAAAGTT  
 GAAACAGAGTGAACTAATGTATATACATTACCATGGCACTGATTTTTTTTAAATGTAAATGACCTGTGATATAA  
 ATATGTGCCATATCATGGTACCTAATAATGGTGATATATTTGTTTCTATGAAAAATGTATTTGTGCTTTGATACTAAA  
 AATCTGAAAAATGTAGTTTGGTAAATTTTTTCTGCTGGTGATTTACATATTAATTTTTTCTGCTGGTGGGA  
 TAAACATTAAAAATTAATCATGTTTCAAAAAA

70/615

## **FIGURE 70**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLEKYMDEDEGEWWIAKQRGKRAITDNDMQ
SILDHNLKLSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNFYCPFRCSGPVCTHYTQVWVATSNRIGCAINLCHNM
NIWGQIWPKAVYLVLCNYSKGNWWGHAPYKHGRPCSA CPSPFGGGCRENLCKEKS DRYPPR
EETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEQSSI CRAAIIHYGII DNDGGWVDITRQGRKH YFIKSNRNGIQ TIGKY
QSANSFTVSKVTVQAVT CETTVEQLCPFHKPASHCPRVYCP RNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSES LQNPPGGKAFRVFAVV
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31

2025-10-27 14:28:50

**FIGURE 71**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGAACGGGACGGGACCCGGCTAGGC  
 TGGGCGCGCCCCCGGGCCCCCGCTGGGCA**ATG**GGGCGCACTGGCCCCGGGCGCTGCTGCTGCCCT  
 CTGCTGGCCCACTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCAACGCTGCC  
 CTCGGGTGGCGCGGCCACGAACCGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCC  
 GAGCGCCACGCGCAGCGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCC  
 GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGACTCTGGCCCGCGGCTACTACCTGGAG  
 ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTT  
 GCCGTGGCAGGAACCCCGCACTCCTACATAGACAGTACTTTGACACAGAGAGGTCTAGCACA  
 TACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACAAAGGAAGCTGGACGGGCTTCGTT  
 GGGGAAGACCTCGTCAACATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAACATTGCCACT  
 ATTTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  
 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA  
 GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT  
 GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATATAAAGGAGACATC  
 TGGTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAATTTCTGAAATTTGGAAATTTGGA  
 GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC  
 ACCACGCTGCTGCGCTGCCCCAGAAAGGTGTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCA  
 TCTCTGATTCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTCTGGACGAAT  
 TCGGAAACAACCTTGGTCTTACTCCCTAAAATCTCCATCTACCTGAGAGACGAGAATCCAGC  
 AGGTCAATCCGTATCAAACTCTGCCTCAGCTTTACATTAGCCCATGATGGGGCCGGCCTG  
 AATTATGAATGTTACCGATTTCGGCATTTCCCATCCACAATGCGCTGGTGATCGGTGCCACG  
 GTGATGGAGGGCTTCTACGTCACTTTCGACAGAGCCGAGAAGAGGGTGGGCTTCGACAGCGAGC  
 CCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCTTTTCTCAACAGAGGAT  
 GTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTAT  
 GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCTGCTGCTGCTGCCGTTT  
 CGGTGTGAGCGTCGCCCCCGTGACCTGAGGTGCTCAATGATGAGTCTCTCTGCTGAGACAT  
 CGCTGGAAAT**GA**ATAGCCAGGCCTGACCTCAAGCAACCATGAACCTAGCTATTAAGAAAAATCA  
 CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAAT  
 CTCGTGTTCTGCTCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTGATTTCAGGCTTT  
 CAAATCCCTCACTTCCAGAAAAATAATTAAAAAAAACCTTCATCTAA

72/615

## **FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493  
><subunit 1 of 1, 518 aa, 1 stop  
><MW: 56180, pI: 5.08, NX(S/T): 2  
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGLALA  
LEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI  
DTYFDTERSSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLP  
GIKWNIGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG  
GIEPSLYKGDIIWYTPIKEEWYQIEILKLEBIGGQSLNLDCREYNADKAIVDSGTLLRLPQKV  
FDAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISYILRDENSSRSFRITILPQ  
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAV  
SEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLIIVLLLPFRQRRPRDPE  
VVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

105536-011502

**FIGURE 73**

GCCGCGGCGGAGAGCGCGCCAGCCCGCGCGC**ATG**CCCGCGCGCCAGGACGCTCCTCCCGCTGCTGGCCCGGG  
 CGCGCGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGCGCGCGGGCGCTGGGGCGCCCGGGCCAGG  
 AGGCGCGCGGCGCGCGCGCGCGCCCGCCCGCGCGCAGCGCGAGGACGGACAGGACCCGACAGCAAGCAAC  
 GTGACACGGCCGACATGTTTCACGACCGGGATCCAGAGCGCGCGCACTTCGT CAT GTTCTCGCGCCCTGGTGTG  
 GACACTGCCAGCGGCTGCAGCCGACTTGGAAATGACCTGGGAGACAAATACAAACAGCATGGAAGATGCCAAAGTCT  
 ATGTGGCTAAAGTGGACTGCACGCGCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCAGGATACCCCACTTTAA  
 AGCTTTTCAAAGCCAGGCCAAGAGCTGTGAAGTACCAAGGGTCTCGGGACTTCCAGACACTGGAAATCGATGTC  
 TGCAGACACTGAACGAGGAGCCAGTGAACACAGAGCGCGAAAGTGAACCGCCAGTCCCGCGAGCTCAAGCAAG  
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAAGCGCACTTTATCAAGTCTTCGCTC  
 CGTGGTGTGGTCACTGCAAGGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCCTGGAACATCCGAAACTG  
 TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTCTGCTCCGGAACACAGGTTCTGGCTATCCCACTC  
 TTCTCTGGTTCGAGATGGGAAAAGGTGGATCAGTACAAGGGAAGCGGGATTGGAGTCACTGAGGGAGTACG  
 TGGAGTCCGAGCTCGACGCCACAGAGACTGGAGCGACGGAGACCGCTCAGCGCTCAGAGGCCCGGCTGCTGGCAG  
 CTGAGCCCGAGGCTGACAAGGCCACTGTGTTGGCACTCACTGAAATAACTTTCGATGACACCAATTGCAGAAGGAA  
 TAACCTTCATCAAGTTTTATGCTCCATGGTGTGTCATTGTAAGACTCTGGCTCCCTACTTGGGAGGAACCTCTCTA  
 AAAAGGAATTCCTGGTCTGCGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGSAACCGAATATCTCGACGA  
 AGTATTCCGTACAGAGACTACCCCACTGTTATTGCTTTTCCGAGAGGGGAAGAAAGTCAGTGAGCACAGTGGAGCA  
 GAGACTTGACTCGTTTACACGCTTTGCTGAGCCAAGCGAAAGCAACTTTAGGAACACAGTTGGAGGTCAC  
 CTCCTCCTCCCGAGCTCCCGCACTCTGCGTTAGGAGTTCACTCCACAGAGGCCACTGGGTTCCCGAGTGGTGGCT  
 GTTCAGAAAGCGAACAATACTAAGCGTGGAGGTAICTTCTTTGTGTGTGTTTTCCAAAGCCACACACTCTACAG  
 ATTCCTTTAAGTTAAAGTTCTCTAAAGTAAATGTGTAACCTATGGTCACGTGTGTAACATTTTCAGCTGGCGATA  
 TATCCCTTTGACCTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAATAGCGTTGAGGGAAATGAAA  
 TTGCTGGACTATTGTTGGCTCCTGAGTTGAGTGATTGTTGGTGAAGAAAGCACATCAAAGCATAGTTTACGTGC  
 CCACGAGTCTTGAAAGGTTGGCCTTTGTGGCAGTATTGACGTTCTCTGATCTTAAAGTCACAGTTGACTCAATAC  
 TGTGTTGTCGATGAGCATGGAGCAGATGAAATGCAAAAACCCACACTCTGGAAGATACCTTCAAGCCGCTGC  
 TGGAGCTTCTGTTGCTGTGAATCTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTCTGACC  
 GTGCGTGAGTAAGAGAATGTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTTCAGGGGAT  
 CCTCTGTTTCTCACGGGGTGAACATGTCTTTAGTTCCTCATGTTAAACGAAAGCCAGAGCCACATGAACCTGT  
 TGGATGTCTTCTTGAAGAGGTTAGGCATGGAATAATCCACGAGGCTCATTTCTCAGTATCTCATTAACTATTGA  
 AAGATTCCAGTTGATTTGTCACTCGGGTGACAAGACCAGACAGGCTTTCCACAGCCCTGGGTATCCAGGGAGGC  
 TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAG  
 CTGTCTATCTTGGCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAAATGGGATGCAATTGATCTCAAGAC  
 CAAAGACAGATGTCACTGGGCTGCTCTGGCCCTGGTGTGCAGCGCTGTGGCAGCTGTTGATGCCAGTGTCCCTCTA  
 ACTCATGCTGTCCTTGTGATTAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA  
 GATAGGCTGTTGTCTTTTACCATCGAGCTACTTCCCATATAACCACTTTGTCATCAACACTCTCCACCCCT  
 CCCATACGCAAGGGGATGTGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAAGCACTTATA  
 CTGCTGTCTGAGGCAAGATAAACAGCAGCACTCTGCACAGCCTCTGCCTTAAAGGAAATCTTTATTAAATCAG  
 TATGTTTCAAGATAATCTTTTTTAAAAAAACCCCACTCTAGAGAGCACTGTCAGAGTCTTTGTACA  
 CACAACCTCAGCTTTGCATCAGAGCTCTGTATTCCAGAAAAATCAAAGTGGTACAAATTTGTTTGTACACTAT  
 GATACCTTTCTAAATAAATCTTTTTTTTTTAA

74/615

## **FIGURE 74**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAADGPPAADGEDGQDPHSK
HLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAHS
VCSAQGVRGYP TLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPELKQ
GLYEL SASNFELHVAQGDHFIFKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQHYE
LCSGNQVRGYPTLLWFRDGGKKVDQYKGRDLESLEREYVESQLORTETGATETVTPSEAPVLA
EPEADKGTVLALTENNFDITAEGITFIKFYAPWCGHCKTLAPTWEELSKEFFGLAGVKIAE
VDCTAERNICSKYSVRGYPTLLFRGGKKVSEHSGGRDLDLSLHRFVLSQAKDEL
```

**Signal sequence:**  
amino acids 1-32

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 75A**

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCAAG  
 CAGTTTTCAGCGCCTTCGCGCGGTTGCGCCAACTACGCAAGCAACGAGCGGCTCCGCGCGGACGCGCGCGCGGGG  
 TAGGGAACCGCGTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAGAAATTTGTCGCGCGAGTTTTCGCGGAGGT  
 GAGGGAGATCAGGAAACGCGCTTCTTCTCCTCCTTCGCCGCTGGTGAGTGTCTGGGGAGATTGGCAAAACGCTTAGG  
 AAAGGACTGGGGAATAAGCCTGGGAAAGTGAGAAAGGTGATCAGGAGGCGGCTCCATCAGCGCATTTTATCTGT  
 TCTGATCAGACGACGACGCGCGCTCCACTTCGCGAGTCTTTCCAGAGTGTGGGACGCGCAGGACGACGCGCCGA  
 TCCCGCGCGCTCCGATCAGCAGCATCCGAGGAGAGTCAGCCTCGCTCCCAACGCTGAGGGGCGCTCTGGGCACGA  
 AAGTTCTCTGTCACGTGATTTCTCAATTCTTCTGCTGGTTTTTTTCTCCAGAGAACTTTGGGTGGAGATATTA  
 ACTTTTTCTTTTTTTTTTCTTGGTGGAAAGTGTCTTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC  
 TGGAGAAGAGCGAGCGCTCTTGTCTCCGAGTCCCATTAAAGCCATCACTTCGGAAGATTAAAGTTGT  
 CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCAACGCTGTGTGGGTGCATG  
 TGTGCGCCCGCAGCGCGCGGGGCGGTGGTTCTCCGCGTGGAGTCTCACTGGGACCTGAGTGAATGGCTCCCA  
 GGGGCTGTGCGGGGCATCGCCTCCGCTTCTCCACAGGCTGTGTCTGTCTGGAAAGATGCTAGCAATGGGGG  
 CGCTGGCAGGATTCTGGATCTCTGCTCTCCTCACTATGGTTACCTGTCTGGGGCCAGGCGCTAGAGAAGGAGG  
 AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCACGCAAACTTCAACCTCCAGCGCCCATCTCA  
 TTTTCACTCCTAGCGGATGATCAGGATTTAGAGATGTGGGTACCAAGGATCTGAGATTAAAAACCTACTCTTG  
 ACAAGCTCGCTGCGGACGAGGATTAACTGGAGAACTACTATGTCAGGCTATTGCAACACCTACAGGAGTCAGT  
 TTAATCTGAGGATCTAGATACACACCGGACTTCAACATTTCTATCAAGAAGCTACCCAAACCACTGTTTAC  
 CTCTGGCAATGCCACCTTACTCAGAACTGAAGGAGTTGGATATTCACGCGATATGGTGGGAAATGGCACT  
 TGGGTTTAAACAGAAAGAAATGCAATGCGCCACGAGAAGGAGTTTGATACCTTTTGGTTCCTTTTGGGAGTG  
 GGGATCTACTATCACTACATAAAATGTGACAGTCCCTGGGATGTGTGGCTATGACTGTATGAAACAGCAATGCTG  
 CTTGGGAGTATGACAAATGGCATATCTCCACAGATGTACACTCAGAGATCAGCAAACTTTAGCTTCCCAATA  
 ACCCAACAAAGCGCTATATTTTATATACTGCCATCAAGCTGTTCATTCCACCTGCAAGCTCTCGGCGAGTTAT  
 TCGACAGATCAAGATCCATTATCAACTAAACAGGAGAAGATATGCTGCCATGCTTTCTCGCTGTAGATGAGCAA  
 TCAACAACGCTAGATGGCTTAAAGACTTATGGTTTTCTATAACAACAGCATCATATTACTTCTCATGATATG  
 GTGGCCAGCTTACGCGCAGGAGGATTAAGCGCTCTCAGAGGTGCAAGGAAACATATTTGGGAAGGAGGATCC  
 GGGCTGTAGGCTTTGTGCATACCCACTTCTGAAAAACAGGGGAACAGTGTGTAAGGAACCTGTGTCATCACTG  
 ACTGTGATCCACTCTCATTTTCACTTGGCTGAAGGACGATTGATGAGGACATTCAAGTATGAGCTATGATATGT  
 GGGAGACCATTAAGTGGGCTCTTGGCTCACCCGAGTAGATATTTTGCATAAATGAGCCCTATACCAACAGGC  
 AAAAAATGGCTCTGGGCGACGAGCTATGGGATCTGGAACACTGCCATCCAGTCAGCCATCAGATGCGACACTG  
 GAAATGTCTAACAGGCTCTCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACGGAACCG  
 GTGGCACTAAGACGATCACTTTGTCAACTGGCAAAAGTATGGCTTTTCAACATCAACAGCCACCATATGA  
 GAGGGTGGACCTATCTAACAGGATATCCAGGAATCTGAGAAAGCTCTACGAGGCTCTCAGTGTCAACAAAG  
 TGCAGTGGCGGTGAGTATCCCGCCAAAGACCCAGAAAGTAAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
 GTATAAGAGGAGAAACCAAGAAAAAGCCCAAGCAAAATCAGGCTGAGAGAAAAAGCAAAAGAAAGCAAAAGAA  
 GAGAGAAAGAACAGCAGAAAGCAGTCTCAGGTAAACCGCAAAATTTGGCTCGATAATATCTGCTGGCCTAAAGGCTCA  
 GGCCTGTTTTCTAGTGTGGCCACTCCAGAGACTTCTGCCACTGGCCCGCAAGCTGAAACCTGTCTCTGAGT  
 CCAAGGCTGCTACTCTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAAAGTGT  
 GTGAGTCTCGAGTTCAGTGTGTGCTTCAGTCACTGACCAACACTGCTTTGAATGTATAGGAGGAGAACATA  
 ACTCAACATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTGAATGATTAACACTCTTGTATATAATTTAC  
 AGTCAAAAGTTTGTGTCACTCAAAGGCTTGAAGAAATATTTTTCTGCTGATTTTTGTATGTCTGTCAATGA  
 CACTTGGGTTTGTATTAATTTATTTATATATATAATATATATGTTTTCTTCTGTGAAAAGCTGTTTTTCT  
 CACATGTGAACAGCTTCGACCTTATTTTACATCGCTGAGGGAATGGCAATGAAGATGTTTGTGACACACTGCC  
 ACAATGAATGTAATCTATTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAACTTAATTTATTTTACA  
 GAAAAATATTTTGTGTTTTTATAAAAAAGTTATGCAAAATGACTTTATTTTTTCTGCAATCACTATGAAGA  
 ATTTTATTTCACTTTCTCAAAATATCAAGCATGTAATCATATAAATTAATGTAATCTGTGTGAATTCAGACTA  
 TAAAAAACACTATTGAGAACTTTATATCTGTCAATGTTTCAATCAAGATTTGAAATGATTAAGATGAATATAT  
 ATTTACTTGAATAATCAATGTTGTGACAGAGTTGAGACAACTTATTTGTTTCTATCAATAAATCTTATGTATCTT  
 AATTAATAAAATGATTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTCTGATCTAACTCTACGTAAAAAT  
 GTATCATTTGGCTTAAATAAATAAATCTTTACTAATAGGCAATTGAAGAGATGGTTGCTAACCAACACAGTAA  
 TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCAATAATAACATA  
 TATTTATATAGGTGGTGCAAAACTGTTGCGGTTTTTCCCAATAAAGTAATAACCTTACTCTTATCAATAAG  
 GGACACTTGGGGAGATACAGAGAAATGGAAGATACGGATCTGCTGGAGTGGTAACTTCTGTGGAAACCC  
 ACATGCAAAAGCTCATGAGGAGAAATAAAGGAGATTTATCAGTATGAAGTTTATCATGGGTCATCAATGAGCATA  
 GATTGGTGTGATCTGTAGACCTGGTGTTTCTTTGAAGTGCCTCTCCTAATGACAGAGGCTTGAAGCTTAC

[illegible]



77/615

## FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGACGHPPPPSPQACVCPKMLAMGALACFWILCLITYGYLSWGQALEEEEEGALLAQAGEKLEPSTTSTSO
PHLIFILADDQGGFRDVGYSSEIKTPTLDKLAAGVKLENYYVQFICTPSRSQFITGKYQIHITGLQHSIIRPTQP
NCLPLDNATLFPQKLKEVGYSTHMGVKGWHLGFNRKECMPTRRGFDTPFGSLLGSGDYTHYKCDSPGMCQGYDLYEN
DNAANDYDNGIYSTQMYTQRVQQILASHNPTKPIFLYTAYQAVHSPVLPQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGYFNNSILITYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLNKKGTACKELV
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRGTGTMNGSPCQLAKVYGFSTSQPTHMRGWTYLTGIQES
```

### Important Features:

#### Signal Peptide:

amino acids 1-37

#### Sulfatases signature 1.

amino acids 120-132

#### Sulfatases signature 2.

amino acids 168-177

#### Tyrosine kinase phosphorylation site.

amino acids 163-169

#### N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

10052536, 211502

**FIGURE 77**

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCTTTTGAAGAACAGTACTGTGGA  
 GCTATTTTAAGAGATAAAAAAGAAATATCTTTCTGGGAGTTCAAGATTGTGCAGTAATTTGGTTAGGACTCTGAGC  
 GCGCCTGTTTCAACATCGCGGAGAGAAAAAGCGGAGATCTGTCTCGCCTTGCACGCGCTCGAAGACCAAGTCAGAT  
 AGCTAGGAATGAACCATCTCCCTGGGAGTATGTGGAAAACAACGGAGGAGCTCTGACTTCCCACTGTCCCAATCTAT  
 GGGCGAAGGAAGTCTCTCTGACTTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAAGATTGAT  
 TCTCTGCGGACTGCACCGGGACTCAAAAGGGCTTGTCTGTCTGGGAATCTCTCTGGGGAGCTCTGTGGGAGACCGG  
 ATGCACCCAGATACGCTATTAGTTCCGGAAGAGCTGGAGAAAAGGCTCTAGGGTGGCGACACTCTCCAGGGACCT  
 GGGGCTGGAGCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCGAGCTTTTCCGCCCT  
 GAATCCGCGCAGCGGAGCTTGGTCAACGCGGCGGAGGATAGACGGGAGGAGCTCTGTATGGGGCCATCAAGTG  
 TCAATTAATCTAGACATTTCTGATGGAGGATAAAGTGAATAATATATGAGGTAGAAGTAGAAGTAAGGGACATTAA  
 CGCAATCGCCTTACTTTTCGTGAAAGTGAATTAGAAAATAAAATTTAGTGAAAATCGACCCACTGAGATCGGTT  
 CCTCTACCCACGCTTGGGATCCGGATATCGGGAAGAACTCTCTGAGAGCTACGAGCTCAGCCCGAAACATCA  
 CTCTCTCCCTCATCTGCAAAAATGGAGCCGACGGTAGTAAGTACCCGAATTGGTGCTGAAACGCGCCTTGAGCG  
 CGAAGAAAAGGCTGTCAACCACTTGGTCTTACGGCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
 CATCCGCGTGATGTTCTGGATGCGAACGACACCGAGCGTTTGTCTCAGCCGAGTACCGCGCGAGCGTTCC  
 GGAGAATCTGGCCTTGGGCACGAGCTGTCTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT  
 GAGGTATTCCTTCCGTATGTGGACGACAAAGCGCGCCCAAGTTTCAAACTAGATTGTAATTCAGGGACAATATC  
 AACCAATAGGGGAGTTGGACACGAGGAGTCAGGATTTACACAGATGGAAGTGCACAGCAATGGATAATGCAGGATA  
 TTTCTGCGGAGCCAAAGTCTGTATCACTGTTCTGGACGTGAACGACAAATGCCCCAGAAGTGTCTCCTACCTCTCT  
 CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGGCCCTTTTAAATGAAATGACCAAGATTCTGA  
 GGAAAAAGGACAGTGTATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAATTTACTA  
 TAGTTTATGTCACAGACATAGTCTTGGATAGGGACAGGTTCTAGTACAACATCAAGTGAACCCGCACTGACCG  
 GGAACCCCGCCCTATCCACGGAACTCATATCTCGTGAACGTGGCAGACACCAACGACCCCGCGGCTTCT  
 CCTCAGGCTCTCTATTCCGCTTATATCCAGAGAAACAATCCAGAGGAGTTCCCTCGTCTCTGTGACCGCCCA  
 CGACCCGAGCTGTGAAGAGAAGCCGACGATCACTTATTCCTGGCTGAGAACCACTCCAAGGGGCAAGCTATC  
 GTCTTACGTGTCTCATCACTCCGACACTGGGGTACTGTATGCGCTGAGCTCTCTCGACTACGACAGTTCGCGAGA  
 CTGTGAAGTGAAGTGTATGGCGGGGACAAAGGACCCCGCCCTCAGCAGCAACCTGTGCTGTAGCTGTGCTGT  
 CTGCGACGAGAAGCAATGCGCCGAGATCTGTATCCCGCCCTCCCAAGGACGGTTCACCTGGCGTGGAGCT  
 GGCTCCCGCTCCGACAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGAACAGAGACTCCGCGGACCAAGC  
 CTGGCTGTCTTACCGCTGTCTCAAGGCCAGCGAGCCGGGACTCTCTCGTGGGTCTGCACACGGGCGAGGTGCG  
 CACGCGCGAGCCCTCTGTGACAGAGACGCGCTCAAGCAGAGCTCTGTAGTGGCGCTCAGGACCAACGCGACCC  
 CCTCTCTCCGACACTGTCAACGCTACCGCTGGCGGTGGCCGACAGCTACGATCACTCTGCTGTAGTGGTGGCGGCTCTGT  
 CGTCTTCTGCGCTCTGCTATCTTGTCTGTGCGCTCAGGCTCGCGCTGGCAGTGAACGCTCAGCCTGTCTGACG  
 TTCAAGAGGGGCTTGAACAGGACCGCGCGTGCACCTTTGTGGGCTGGACGGGGTGCAGGCTTTCTCTGAGAC  
 CTATTTCCACAGAGTTTCTTCCACACGAGCTCCGGAAGAGTCACTGATCTTCCCCCGCAACTATGACAGA  
 CATGCTCTGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTCTGAGGTGATTTCGGTATTTTCAAAGA  
 CAGTCACTGGTTAATTGTAGGTGAGTTTATATCAAACTCTCTTTCTTTTAAATGCTCTGTCTCCCAAGC  
 TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCTCAAACCTTAGGCTCAAGCAATATCCCACTTTGCTCT  
 CGGTGTAAACAGGACTACAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT  
 CTATCTATCTATCTATCTATCTATCTTCTGTACAGAGCGGAGTCTCACGCTGTGAATCCAGTACTTTGGGAGGC  
 CGAGCTGGTGGATCACCTGAGGTGGAGTTTGGAGCCAGCGCTGAACCACTGGAAGAACCCCGTCTATACCTAA  
 AAAAAATACAAAATTAGCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
 TGCTTTAACTGGGAGGTGGAGTTGCAATGAGCTGAGATTGTGCCATTGCACTCAGCCTGGGCAACAGAGTGA  
 AACTCTATCTCA

79/615

## FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306  
><subunit 1 of 1, 916 aa, 1 stop  
><MW: 100204, pI: 4.92, NX(S/T): 4  
MIPARLHRDYGKGLVILGILLGTLWETGCTQIRYSVPPEELEKGSFVGDISRDLGLEPRELAERGVIIPRGRQTQLF  
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM  
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVVKRALDREEKAHHLVLTASDGGDPVRTGT  
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGT  
ISTIGELDHESGFGYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVNDQD  
SEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLVNADTNDNPP  
VFPQASYSAYIPENNPRGVSLSVSTAHPDCEENAQITYSLAENTIQQASLSSYVSINSDTGVLIALSSFDYEQF  
RDLQVKVMARDNGHPPLSSNVSLFVLVDQNDNAPEILYPALPTDGGTGVELAPRSAEPGYLVTKVVAVDRDSGQ  
NAWLSYRLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSI PQVLADL  
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALRLRRWHKSRLLQASGGGLTGAPASHFVGVDGVQAFL  
QTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLTEVSLYQIFLFFFFNCVS  
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLSCTDGS�TPVIVLW  
EAEAGGSPEVGSRLPA

### Signal sequence:

amino acids 1-30

### Transmembrane domains:

amino acids 693-711, 809-823, 869-888

1052555.011501

**FIGURE 79**

AGCGGCTGCCCGGGCGGGCGGCCGCGGGCGGCACCA**ATG**AGTCCCCGCTCGTGCTGCGTTCGCTGCGCCTCCTC  
 GTCTTCGCGCTCTTCTCAGCGCGCGCGAGCAACTGGCTGTACTCGGCCAAGCTGTCGTGGTGGGGAGCATCTCA  
 GAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACTCGGAAGTC  
 ATGGACTCGGTGCGCGCGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAAGTTCCGGAAACCGGCGCTGGAAC  
 TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGGACTCGGGAGGGCGGCCTTCGTGTAC  
 GCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACGAGTGGGGAGCTGGAGAAAGTGCGGCTGT  
 GACAGGACAGTGATGGGTGAGCCACAGGGCTTCAGTGGTCAGGATGCTCTGACACATCGCCTACGGTGTG  
 GCCTTCTCAGTTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC  
 CACAACAATGAGGCGCGCAGGAAGGCCATCCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTCAAGG  
 TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCGCAGGTGGGTACGCACTGAAGGAGAAGTTT  
 GATGGTGCCACTGAGGTGGAGCCAAGCGCGCTGGGCTCCTCCAGGGCACTGGTACCAAGCAACGCACAGTTCAAG  
 CCGCACACAGATGAGGACCTGGTGACTTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG  
 CTGGGCACGAGGGGCGGCACATGCAACAAGACGTCCAAGGCCATCGAAGGCTGTGAGCTGCTGTGCTGTGGCCG  
 GGCTTCCACAGCGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCGTCAAGTGC  
 CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGAT**GA**CGCCTGCCTAGCCCTGCGCGGCAACCACTTA  
 GTGGCCAGGGGAAGGCCGATAATTAAACAGTCTCCCAACCACTACCCCAAGAGATACTGGTTGTATTTTGGTT  
 CTGGTTTGGTTTGTGGTCTCATGTTATTATTATGCGGAAACAGGCGAGGCAACCCCAAGGGCACCAACAGGGC  
 CTCGCCAAAGCCTGGGCTTTGTGGCTGCCACTGACCAAAGGGACCTTGTCTGTGCGCTGGCTGCCCGCATGTG  
 GCTGCCACTGACCACTCAGTTGTTATCTGTGTCGTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTA  
 TTACCAACCATGCTACTGACCGGTGTCTCGGGGAAGAGGGGGCCTATGGCAGGGAAAAATAGGTACCGACTTG  
 ATGGAAGTCACACCCTCTGGAAAAAGAACTCTTAACCTCTCCAGCACATACATGAGCTCCTGGCAGCTTGA  
 CCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAAGTCAAGGGCACAGGTTCAAT  
 TCAGCCCTTACATGGACAGCTAGAGGTTTGAATATCTGTGGGTCTTCCAGGCAAGAGAGGGAGATGAGAGCAAG  
 AGACGACTGAAGTCCCAACCTAGAACCCAGCCTGCCCAAGCCTGCCCTCGGAAAGGGAACCTTAACCACTCCC  
 AGACCCACTTAGGCAGGCATATAGGCTGCCATCTGGACCAAGGATCCCGGCTGTGCCCTTTCAGTCTATGCCCA  
 GTCACTTTTACAGCGCTGTCTCTCATGAACTGAAAAACACACACACACACACACACACACACACACAC  
 TCACCTTTACAGCACTGTTCTCT

81/615

## **FIGURE 80**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLSRLRLILVFAVPSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFYVAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGCSDNIAYGVAFSQSFDVVRERSKGASSSRALMNLHNEAGRKAILTHMRVECKCHGVSGSCEVKTCTWRAP
PFRQVGHALKEKFDGATEVEPEPRRVGSSRALVPRNAQFKPHTEDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCCKFWCCFVKCRQCQRLVELHTCR
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

2025-04-20 14:30:00

**FIGURE 81**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATTGGGCGTGAGTGCAATCTACGGATCAGTCT  
 CTGTGTTGGTGGTCTGTTAACTCTCAGTGGGGACTCCAAGATTCCATGAAGAAAATCAGTGTCTTCAATTCAGAAT  
 TGGGCTCTGGCTCAGAAATCTGCTGCAGCTGCTGAAATCTGTTTCTAGAAGAGGTTTAAATTAATGCTCGACTCT  
 GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCCGCTTCT  
 TGCTGCTCTGCTGGCTGGCTGGCTGGCTGGCTTTTGGAGCCTTCAGCTCGAGTCTTCCGACCTGATCCCGGTGT  
 CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCAAGAGAAATCATGCCCGACCCCTGTGACGAGGCCCCCTGGA  
 CAGACCCCGTTTATGAAGCTCTTTGTACTGCAACATCCCAGTGTGGCCGAGGCGAGCATGGAAGGTCATGCC  
 CGCATCATTTTAAGCTGGTCTCAGTGCACTGTGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCTCA  
 AAACAAAGCGACCAAGAAATGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTC  
 TTAGTCACATGTCAAAGAGTCCGGAGCCTCTTTCGAAAGCCCTTTGAACCTCCTTGCTCTTTACCCAAATCAC  
 CATTTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACCGTTCAGCTGCTGAGGGATA  
 TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTTGGTCTGCAGACCAAGCTCTATTAGAGACCACTGGGAAA  
 GCCGACCCCTACAAAGTGGGCTGGCTGGCTTGTCTTATGGCTTTCTCCAGATTTTGAATGGAAGAGATTATTTCA  
 GGCACACGCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTGAAGAACAGCATATCTGGAAGAGGAGC  
 AGCGTCGTGAGTACCTCTACGTTTGAACACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAAGTCTGTGG  
 ATGTCCTCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTCACT  
 TTCCCTGTACCAAGAAATGGCTGTGTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGA  
 GGGAAAGACGGGAGAAGAAATGTACTTCGGGTAATTTCTCTCTGGGTGCCACCCCATCCTGAACCAACCATCG  
 GCCGGATCGAGCGTGCCACCGAGGGCAGGAAAGAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT  
 CACCAAGTTCTCAGTGCCTTTGGGCCCTTTCAGAAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTT  
 GGCAAGACAGAGAAAAGCCCAAGCTGAACATTCGCTCCGGATCTTTACAATGGCGTCGATGTCACATTCACACT  
 CTTTCTGCGAAGACCCACCAAGGCTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAA  
 GGGACATGTTTGTAGCCTTGGTGGCTGGTACAAATTTATGATGTCATGTACAGGGAAGGATCTCTAAAGG  
 TAGGAGTAGAAGATTATTCCTTTTAAAGGCTAAATTTGTTTGGGAACCCACAGATGTTGGGTTGAAGCAGT  
 AAGCACTTGCCTGCAATGTCTACGTGAATGCTTGGTACAAAATGGCCAGTTACAGAGAGAAATAGAAGTACTT  
 TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATAGTTCAAGACCTGAAATGGCAATCAAGTTTGCAC  
 TCTCTTGGCCCTGCCCATGTGTACATGTGATGGAACCAAGCACCTTCAACCAAAATTTTAACTCTTAGACAT  
 TTTATCTTGCTCTGTGTTAAGAAATTTCTGAAGTGATTTATCTAAAATAAAGGTTGGCAACTTTTCTGTAAAG  
 CGCAGATTGTAAATATTTTACAGCTGTGTGGACCAAAAGGCCACATACAGTCTCTGTACATACTACTCACTCTGT  
 TTTCTGAAGCAGGAAGGCCACACAGACAGTACATAAAGGAATATGTAGCTGGTTCGAGGCCAGACAAAACA  
 GATGCTGACACAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCAAGCTTAAATAAGGCTATATCAAAATTC  
 ACTTCCAGCACTTTGGAACAGGAGTTGAATACCAAGAATTAATCAATGGTCTCCCGAGTAACTCTGCTAGAAACA  
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGTTAAATAAATGAAATAGAATGAATCATAGAA  
 AACTGATTAGAAGAAATCTGTATGTTTATGATGATTTGGGTACAAGATAGATTTTAAGTATGTTCTAAATATTTGT  
 CTGCTGTAGTCTATTGTTGATATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTGAAGAAATATTT  
 TTTAAGACAGTTTATGATGACTCTATTCTCTGTAGTAATATTCATTTTGTGTACCTGCTTGGTGGTTAGAAG  
 GAGGCTAGAAGATGAATTCAGGCACTTCTTCCAATAAAACATAATATGGCTCAITTCGCTTTGACAAAGCTGTAGA  
 ACTGATTCATTTTAAACCAATTTTCATCAGTTTCAAATGGTAAATTTCTGATGATTTTAAATGCGTTTGTGA  
 AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTTTATATATTAGAAGCAATATAGAATACATCTG  
 TGATTTCTGAACATTAATGGTGTCTAATTCAGAGAAATGGAAGTGAAGTGAAGTTCTCTGTTGTCATCGGCATCTC  
 AACTTTCTCTCTTGGTTTGTGCAGTGTGCAATTTGAATATGCTGTTTCTATAAATAATTTTAAAGAAAT

83/615

## **FIGURE 82**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLAALLAFVSLSLQFFHLIPVSTPKNGMSKSRKRIMPDPVTEPPVTDPVYEALLVCNIPSVAE
RSMEGHAPHHHFKLVSVHVFIRHGDRYPLIVIPKTKRPEIDCTLVANRKPYPHPKLEAFISHMSKGGSGASFESPLNS
LPLYPNHPLCEMGELTQTGTGVVQHLQNGQLLRDIYLLKKHKLPLNDWSADQLYLETTGKSRTLQSGLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMCL
HFCHNVSPFCTRNGCVDMEHFVKIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSPCQDHHKRSKPKMCPLE
NLVRFVKRDMFVALGGSGTNYDACHREGF
```

**Signal sequence:**

**amino acids 1-18**

1055256.04502

**FIGURE 83**

TCTCGCAGATAGTAAATAATCTCGGAAAGCGAGAAAGAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT  
 GACGTTGTGGAGATGGGGAGCGTCTGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGGGAAGTGGC  
 CCGTGTTTGTCTATGCGCAGTGTCTGCTTCTAGTGGAAACAACCTCCACTGTAACATGATGTACTATGCACCTTTTCTTG  
 CTTTGTGGAGATATGTGTAGCTTGTGTAAATGTTGTATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTT  
 TGTGAGAATGAGAAAGGTGTGTCCCTTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGT  
 TGCGCTATGTTCTATCTCTCTCTCTTACTATGATCAAAAGTGAAGAGTGCAGTGTATCTGAGAGCTGCAGTG  
 CCAATAGGATTTTAAAGTCTTTTGGTCTGTCAGCAATTCGAATATATATGGGCGCATCTCTCTCTCCAGAAAG  
 ACTTTTCAACTGTGTGGTTTATGTAGGCTAGGCGAGTGCCCTTTGTCTTTCATCCATACAACATAGTCTTACTT  
 ATTGATTTTGCACATTCAGGAATGAATCGTGGGTGAAAAAATGGAAGAGGGAACCTCGAGATGTTGGTATGCA  
 GCCTTGTATCAGCTACAGCTCTGAATATCTGCTGTCTTTAGTTGCTATCGTCTGTCTTTGTCTACTACACT  
 CATTCCAGCCAGTTGTTTCAGAAAAACAAGGCGTTTCACTAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG  
 TCTATATGCGCAAAATCCAGATATCAACACCAAGTCTGTTTGTACAGTCTCTTCAGTAATTCAGTCTACACA  
 ATGTATTTTGACATGGTCAGCTATGACCAATGAAACCAAGAAACAAATTGCAACCCAGTCTATCAAGCATATTTGGC  
 TACAATACAACAAGCACTCTCCCAAAGGAAGGCGAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTTATAGACTA  
 ATTCTCTTTTGTGTGTGTATTTTATCCAGCATCCGTAACCTCAAAACAATAGTCAGGTTAATAAACTGACTCTA  
 ACAAGTGTATGAATCTACATTAAATAGAAGATGGTGGAGCTAGAAGTGTATGGATCACTGGAGGATGGGGACGATGTT  
 CACCGAGCTGTGATATAATGAAAGGGATGGTGTCACTTACAGTATATCTCTCTTTCACCTTCATGCTTTTCCGTGGCT  
 TCACTTTTATCATGATGACCTTACCAACTGCTCCAGGTATGAACCTCTCTCGTGAATGAAAGTCAAGTGGACA  
 GCTGTCTGGGTGAAAAATCTCTTCCAGTTGGATTGGCATCGTGTGTAATTTGGACACTCGTGGCACCACTGTT  
 CTTACAATTCGTGATTTTGAACGAGTGTGAGACTTCTAGCATGAAAGTCCCACTTTGATTATGCTTATTTGAAAC  
 AGTATTTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTTCCATGTAACTCTCCAGTGTCTTGGCATGAATTA  
 GATTTTATCGCTTGTGATTTTGTATTTTCTTACCAAGTGCATGTATGTGGAAGTAGAATGAATTCGACAGGAA  
 AGTTTTATGAATATGGTGATGTAGTTAGTAAAGTGGCCATTTTGGCTTATCTCTGCTCTATAGTTGTGAAAT  
 GAAGATGAAACAATAATTTGTGTACTATTTTAAATATATATAGACTTAACTTTTAGCAGTATGTAAGC  
 AAATGTATGGCTGCTTTTGAATATTTGATGTGTGCTGGCAGGATACCTGCAAGAACATGTTTATTTTAA  
 ATTTATAAACCAAGTCACTTAAATGCGAGTTGTCTGAAAAATCTTATAAGGTTTTCACCTTGATACGGAATTTACA  
 CAGGTAGGAGTGTTTAGTGGACAAATAGTGTAGGTTATGGATGGAGGTGTCGGTACTAAATTTGAATAACGAGTAA  
 ATAACTTACTTTGGGTAGAGATGGCTTTGCGCAACAAGTGAACCTGTTTGGTGTGTTTAAACTCATGAAGTATG  
 GTTTCAGTGGATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTGAAGAGGATAATCATGGGTTAGARGGAA  
 GTGTTTGAAGATCACTTGAAGTGTGTTGGCCACACGAGTGAAGTCACTTCTGATATCCGACACTTGTG  
 GGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACAGCTTGGCATAGTGAACCTGTTCTATAAAA  
 ATAACTGTGCTTTGAGCATATGCTCTGGTCCAGCACTGAGAGGCTAGTGAAGATGCTGAGCCACAGAGCCAAAG  
 GTTGCAGTGAGCAAGTCACTGCACTGCACTCTAGCTGGCACAGAGTGAAGCCAAAAAATATATATATATTGAAAT  
 CAGGAGGAGCAAAATTTGACAGGGGAAGGAACTACTGCAAAACCACTAGGCTTTAGTAGGTACTTATATAAAATC  
 TACTCACTCTCTATTTAAAAAATGAGACACTGAAATACAGCTTAATATAGCTCAGATAGCTAATTAGGAA  
 ATTTCAAGTTGGCCAAATAGCAATCTCTCTGACATTTAAAAATAAATTTCTATTCAAAATACATGCAATTTGAT  
 TTACACCTCATCTGTGATAATTAATGTGATGTGGATTGCTGTGTCCAGCATGACCCATAAACAGGTGAGAGA  
 ATGATGGAATGTTTTAGAATAAACTCTGCTTATAGTATACACAGTTCAAGAGATGTTTAAAAATGCTTTTGT  
 ATTTACTGCCATGTAATTTGAAATATATAGATTATTTGAACCTTTCAACCTGAAATACAGCAGTATGAGAGTTTA  
 GTTATTTGATGTGCTAGTGTCTAATGAAGCTTTTAAATCTCAAAATTTCTCTTTTAAAAATATTTAAT  
 TGAAGGGAATATGAACATTCAGCTTAATTTCCCACTTATCTGTGTGAGACATTTGATCCCAATTTTGA  
 ATGGCTGTGTTTTACTCTTAAATAAATGAATTCAGAGAAAAAATAAAAAA



85/615

## **FIGURE 84**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE  
KGVVPCNIIIVGYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTT  
VWFYVGMAGAPCFILIQVLVLLIDFAHSWNESWVERMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS  
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIIGYNTT  
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV  
DNERDGVITYSYSPFFHFMFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGIVLYVNTLVAPLVLTNRDPD

10052586.013502



87/615

**FIGURE 86**

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFRRRGHLGIFHHHRH  
PGHVSHVPNVGLHHHHHPRHTPHLLHHHHHPHRIHPRIAR

10052586.011502

**FIGURE 87**

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTATTTGCAACGGTCAAGGCTGGCTTGT  
 GCCACAGCCGGCGCCCGCGCGGCACGACGACACACACCGGGGGAACCTTTTAAAAATGAAAGCTAGAAGA  
 CTTCCAGCGCGCGCCCGCGCTCGCGCAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAATCCCTCGCGTCCGGA  
 CGCCCGGGCCCCGGCTCGGCGCCCGCTGGGATGCTGACGCTCGCGCCCGGGCCCCAGAGCTGCTGCATCGAAG  
 GCGCGCGACGCTGCGAGCGCGCCCGCTGCGCCGTGTCCTCCCGCCCGCGGCCCTCTGCTCGCCCTGGCGGTGCTCT  
 GCTCGCGCCCTCGCAGGCGCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCTAGTGCCTCTGT  
 TCGAGTGGGAGCTCTGGATCCCACTGAGAGGCTTCGACTCCCAAGAAATCATCCAGAAAGTGTGTAATTCGACT  
 ACAACGGGAAGCAAGAACTGATCATAAATCTGGAAGAAATGAAGGTCTCATTTGCCAGCAGTTTTCACGGAAC  
 CCACTATCTGCAAGACGGTACTGATGCTCTCCCTCGCTCGAAATACACGGGTCACTGTTACTACCATGGACATGT  
 ACGGGGATATTCTGATTACGACGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAATAATGA  
 AAGCTATGTTCTTAGAACCAATGAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAAAGCTGAAAGCGGT  
 CCGGGATCATGTGGATCACATCACAAACACCAAACTCGCTGCAAGAAATGTGTTTCCACCACCTCTCAGAC  
 ATGGGCAAGAGGCATAAAAGAGAGACCTCAAGGCAACTAAGATATGTGGAGCTGGTGTATCGTGGCAGACAACCG  
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAATAAGTTAAGCAGCGATTAAAGAGATTGCTAATACAGTTGACAA  
 GTTTTACAGACCATTGAACATTCGGATCGTGTGTGTAAGCGTGGAAAGTGTGGAATGACATGGACAAATGCTCTGT  
 AAGTCAGGACCCATTACAGCCCTCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA  
 TGCAATGCGCAGCTTTGTAGTGGGGTTTATTTCGAAGGACCAACATCGGCATGGCCCCAATCATGAGCATGTG  
 CACGGCAGACAGCTCTGGGGGAATTTGTATGGACCATTCAGACAATCCCTTTGGTGCAGCCGTGACCTGGGACA  
 TGAGCTGGGCCACAATTTTCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCATGGTGTTCAGCAGTTGACGAGGAAGGACTT  
 GGAGACCGCTCGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCGCGAAGTCAGGGAGCTTTTCGGGGGCCA  
 GAAGTGTGGGAACAGATTTGTGGGAAGAGGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG  
 CTGCAATGCCACCACTGTACCTTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGAGTGCACGT  
 GAAGCTCGCAGGAACAGCGGTGACGGACTCCAGCAACTCGTGTGACCTCCAGAGTTCTGCAACAGGGGCCAGCC  
 TCACTGCCAGCCAAATGTACTTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
 CTGCGCAGACTCAGGACGAGCTGTGTACGCTCTGGGGACAGGTGCTAAAACCTGCCCTGGGATCTGCTTTGA  
 GAGAGTCAATTTCTCAGGTTGATCTTATGGCAACTGTGGCAAGCTTCGAAGAGTTCCTTTGCCAAATGGGAGAT  
 GAGAGATCTCAAATGTGGAATAAATCCAGTGTCAAGGAGGTGCGACGCCGCCAGTCATTTGTGCAATGCTCAATGTCA  
 CATGAAACAAACCTCCCTCTGCAGCAGGAGGGCCGATTTCTGTGCCGGGGGACCCAGCTGTACTTGGGCGATGA  
 CATTGCGGACCCAGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAATAATCTGCTGAATCGTCAATGTCA  
 AAATATTAGTGTCTTTGGGTTTCACAGTGTGCAATGCAATGCGACCGCAGAGGGGTGTGCAACCAACAGGAAGA  
 CTGCCACTGCGAGGCCCACTGGGCACTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC  
 CATCCGGCAAGCAGAAGCAGGAGCGAAGCTGCAGAGTCCAACAGGGAGCGCGCCAGGGCCAGGAGCCCTGGG  
 ATCGCAGGAGCATGCTCTGATGCTCTCACTGACATCATCTGAAGCCCTCCCATGACATGAGGAGCCGTGACCACTG  
 CTGCTGCAGAGGAGTGCAGCGTCCCCAAGGCTCTGTGACTGCGCAGCATGACTTGTGGCTTTGGCATGCTT  
 TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCTACCAGGACGCTGTGAGAA  
 CAGTGCAGGAAGAGGCGAGCATCTCTGGTTGAGCTTCTGCTAAAACATGGAGATGCTTCAGTGTGCTGCTCTGAG  
 AGAGTGCAGAGTTTACCACTCTGGCAGGCCCGAGCCCTGCAGCAAGGAGGAGGAGGATCAAAAGTCTGGCTTTTC  
 ACTGAGCTCCACAGCAGTGGGGGAGGAAGCAAGGGTGGGGCCAGTGTCCCTTCCCCAGTGACCACTCAGCT  
 TGGCAGCCCTGATGACTGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATATGAAAT  
 AGCAGGGTTTATGTTTAAATTTACAGACCCCTGCCACCAATTCATCTCAAGCAAACTGAATGGCAA  
 TGAACCAAACTGGAGGAAGAAGTAGGAGAAAGGGCGGTGAATCTGGCTCTTTCGCTGTGACATGCGTGAACGAGC  
 AGTACTCAGGTTTGAAGGTTTGCAGAAAGCAGGGAAACCCACAGAGTCAACCAACCTTCATTTTAACAAAGTAGAA  
 TGTGTAATAAGTGAAACAATGTAAGAGCTTAATCCATCCCCGTGGCCATTACTGCAATAAATAGAGTGCATTT  
 GAAAT

89/615

## FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLIALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIIPVKSFDSKNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYHGHVGRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHENTPNLAAKNVFPFPPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQKQKLEKVKQRLIEIANHVDFYRPLNTRIIVLVGVEVWMDMDKCSVSDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTITGMAPIMSMCTADQSGGIIVMDHSDNPLGAAVTLAHELGHNFGMNHDITLDRGCSCQMAVEKGCC
IMNASTGYFFPMVFSSCSRKDLTSLEKGMGVCLFNLPVRESFGGQKCGNRFVEEGEECDGEPPECMNRCCNA
TTCTLKPDVAACHGLCCEDCQLKPAGTACRDSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQVDGYCYNGICQT
HEQQCVTLWGPAGKAPAPGICFERVNSAGDPYGNCGKVSFSAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPLOQGGRIILCRGTHVYLGDDMPDPGLVLAGTKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVCNNRKNCHC
BAHWAPPFCDFKFGGGSTDSGPIRQAEARQEAESNRERGGQGEFVGSQEHASTASLTLI
```

### Signal peptide:

amino acids 1-28

10052535.011502

**FIGURE 89**

CTGCTGCATCCGGGTGCTCGGAGGCTGTGGCCGTTTGTGTTTCTTGGCTAAAAATCGGGGAGTGAGGCGGGCCGG  
 CGCGGCGGACACCGGGCTCCGGAACTGCACGACGCGGGCTGGACTGACCTGAAAAAATGCTCGGATTTCCTA  
 GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA  
 CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCAACCATGAAAAGATTTCAACCACTCA  
 TACCATGCCTCTGGTGTTATAGCAACCATAGCCTTCTTAATGATTAAATGCAGTATCGAATGGACAAGTCCGAGGT  
 GATAGTTACAGTGAAGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCTTT  
 GGTATCTGATTGCACTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCCTGGA  
 ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA  
 TGGCAGTGAACACATCTGATTTCCCAAGCACAAACAGCCCTGCATGGGTTTGTGTTGTTTTTACTGCTCACTCC  
 CAACCTTTGTAAATGCCATTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAATC  
 ACGAGAACACCTAAACAAACCAAAAACTTATTGTGGTATGCACCTGATTAACCTTATAAAATGTTAGAGGAAAC  
 TTTACATGAATAATTTTGTCAAATTTTATCATGGTATAATTTGTAATAAAGAAATTAACAAAGAAAT  
 ATGGATTTGTCAATGTAAGTATTTGTCTATCTGAGGTCCAAACCAACAAATGAAGTGTCTGAAGATTTAATGT  
 GTTTATTCAAATGTGGTCTCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTAGTTTTTAAAAATATCC  
 GTGGTCAAATTTCTCTCACTATAATTGGTATTACTTTTACCAAAATTTCTGTGAACATGTAATGTAACCTGGC  
 TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACAGGCTCCCTG  
 TGTCCCTTCCATGGGAAGGTCTCCGCTGTGCTCTCATTTCAAGGGCAGGAAGATGTGACTCAGCCATGACACG  
 TGTTCTGTGGGATGCACAGTCACTCCACATCCACCACTG

10022536-07502

91/615

**FIGURE 90**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAYIPTMKDFNHSYHACGVIATIAFLMINAVSN  
GQVRGDSYSEGLGQTGARIWLPVGFMLAFGSLIASMWILPGYVAKEKDIVYFGIAVFFQNAPIFFPGLVFKFG  
RTEDLWQ

105256-01502

**FIGURE 91**

CGACGCCGGCGTGAITGGCTTCCGCTGGTGTGCTCTCTGGCTGTCTGCTGCTGGCCGCTCTCTCTGCAAAAGTTTA  
 CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGGCCCCAGCGCCCTGGTAAAC  
 TGACAAGGAGGCCAGGAGAAGGTTCTCAAACAAAGCTTTTTCAGCCAAACAAAGTGC CGGAGAAGCTGGATGTGGT  
 GGTAAATTGGCAGTGGCTTTGGGGGCCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAGCGAGTCTCTGGTGT  
 GGAAACACATACC AAGGCAGGGGGCTGCTGTATACCTTTGGAAAGAAATGGCCCTTGAATTTGACACAGGAATCCA  
 TTACATGGGCGTATGAAGAGGGCAGCATTTGGCCGTTTATCTTGGACAGATCACTGAAGGGCAGCTGGACTG  
 GGCTCCCGCTGTCCTCTCTTTTGACATCATGGTACTGGAGGGCCCAATGCCGGAAGGAGAACCCATGTACG  
 TGGAGAGAAGCCATCACTCAGGGCCCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA  
 GCTGGTTAAGGTGGTATCAGTGGAGGCCCTCATGCCATCCTGTTGAAATTCCTCCCATGGCCGCTGGTTACGCT  
 CCTCGACAGGTGTGGGCTGCTGATCGTTTCTCTCCATTCCTTCAAGCATCCACCCAGAGCCCTGGTGGAGTCTCT  
 GCAGCAGCTGGGGCCCTCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCACCTTACGCTGTGACCCCCAA  
 CCACAGTGGCTTTTTCATCACGCCCTCTGTGTCAAACATACATGAAGAGAGGCTTTTATCCCGAGGGGGTTC  
 CAGTGAATTTGCTCTCCACACCATCCCTGTGATTGAGGGGGCTGGGGGGCTGTCTCTCAAAAGGCCATGTGCA  
 GAGTGTGTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGAAGAAGGGCATGAGCTGGTGAAACATCTA  
 TTGCCCATCTGGTCTCAAACGAGGACTGTTCACACCTATGAACACCTATGCGGGGGAAGCCCGCTGCTCT  
 GCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGCCCGGCTTAGGCATGACCTCTGTTTTCATCTGCCGTGGAGG  
 CACCAAGGAAGACCTGATCTGCTGCCCTCCACCAACTACTATGTTTACTATGACACGGACATGGACCAGGCGATGGA  
 GCCTACTCTCTCATGCCAGGGAAGGGCTGGGAACATCCCTCTCTCTCTGCTTCTCCATCAGCAA  
 AGATCCGACCTGGGAGGACCGATTCCCAGGCCGCTCCACCATGATCATGTCTATACCCACTGCCATGAGTGGTT  
 TGAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGACTATGAGACCTTCAAAACTCCTTTGTGGAAGC  
 CTCTATGTCAGTGGTCTCGAAACTGTTCCACAGCTGGAGGGGAAGGTGGAGAGTGTGACTCGAGGATCCCACT  
 CACCAACAGTCTTATCTGGCTGCTCCCGAGGTTGCCCTGCTACGGGGCTGACCATGACCTGGGGCGGCTGCACCC  
 TTGTGTGATGCGCTCTTGAAGGCCAGAGCCCATCCCAACTCTATCTGACAGGACAGGATATCTTCACTGT  
 TGGACTGCTCGGGCCCTCAAGGTGCCCTGTGTGTCAGGAGGCCCTCTCTGAGGCGGAATCTCTCTCAGACCT  
 TAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAGAAATAGTTCCATCAGGAGAGGATCAGAGGAATTTG  
 CCAATTTGGTCTGGGGCATCTCCCTGGACTTACCATAATGTCTTTCTGCAATAGTTCCTTGACAGTATAAAGCACT  
 CTAATTTGGTCTGATGCCCTGAAGAGAGGCCCTAGTTTAAATCACAAATCCGAAATCTGGGGCAATGGAATCACTGC  
 TTCCAGCTGGGCGCAGGTGAGATCTTTACGCCCTTTATAACATGCCATCCCTACTAATAGGATATGACTTGGATA  
 GCTGTGATGTCTGATGAGAGGGGGCTCTGCATCCCTCAACCATCTCTCTAACTCAGTGTACAGCAAGTAATTT  
 CCATCTGTGATAGAACCCCTGGCAGTGTGTGACGTCAACCTGTGGTTCAGTTCTGTCTGAGCTCTGCT  
 CTCTATCTATTGATGCTACGCTCAGCTCAGTTCTACACTGTCAAGGGAAAGGAGAGCTAATGAGGCTTAACTCAAA  
 ACCTGGGGCTGGTTTTGGTTCGCAATCCATAGGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCACTGGCT  
 CTTCAAGGGACAGGAAATGCCGTGTCTGGCCAGTGTGGTCTTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT  
 TAGTAGGGTGCAITGTGATGATCATATCCAATTCTATGGAAGTCCCGGCTGTGCTCTCTTATCATCTGGGGTG  
 GCGAGTGTGCTCAATGTCCAGCAGGAGCTCAGTACTGAGCTCATCAAGCTGATCAACCAATCAAGG  
 GAAGGCTGATCAGGGAAGGGTGTACATCAGGAGTCAAGGCTCAGGCTAGGACTGGTAAGATGAATCTTTGCTGGGCTGAA  
 GCAGGCTCGAGGGCAITTCAGCCAAAGGGCAGCAGCAGGGGACAGTGCAGGAGGTTGGGGTAAGGAGGGAGTCA  
 ACATCAAGAAAAGGGAAAGCAAGGAATGTGTGTGAAGCCCAAGAAATGGCAATTTGCAATTAATTAGCAGATGTGAG  
 GGTTAGACAGGTAGTGTGATGCAGGCTCAAGGTTTGGAAAGAAAGTCTTTTCAAGTATTTTGGTATCAGACAT  
 ACAGAAAGTCTTTTGTAGTTCTGTTTAAAGTAAACATTAATAAATTTATGATTCATGCTTTGAAAAA  
 AAAA



93/615

## **FIGURE 92**

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDKRPPAPLVTDKKARKVLKQAFSANQVPEKLDVVVIGS  
GFGGLAAAAIILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIGRPTILDQITEGQLDWAPLS  
SPFDIMVLEGPNGRKEYPMYSGERKAVIQGLKEKFPQBEATIDKYIKLVKVVSSEGAPHAILLKFLPLPVVQLLDRC  
GLLTRFSPFLQASTOSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAPFSMHALLVNHYMKGGFYPRGGSSEIA  
FHTIPVITQRAGGAVLTKATVQSVLDDSAGKACGVSVKKGHELUNIIYCPITVVSNAGLFNTYEHLLPGNARCLPGVK  
QQLGTVRFGGLGMTSVFICLRGTKEDLHLFSTNIYVYYDTMDQAMERYVSMFREEAAEHIPLLFFAPPSAKDPTW  
EDRFPRSTMIIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLFQLEGKVESVTAGSPLTNQF  
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPINLYLTGQDIFTGCLVGLALQGALLCSSAILKRNLYSDLKNLD  
SRIRAQKKKN

10052586.011502

**FIGURE 93**

GGGAAAGATGGCGCGCACTCTGGACCCCTTGGGTCGTGGCAGCAGTGGCGCGCATGTTTGTGCGGCTCGGGATGG  
 GTCCAGGATGTTACTCCTTCTTTTGTGGGGTCTGGGCAGGGGCCACAGCAAGTCGGGCGGGTCAAACGTT  
 CGAGTACTTGAACCGGAGCACTCGCTGTGCAAGCCCTACCAAGGTTGGGCAAGGCAGTTCCTCACTGTGGAA  
 TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCTTACCCAGATATGCAAAAGTAAACAGGGTGCCCT  
 GTGGAAACCGGGTGCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAAATCCATGGACAAGGAAAGAA  
 GAATCTGCATGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCTGTGTTTGGAAACAT  
 GGAACAAATTTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC  
 CTACATCTCAGCCATGGTGAAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGGCGGCCCTACAGAGCTGGG  
 AGGCTGCACAGCCATTGTCCGCAATCTTCAATACGACACCTTCTGTGATTCGTACGTCAAGAGGCATTGTGAC  
 GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCTGCCCGCGG  
 CTACTACTTCCGCACTCTCCATCACTGCGGGATCTCTCAGATAATCATGATGTCACTTCCCTGAAGTGTGTTGA  
 ACTGACAGTGGAGAGAACCCAGAGAGGAAAGCTCCATCGAGATGTGTTCTTGGCCCTCAGTGGACAATATGAA  
 GCTGCCTGAGATGACAGCTCCACTGCCGCCCTGAGTGGCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGT  
 GTTTTCTGTATTTGCCATAGTCATTGGTATCATACTCTACAACAATGGCAGGAACAGAGCCGAAAGCGCTTCTA  
 CTGAAGCCCTCTGCTGCCACCACTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCCTGGCCTGAGCA  
 TGCAGCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTGAATGCAGG  
 GACCCCGCATTCCTCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT  
 GCTGTGATGTGCCTTCCCTCGATCCTTCCATGTGGGAGCAGAGGTGTGAAGAGAATTACGTGGTTGTGATGC  
 CAAAATCAGAGAACAGAATTTCTAGCCAGGCTCCGTTGTTTGTACTCAGAAGGCCCTTCTACTTCACTTTT  
 GAATCCACAAGAATTAATAAAGTGTAAACACACAGGCTTTCTGACCATCCATTCGTTGGGTTTGTGATTGAAC  
 CAACCCCTCTGCTACTCTGAGGAGCTTTCTTGGAAACAGGATGGAACCTTCTCCCTGCCTTACCTTCTCTTCA  
 CTGCATTCACTGCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTGGATGCCTCTCTGTTGGGGCTGGGG  
 CTGCAGAACACACTGCTTTCACTGGCCTTCAATAGGTGGCCCTTAGGGAGATGGCTTCTGCTTGGATCACTG  
 TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTCAGGCCCTCAGTGAA  
 GTTTGGCTAAAGGTTGGTGTAATAAATCAAGAGAAGCTGGAAGACATCATGGATGCCATGGATTAAGTGTGCAAC  
 TGACAGCTCCAGGTTTGTATCAAAACCAAAAGCAACATTGTGATGTGGTCTGACCATGTGGAGATGTTTCTGGAC  
 TTGCTAGAGCTCTGCTAGCTGCATGTTTGTAGTTACGATTTTGGAAATCCCACTTTGAGTCTGTAAGTGTGAAG  
 GAAGCTTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTCTTCTTAAATGGACAA  
 GAGACAGTTGCTGTCTCATGTTCCAAAGTCTGAGAGCAACAGACCTCATCATCTGTGCTGCAAGAGTTCACTG  
 TCAATTGAGCAGCAGCGCTGAGTCTGGCTCTGTCAACCTTATTCCACTGCTTATTTGACAGGGGTATCAT  
 GCTGCTCACTTACTGCTCTGGGATTAATCACTTACAGGCCAGAGTCTCTTGGAGGGCCTGGAACCTCTGAGTC  
 CTCTTAAGACCTCTGTAGCTTAATGAAATCTTAAATCACCAGTGAACCAAAAAAAGGGGCG  
 GCGCGCATCTGAGAGTCAGCTGAGTGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

95/615

## **FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSA RDGSRMLLLLLLLLGSGGQGPQQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGGALWNRVPCFLRDWELQVHFKIHQGGKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDITYPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFYTSSITGDLSDNHDVISLKLFEFLTVERTPEEEKLRDVFPLPSVDNMKLP
EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
```

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

2025-10-08 14:55:00

**FIGURE 95**

CCTGTGTTAAGCTGAGGTTTCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA  
 ACCTCGAGCTCACACCAACAGACACAGCGCGGCATACACACTCGCTCTCGCTTGTCATCTCCCTCCCGGGGGAG  
 CGGGCGCGCTCCCACCTTTGGCGCACACTCCGGCGAGCCGAGCCGCGCGCTCCAGGATTTCTGGGGCTCGGA  
 ACTCGGATTCGAGCTCTGAACCCCATGCTGGTGTCTTTAAACACTCTTTTCCTCTCTTCCTCGTTTGTATGTC  
 ACCGTTTCCATCTGGGGCTAGAGAGCAAGCGCAGCAGCTTCCAGCGAGCCCTTGTGGCTTGGCATCTGCCA  
 TCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGGCTGCTGCTCCCTCCGCTGGCAGAAAGGGGTG  
 ACGCTGGGCAGCGCGAGGAGCGCGCTGCCCTTGGCGGGCTTTCGGCTTGAGGGCAAGGTGAAGAGCGCAC  
 CGGCCGTGGGGTTTACCGAGCTGGATTGTATGTTGCACCA**TG**CCCTTCTTGGATCGGGCTGTGATCTCTCCCT  
 CTTGGGGCTGCTGCTCTCCCTCCCGCGGGCGGATGTGAAGGCTCGGAGCTCGGAGAGGTCCGCCAGGCGTA  
 CGGTGCCAAGGGATTTCAGCTGGCGGACATCCCTACAGGAGATCGCAGGGGAACACTTAAGAAATCTGTCCTCA  
 GGAATATACATGCTGCACCAAGAAATGAAGACAAGTTAAGCCAACAAGCAAACTCGAAATTTGAAAACCTTGT  
 GGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCAGGCATAAGAAATTTGACGAATTTTTCOGAGAGCT  
 CCTGGAGAAATGCAGAAAAGTCACTAAATGATATGTTGTACGGACCTATGGCATGCTGTACATGCAGAAATTCAGA  
 AGTCTTCCAGGACCTCTTACAGAGCTGAAAAGGTAACAATGGGGTAATGTGAATCTGGAGGAAATGCTCAA  
 TGACTTTTGGGCTCGGCTCTGGAAACGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGAAGACTACCT  
 GGAATGTGTGAGCAAATACACTGACCACTCAAGCCATTTGGAGAGCTGCCCGGAAACTGAAGATTCAGGTTAC  
 CGCGCCCTTCACTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAAGTTGCAACCCAGGTTTCCAA  
 GGTGAGCCCAACCCAGGGGTGATCCGTGCCCTCATGAAGATGCTGTACTGCCCATCTGTGGGGGCTTCCAC  
 TGTGAGGCCCTGCACCAACTACTGTCTCAACGTCATGAAGGGCTGTTGGCAAATCAGGCTGACCTGCACACAGA  
 GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCA  
 GGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAACAGCATGCAGGTGTCTGCAAAAGGT  
 CTTTCAGGGATGTGGTCAGCCCAACCTGCTCCAGCCCTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATAC  
 ACGTTTCAGGCCCTTACAATCTGAGGAAAGACCAACAACCTGCTGACGGCACAAGCTTGGACCGGCTGGTACAGA  
 CATAAAGAGAAATTTGAAGCTCTTAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAGGACGAGAGCGT  
 GACAGCGGCGACGTCCAACGAGGAGGAAATGCTGGAAACGGGCACAGCAAGGCAGATACTTGCCTGAGATCATGAA  
 TGATGGGCTCACCAACAGATCAAGCAATCCGAGGTGGATGTGGACATCACTCGGCCGTGACATTTTATCAGACA  
 GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGA  
 CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGATGATGCTGTGTCACCCAGGATTTGAGTT  
 TGTCCACCAAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGATCTTTCTGCGCCAGCGGTGGCCACTC  
 CTTGCTCTCTGGCTCTCACCTGCATGCTTCCCTGGCACTGCAGAGACTGTGCAGATA**TAAT**CTGGGTTTTTGGTCA  
 GATGAACCTGCATTTTAGCTATCTGAATGGCAACTCACTTCTTTTCTTACACTCTTGGCAATGGACCATGCA  
 CAAAACTTACGTTTTTCTATGAGAAAGAGACGATGATGCAATCTGCCCTCCCTTTTGGTTTTCCCAAGAGTACC  
 GGGTGCCAGACTGAAGTCTTCTCTTTCTTCTCAGCTATCTGTGGGACCTGTGTTATTCTAGAGAGAAATCTTCA  
 CTCAAAATTTTTCGTAACAGGAGATTTTCTACCTTCATTGCTTTTATGCTGCAGAGTAAAGGAATCTCAGGTT  
 GTGAGGGTTTTTTTCTCATTTAAAAAT

97/615

## FIGURE 96

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWGAVILPLLGLLSLPAGADVKAQSCGEVROAYGAKGFSLADIPYQEIAGEHLRIPCPOEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELENAEKSLNDMFVRTYGMLYMONEVFPDLFTELKRY
TGGNVNLEEMLNDPFWARLLERMFLINPQYHFSEDYLECVSKYTDQLKPPGDVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMMKGCLANQADLDTEWNLFIDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNMQENSMQVSAKFVQCGQPKPAPALRSARSAPENFNTRFRFPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGMDDVCPTEFEFVTTTEAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

### **Signal peptide:**

amino acids 1-23

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

AGCGGCTCCGTGAGGGGGCCCTTTGGAGCGGGGTAGTGTGTTGGTGTCCCTGTCTTCGGTGATATGGACAACATG  
AAGCTTTCTCGACCACTGGACTTGAAGAAAGATGACTCTGTAAGCGGACAGACTTTACTTGGCCGGCCGGCGCTCT  
TCATCCCCCGTAAGGAGCGAGTCTCTTTGTACTGACATCCAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAA  
TGGGAAGGTTTGTATGAAAACTACAGCTGAGAGATTCAGACATAGAGTTGGTGTCCAAAGAAGCTCTCAAAAGCTTG  
CAGAAATTTATCAACCTTTGTTGGAAGCTTATTATGACATACCAATTTTTCATAGATTTGGCTCGGTGTTCAT  
AGTCCAGGCGGAGATCTCTCGGACAGAGGAGTGTGGAGATCTATCTATGAGGAGCCCATCAAGATGAGTCT  
TCATTCCAGGTTGCTCTTTAATCGGACAGAGAGTGGTGTGCATGCGCAATCTGCTGTTCTCATGATATGCGACCA  
GTCTTTCTTCACATCGGGTGCAGACAGATGAATTAACATTAAGCATACCATCTCTTGGAAAGGTTTACAGGGGATCA  
AGTATAAACAATGTGTGCGACTGTCAAGAATGAGACATGATGATGACGAGAAGACACATATCCACAACAAATAAA  
AAGCTGTGAGGTTTGTGTTAACTCTTTGATGACATCTTCCAGGGAAGATTAAGAGGCTGAAAAAGAGGAAAC  
AGAGGAGGAAGTAAAGAAATGAAACCAAGGACAAAAAATTTAGTTACTTTCATTTGGAGAGGAGAGCTGA  
GGAATGAGGAGGAGGATGAATTCAGTTAGTCAGAGCATGAGAGGCGAAAAGCAAAGATGATGATCTGCTTAA  
GGAATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAGAGGATGTGACACAGATTTAGTTGATGATGG  
AGAAGATGAAGTGCAGACAGATGATGAATATTTGATGGTGAATGAAAGAACTGATGAGAGAGAAAGATGCCACA  
AAAAATAAAAAGACACAAGTGCAGATTTAAATTCAGCTGGAGAGGAGAAGTGGAGAAGAAATCATGTCAGCG  
CAGTGAAGAGCTCAGAAAAGAACCAAGACATTAAGAACCGGAACCTTTACGACAGACAAAAAAGATGAGAAA  
TGCAGCAAAACCAAGCAAAAAAGAGTGAAGAGGAGAGGCCCTCCAGATGTTGTGTCGCAATACAGAG  
AGAAAAGCAAGAGATGAAGCTTTGAGGAAGCAACAGTCAAGAGAGGGAATCTCCCGGAGAGATCAGACCTTGC  
ACTGCTGAACACGTTTAAATCTAAATCACTCAAGCAACTTGCCTGAACACCTGAAATGACATTTCTGAAACAGA  
AGTGAAGACATGATGAAGGATGATGTCATGTACTTCAGTTTGAGGATAAAGACAGAAAGTGTGAAGATGCAAG  
CATCGACAGATCATGATACATTTGAAATCTGATGTTCTCGGAATCCAGTGATTAATAAGAGGAGGAGAAAGACAA  
AAAGCTGTAGTAGAGACAAAAAAGGAAGAGCAATAAATGAGATATGATACACAGCAATCTGCTGGAATTTGTCCT  
ACATGTGCCCTTTGAACACGCAATTTCCCAACAGCATCACTAGGGGTGTGAAAAGAGATTTTGTGAACCTGTT  
GTCTGGTTTGAAGAACCAATATCTGTTTGAACATGTGGAATGATGAGCAAAATGCTTTTGGTATCTGGTAT  
CATGTGTTTTCCTGATGACCTTTTATATTTGCTAAATCTGAAATAAAATAACTTTCCTTCACAAAAAAGAAAA  
AAAAAAGAAAAAAGAAAA

99/615

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESYIGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFNFPDDIIPREIKRLKKEKPEEEVKLLKPKGTKNFSLLSFGEEAEVEEVRVVSQSM
KGKSKSSHDLLKDDPHLSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMREIRIAKKLKKDTSANVKS
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKVENAAKQAEKRSEEEAAPPDGAVAEYRREKQKYEALRKQQS
KKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQDSDTFEIYDPR
NPVNKRREESKKLMREKKERR
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

2025.01.15.01.00.00

100/615

## FIGURE 99

CTTTCTGAGGAACCAAGCAATGAATGGCTTTGCATCCTTGCTTGAAGAAACCAATTTATCCTCCTGGTACTA  
TTTCTTTTGCAAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCCTACCGCTGAAGTCTGTGCCACACACA  
ATTTACCAGGACCCAAAGGAGATGATGGTGAAGAGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA  
CGCATGGGGCGAAAGGAATTAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCC  
ATTGGGAAGAGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAGCAGGTACTGTC  
TGTGATTGTGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG  
TTTGTCAAGAAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATTTCTACTACATCGTGCAGGAAGAGAAGAAC  
TACAGGGAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACA  
CTCATCGTGAATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGA  
CAGTACATGTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT  
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT  
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCTACGTATTTGCTATTTTCCTGTGACCGTCATTA  
CAGTTATTGTTATCCATCCTTTTTTCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAA  
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

10052586-011502



101/615

## **FIGURE 100**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQISLGLDIDSRPTAEVCATHTISPGPKGDDGEEKGDPGEEGKHKGVGRMGPKGI
KGLGDMGDQGNIGKTGPIGKKGDKGEKGLIGIPGEKGAGTVCD CGRYRK FVGQLDISIARLKTSMKFVKNVIA
GIRETEKFFYYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDL LEREGQYMSTDN
TPLQNYSNWNEGEFSDFYGHEDC VEMLSSGRWNDTECHLIMYFVCEFIKKKK
```

**Signal peptide:**  
amino acids 1-25

1002585.01302

**FIGURE 101**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGAGCCCCAACCCCGACCCAGAGCTTCTCC  
 AGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCCTTAACTTCTCCGCGGGGCCCAGCCACCTTCGGGAGTCCGGGTT  
 GCCACCTTGCAAATCTCCGCTTCTGCACTGCCACCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCA**ATG**GCCA  
 ACGCGGGGCTCAGCTGTTGGGCTTCAATCTCGCCTTCTGGGATGGATCGCGCCATCGTCAGCACTGCCTGTC  
 CCCAGTGGAGGATTACTCCTATGCGCGGCGACAAATCGTGACCGCCAGGCCATGTACAGAGGGGCTGTGGATGT  
 CCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCAATTGC  
 AAGCAACCCGTGCTTGTATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGCATGA  
 AGTGATGAAGTGCTTGGAAAGACATGAGGTGCAGAAAGATGAGGATGGCTGTCAATGGGGGTGCGATATTTCTTC  
 TTGCAGGTCTGGCTATTTTAGTGGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAATCTATGACCCATATGA  
 CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCTTCTGG  
 GAGGTGCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAAACCAAGGCCCTATCCAAAACTG  
 CACCTTCCAGCGGGAAAGACTACGTGT**G**ACACAGAGGCAAAAGGAGAAAAATCATGTTGAAACAAACCGAAAAATGG  
 ACATTGAGATACATCATTAACATTAGGACCTTAGAATTTGGGTATTGTAATCTGAAGTATGTTATCAAAAC  
 AAACAAACAAACAAAAACCATGTGTTAAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTCTTTTC  
 CTCATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCAATTGAGTAATCATACTCAAAATGGGGGAAGG  
 GGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTCTATTAAAAATAGACAGTAAAAATACTATTCT  
 CATTTATGTGATACTAGCATACTTAAAAATCTCTAAAAATAGGTAAATGTATTTAAATCCATATTGATGAAGATG  
 TTTATTGGTATATTTCTTTTTCGTCTTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCAATAGC  
 TTTGGGTGCCTTTGGCCACAAGACCTAGCCATAATTACCAAGGATGAATTTCTTCAATCTTTCATGCGTGCCCTTT  
 TCATATACTTATTTTATTTTTTACCATAATCTTATAGCAGTTGCATCGTTATTAAGCCCTTATTGTGTTTTGTTT  
 TCATTGGTCTCTATCTCCTGGAATCTAACACATTTATAGCCTACATTTTAGTTTCTAAAGCCCAAGAAGATTAT  
 TACAATACGAACCTTTGGAGGCAAACTTTCTGCATGAACAAAGTGATAAATCCGTGTGACCTTCCACACAAT  
 CCGCTACTCTGACCCATAGCAGCTTTGTTTGTCTTTGAAATAATTTGTCATTTAGTATGCTAGCTGCTGTCC  
 CCAGGTGTGTAACACAACCTTATTGTATTGAATTTTTAAGCTACTTATTCTATGTTTTATATCCCCCTAAACATC  
 CTTTGTGTCGCCATTCCTTAATTTGATTTGTTTTTCCCAAGTGTAATATCATCGGTTTTATATCTTCTTAATAAG  
 GTGGGTCTGTTTTCTGTAACAAAGTGCTAGACTTTCTGGAGTATAATCTGGTGACAAATATTTCTCTGTAGC  
 TGTAAGCAAGTCACTTAATCTTTTACCTCTTTTTTCTATCTGCCAAATGAGATATGATACTTAACAGTTAG  
 AAGAGTGTGCTGAATATAATTAGTTTTATATTACTCTTATCTTTGAACATGAACATATGCTATGTAGTCTT  
 TATTTGCTCAGCTGGCTGAGCACTGAAGAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATTCAGTG  
 CCTTCTCTCTCTACAGTCTATTTCCACTGAACAAACCTACACATACCTTCATGTGGTTCAGTGCCCTTCTCT  
 CTCTCTACAGTCTATTTCCACTGAACAAACCTACGCATACCTTCATGTGGCTCAGTGCCCTTCTCTCTCTA  
 CCAGTCTATTTCCATTTCTTCACTGTGTCTGACATGTTTTGTGCTCTGTTCCATTTTAAACAAGTCTCTTACTTT  
 TCCGCTCTGACAGAAATGCTATTTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG  
 ACCTGGATTTGAGTCTTTGGTCTATCAATCACCGCTCTGTGTTTGGAGCAAGGCATTTGGCTGCTGTAAGCTTATTG  
 CTTCACTCTGAAGCGGTGGTTGTAAATCTCTGATCTCCCACTCAAGTGTGTTGTGGGGATCCAGTGAGATA  
 GAATACATGTAAGTGGTGGTTTGTAAATTTAAAGTGCTATACTAAGGGAAGAAATTTAGGAATTAATGTCATAC  
 GTTTTGGTGTGCTTTTCAAATGTTTGAATAAAAAAATGTTAAG

103/615

## **FIGURE 102**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCVSVQSTGQIQCKVFD SLLNLSS
TLQATRALM VVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMIPVNARYEFGQALFTGWAAASLCLLG GALLCCSCPRKTTSYTPRFPYKPPAPSSGKDYV
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

**N-glycosylation site.**

amino acids 72-75

**PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

**ABC-2 type transport system integral membrane protein**

amino acids 119-133

103/615-01502

**FIGURE 103**

CCCACGCGTCCGCGGACGCGTGGCTGGACCCAGGCTCTGGAGCGAATTCCAGCCTCGAGGGCTGATAAGCGAGG  
 CATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTTGGTGGTTGGAGGCGCGCAGTATAGAGCAGCAGCACAGGCGCG  
 GGGTCCCGGAGGCGCGCTCTGCTCGCGCGGAGATGGGAATCTCCTTCACGAAACCGCATCGGCTGTGGCCACC  
 GCGCGCGCCCGCGCTGGCTGTGGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTCTCTCGGCTTCCCTCTTC  
 GGGTGGTTTATAAAATCCTCCAATTGAAGCTACTTAACATTACTCCAAAGCATAATATGAAGCATTCTTTGGATGAA  
 TTGAAAGCTGAGAAACATCAAGAACTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC  
 TTTACAGCTTGCAAGCAAAATCAATCCAGTGGAAAGAAATTTGGCTGGATTCTGTGGAGCTAGCTCATTATGAT  
 GTCTCTGTTGCTTACCCAAATTAAGACTCATCCAACTACATCTCAATAATTATGAAGATGGAAATGAGATTTTC  
 AACACATCATTATTTGAACCACTCTCTCCAGGATATGAAAATGTTTCGGATATTTGTACCACCTTTTCAGTGCTTTC  
 TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGATGTTAACTATGCACGAACTGAAGACTTCTTTAAATTTGAA  
 CGGGACATGAAAAATCAATTGCTCTGGGAAAAATTTGTAATTGCCAGATATGGGAAAGTTTTCAGAGGAAAAATAGGTT  
 AAAAATGCCAGCTGGCAGGGGCGAAAGGAGTCAATCTCTACTCCGACCCTGCTGACTACTTTGCTCCTGGGGTG  
 AAGTCCATTCACAGCGTTGGAACTCTCTGGAGGTGGTGTCCAGCGTGGAAATATCTCAAAATCTGAATGGTGCA  
 GGAGACCCTCTCACACCAAGTTACCCAGCAAAATGAATAGCTTATAGGCGTGGAAATTCAGAGGCTGTTGGTCTT  
 CCAAGTATTTCTGTTTATCCAATTGGATACTATGATGACACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGCACCA  
 CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAAACTTTTCTACA  
 CAAAAGTCAAGATGCACATCCAATCTACCAATGAAGTGAACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA  
 GCAGTGGAAACACAGACAGATATGTCATTCTGGGAGGTCAACGGGACTCATGGGTGTTGGTGGTATTGACCCTCAG  
 AGTGGAGCAGCTGTTGTTTATGAAATTTGTGAGGAGCTTTGGAACTGAAAAAGGAAGGGTGGAGACCTAGAAGA  
 ACAATTTTGTGTTCAAGCTGGGATGACAGAAATTTGGTCTTCTTGGTCTACTGAGTGGGCAGAGGAGAAATTC  
 AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAGGAAACTACACTCTGAGAGTT  
 GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA  
 GGCAAATCTCTTATGAAAGTTGAGCTAAAAAAAGTCTTCCCCAGAGGTCAGTGGCATGCCAGGATAGCAAA  
 TTGGGATCTGGAAATGATTTTGGAGTGTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCACGGTATACCTAAA  
 AATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATACAGAGTGTCTATGAAACATATGAGTTGGTGGAAAAAG  
 TTTTATGATCCAATGTTTAAATATCACTCACTGCTGGCCAGGTTTCAGGAGGGATGGTGTGATGATAGCCAAT  
 TCCATAGTGTCTCCTTTGATTGTGCGATATGCTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATT  
 TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTTGATTCACCTTTTCTGCACTAAAGAAATTT  
 ACAGAAATTTGCTTCCAGTTCAGTGAGAGACTCCAGGACTTTGACAAAGCAACCCAATAGTATTAAGAATGATG  
 AATGATCAACTCATGTCTTCTGGAAAGAGCATTATGATCCATTAGGTTTACCAGACAGGCTTTTATAGCAT  
 GTCATCTATGCTCCAAGCAGCCACAACAAGTATGAGGGAGTCAATCCAGGAATTTATGATGCTCTGTTGAT  
 ATTGAAGCAAAAGTGAGCCCTTCCAGGCCTGGGAGAGAGTGAAGAGAGATTTATGTTGACGCTTCCAGCT  
 CAGGCACTGCAGAGACTTTGAGTCAAGTAGCTTAAGAGGATTTTTTAGAGAAATCCGATTTGAATTTGTGTGGTA  
 TGTCACTCAGAAAGAAATCGTAATGGGTATATTGATAAAATTTTAAAAATTTGGTATATTTGAAATAAAGTTGAATATT  
 ATATATAA

105/615

## FIGURE 104

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFDELKAENIKKFLH
NFTQIIPHLAGTEQNFQIAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISITNEDGNEIFNTSLFPPPPPG
YENVSDIVPPPSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVARIYRGKVKRGNKVKNAQLAGAKGV
ILYSDPADYFAPGVKSYPDGNLFGGGVQQRGNILNLNGAGDPLTPGYPANETAYRRGIAEAVGLPSIPVHPIGYY
DAQKLEKMGSSAPDDSSWRGSLKVPYVNVGPGFTGNFSTQKVKMHIHSTNEVTRIYINVIGTLRGAVEFDRIYVILG
GHRDSWVFGGIDPQSGAAVVEHIVRSFGLKKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSKLLQERGVAIY
NADSSIEGNYTLRVDCITPLMYSILVHNLTKELKSPDEGFEGKSLYESWTKKSPSPFSGMPRIKLGSGGNDFFVFF
QRLGIASGRARYTKNWETNKFSGYPLYHSVYETELVEKFYDPMFKYHLTVAQVRGGMVFLANSIVLPFDCRDY
AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFYERLQDFDKSNPIVLRMMNDQMLFLERAF
IDPLGLPDRPFYRHVYAPSSHNYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAEITLSEVA
```

### Signal sequence:

amino acids 1-40

### N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463, 476-480, 638-642

### Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

### N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366, 427-433, 529-535, 707-713

105/615

**FIGURE 105**

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTCTTATTACTGCTGCGTTTATGTGTGGGAATT  
 CCTCTCTTATGGCTTGTCTTGGAGCCACAGAAAACCTCTCAAACAAAGAAAGTCAAGCAGCCAGTGGCATCTCAT  
 TTGAGAGTCGAAGCTGGCTGGCTGTGGAACCAATTTTCTACCAAGAAATCAACACTAGCTACATCACATC  
 GGCAGCTAAGATCTGATTTAGACAATGGAACAATTTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAGT  
 ACTTTTATCATTGATGAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC  
 ATCTTAAGAGCCCAAGTAAATAGACATCGCTATCGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTTCATCAAAGTT  
 TCGATATCAATGACAAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTTGATCCAGAGATGTCTCCAGAA  
 GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATATGCTGCTCTCCCTAC  
 AGCTTACTTCAAGGCCAGCCATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAAATATCTTCTAAATGGAT  
 AGAGAAGTCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA  
 ACAACAAGTGATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAGTTTATACCGCTTG  
 ACTGCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT  
 GCAGAAATGGATTACAGCATTGAAGAGGATGATTCCGAAACATTTGACATTATTAATAATCATGAAATCAAGAA  
 GGAATAGTTATTTAAAAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAAC  
 CATCATGTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAGGTGGAAGAT  
 GTTGATGAGCCTCCTCTTTCTCCTTCCATATTATGTAATTTGAAGTTTGTGAAGAAACCCCAAGGATCATTT  
 GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAAGT  
 TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAATCAGTGCTTGGTACAACCTA  
 AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC  
 AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAATGCAAGCTCTGGTCAGGTAAAT  
 CAGACTATCAGTGCAGTGATAGAGATGAATCCATAGAAAGCACCATTTTTACTTTAATCTATCTGTAGAAGAC  
 ACTAACAAATCAAGTTTACAATCATAGATAATCAAGATAACACAGCTGTCAATTTGACTAATAGAAGCTGGTTTT  
 AACCTTCAAGAAAGACCTGTCTTCTACATCTCCATCTTAATTTGCCGCAATGGAATCCCGTCACTTACAAGTACA  
 AACACCCTTACCATCCATGCTGTGACTGTGGTGAAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG  
 CTTTCCATGGGATTTCAAGACAGAAAGTTATCATTGCTATTCTCATTGCAATTATGATCATATTTGGGTTATTTTT  
 TTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTCTTGAGAAAAGTGAAGATTTCAAGAGAAATATA  
 TTCCAATATGATGATGAAGGGGGTGGAGAAAGAGATACAGAGGCCTTTGATATAGCAGAGCTGAGAGGATAGTACC  
 ATAATGCCGGGAACGCAAGATCTCGGAAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCACTCTTTCGAAGTT  
 GGCCCGCAGTGCCTATTCAGGAAATTCATTCTGGAAGAGCTCGAAGAAGCTAATCTGATCCGTGTGCCCT  
 CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA  
 GCACTCTCTGATCAGGATGAAGAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCTATG  
 TTTGGTTCTGCACTGAGTCAAAATAATAGGGCTTTTACCATCAAAATTTTTAAAGTGCCTAATGTGTAATTCGA  
 ACCCAATGGTAGTCTTAAGAGTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGTA  
 TTCTCCCTGGAGTAATACTCCATGGTTATTTAAGACTACCTACATGCTGTCTGATGAAACAGAGATGTGGGAGGAA  
 TGTAAACATCAGCTCAAGGCATCAATACAACAGATTTGAAGTAAATAATGTGAGGAAGATATTAAGAGTAGA  
 TGAGAGGACACAGAGTGTAGTGCATCTTATGCGATTATATCATTTACTTAGGAAAGAGTAAAAATACCCAA  
 CGAGAAAATTTAAGAGAGCAAAATTTGCAAGTCAAAATAGAAATGTACAAATGAGATACCAATTACATTCTAT  
 CATATTGACATGAAATTGAAAAATGATATAGTCAGAGAAATTTTCATGAATTAATTCATGAAGATATTGTTTCCTTT  
 ATTTAA

107/615

## FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWVWQFFVPEEMNTTSHHIGQLRSDLDNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYLLRAQVIDIATGRAVEPESEFVIKVSINDINDNEPKFLD
EPYEAIVPEMSPECTLVIQVTASDADDPSSGNNARLLYSLQGQPYFSVEPTTGIVIRISSKMDRELQDEYWVVIQ
AKDMIGQPGALSQTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDS
QTFDIIITNHETQEGIVILKKKVDPEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPY
VFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNIINDNGTITITSNSLDRDISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETVCENAGSGQVIQTISAVDRDESIEEHFFYNLSVEDTNNNSFTIIDNQ
DNTAVILTNRTGFNLQEEPFVYISILIIDNGIPSLTSTNTLTIHVDCDGSSTQTCQYQELVLSMGFKTEVILIA
ILICIMII PGFIPLTLGLKQRRKQILFPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTS
AEIRSLYRQSLQVGPDSAIRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQDESVDYL
NELGPRFKRLACMFSAVQSNN
```

### Important features:

#### Signal peptide:

amino acids 1-21

#### Transmembrane domain:

amino acids 597-617

#### N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

#### Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

1005256-01350

**FIGURE 107**

ATCTGGTTGAACTACTTAAAGCTTAATTGTTAAACTCCGGTAAGTACCTAGCCCCACATGATTGACTCAGAGATT  
 CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAGAGCTCCCAAATGCTATATCTATTACAGGGGCTC  
 TCAAGAACAAATGGAAATATCATCTCGTAAATTTAGAAAATTTGGATGCAAGATGGATATACATCAATTACACTTCGACTCT  
 CAAAGCAATACCAGGATAGCTGTTGTTTTCAGAGAAAGGATCGTGTGCTGCATCTCTCCCTTGGGCGCTCAATTGCT  
 GTAATTTTGGGAATCCATATGCTTGGTAATACTGGTAGCTGTGCTGCTGGGATCCATGGGGGGTCTCTTCCAGC  
 CCTTGTCTCTCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTCCAGCATGTCACTAAAATTCCTGGGATGGA  
 AGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCTCTAAAGATAGACAGCTCAAATGAATTTGGGATTTATAGTA  
 AAACAAGTGTCTTCCCAACCTGATAATTCAITTTGGATAGGCCCTTCTCGGCCCCAGACTGAGGTACCATGGCTC  
 TGGGAGGATGGATCAACATCTCTCTTCTAATCTATTTCAGATCAGAACCACAGCTACCCAAAGAAAACCATCTCCA  
 AATTGTGTATGGATTACGTGTGAGTCAITTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG  
 AAGTTTTCATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTAGGAGGACAGAAAACAGAA  
 CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCAACGTGAATCTTAAAC  
 AAGAAATTTAAGGGAGAGGCTGTGATTTCTGTATTTGTCGACCTACAGGTAGGCTAGTATATTTTCTAGTTAG  
 TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTATTTTTTATTTTATTTATTTTTTTGAGATAGG  
 GTCTCACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC  
 TCAAGTAGCTGGGACTACAGGTGCAATGCCACCATGCCAGGCTAATTTTGGTGTTTTTTGTAGAGACTGGGTTT  
 GCCATGTTGACCAAGCTGGTCTCTAATCTCTGGGCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAAGTGTGGGA  
 TTACAGATGTGAGCCACCACTCTGGCCCCAAGCTTGAAATTTTCATCTGCGCATTGACTGGCATTACCTTGGG  
 TAAGCCATAAGCGAATCTTAATTTCTGGCTTATCAGAGTTGTTTATGCTCAACAATGCCATTGAAGTGCACGG  
 TGTGTTGCCACGATTTGACCCTCAACTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAAATATATTTCTGAAT  
 AGCTAAATGAAGAAATGGGAAAAAATCTTACCACAGTCAGAGCAATTTTATTTTTCATCAGTATGATCATAA  
 TTATGATTATCATCTTAGTAAAAAGCAGGAATCCTACTTTTCTTTATCAATTAATAGCTCAGAGAGTATCAT  
 TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTGCCTCTGTGTGCCAGGCTG  
 GAGTGCACCGGCACGATCTCGGCTACCGCAACCTCGGCCCTGGGTTCAAGCAATTCCTCTGCCTCAGCCTCC  
 CAAGTAGCTGGGATTACAGTCAGGCACCCACACCCGGCTAATTTGTATTTTTTTAGTAGAGACAGGGTTCT  
 CCATGTCTGGTCAGGATGCTCCGAACTCTGACCTCAAGTGATCTGCCTGCCTCGGCCCTCCCAAGTGCTGGGATT  
 ACAGGCGTGAGCCACTGCACCCAGCCTAGAAATCTTGTAATATATGTAATTTAGGGGAACTGCCTCATAGGAA  
 GTTTTCTGCTTTTAAATACAAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC  
 TCATTGGAAACAGTATTAACATTTTGGAAATATGTTTTATAGTTTGTGATGACTGTTTACAAATTTTACCAT  
 TTTTTTCAGTAATTTACTGTAAATGGTATTTATGGAAATGAACATATATTTCCCTATGCTGATTTGTGCTTATTT  
 TTTTCATACTTTCCCACTGGTCTATTTTTATTTCCAATGGAATTTCTGTATTACTAGGGAGGCATTTACAGTTC  
 CTCATAGTTGATTTATATGTGAAAGAAATGTACCAATTTTACTAAATATGCAAGTTTAAATGGATGATTT  
 ATGTTATGTGGATTCAATTTCAATAAAAAAACTCTTATCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA



109/615

## **FIGURE 108**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEVHPDLENLDEDCYTQLHFDSQSNTRIADVSEKGSAAAPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLSNWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQLCSVPSPYSICEKKFSM
```

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

10052536-011502

**FIGURE 109**

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCACA  
 ATATCTTAACTCTTCATATTTGGGTTTTGGGACTGCTTTGAGTGCCATCTTCTATTTAAAAAATAACAGAGAC  
 CTACCTACCCGTACGCATACATATGTGTATATATATGTAACCTAGACAAAGATCCGACATCATAAAGCAAG  
 CTCTGCTTTAGTTTCCAAAGAAGATTACAAAGAATTTAGAGATGATTTTGTCAAGATCCCTGTCTGATTTCAGCCCT  
 TTGGGTTACGGTGTCTCAGTGATGACGCCCTACCCCTTGGTTTGGGGACATTTATGATTTGTGTAAGACTCAGAT  
 TTACACGGAAGGGAAGGATTTGGGATTACATGGCCTGCCAGCGGAATCCACGGACATGACAAAAATATCTGAA  
 AGTGAACCTCGATCCTCCGGAATATTACCTGTGGAGACCCCTCCTGAGACGTCTCTGTGCAATGGGCAATCCCTACAT  
 GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTCAGCTGATGTTTGTATTTTGAAGGAAG  
 ACATCCCTCCACATTTTGGCAGTGTGCCACTTGGAAAGGAGTATCCCAAGCCCTCCAGGTTAAACATCACTCTGTCT  
 TTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAATGATCCT  
 GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA  
 CATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGCTCTTAGAAATCATTTGCACAGAAGAGTACTCAAC  
 AGGGTATACAAATAAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTGTCTGGACCTCGCCT  
 ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAAACCAAGAACTCAGAGATTTCTTTACAGTCACAGACCT  
 GAGGATAAGGCTGTAAAGACAGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGCAGCTACTTTTACGC  
 GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTATGACAACAGCAA  
 ATTGACATGCGAATGTGAGCAACAACATACAGGTCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC  
 TTGGAGTCCAGGCTCCTATCTCCCAATCCCAAAAGGCACGTGCAAAATACCTGTATCCCCAGTATTTCCAGTATTGG  
 TACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGACGTGCCACAACACGTGCGCTGCTCTGTG  
 CCCGCCGCATACACGGGCACTCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGGCTCCGACTCTGG  
 CAGGGCGCGCCCCCGCAGCGCACCCAGCGCTGTCTGTCTGACACGCTGTCTGGGAACCCGACGCCCCCTGGT  
 GTTCTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCGGTGGGGAAGCAGACACAAACCAATTTTGCTA  
 CTAACATAGGAACACACACATACAGACACCCCCACTCAGACAGTGTACAACTAAGAAGGCTTAATCTGAACCTAA  
 GCCATATTATTACACCGTGGACAGCATCCGAGTCAAGACTGTAAATTTCTCAGCTCCAGAGGATTTGGCAGCTG  
 TTGATATTATCACTGCAATACATTTGCCAGCTGCGAGCATATTTGTGGATTGGAAAGGCTGCCACAGCCCCCA  
 AACAGGAAGACAAAAAAACAAACAAATCAACCGACTTAAACCAATTGGCTACTCAGCGTGGTGGCGCCCTAGTAC  
 GACTCCGCGCAGTGTGTGGACAACCAAAATAGCATTCTTTGCTGTGAGTGCATTGTGGGCATAAGGAATCTGT  
 TACAAGCTGCCATAATTGGCTGCTTCCGTCCTGAACTCCCTTCAACCTGTGCTTTAGTGAACGTTTGTCTCTGTA  
 CCTCGTTGGTTGAAGATTTCTTTGTCTGATGTTAGTGATGCATGTGTAACAGCCCCCTCTAAAGAGCGCAAG  
 CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCAGACACACCCCATATACAAGAGTGGCTATA  
 GGAAAAAAGAAAGTGATCTATCTTTTGTATTCAAATGAAGTATTTTCTTGAACCTACTGTAATATGTAGATT  
 TTTTGTATTATTGCCAATTTGTGTTACAGACAATCTGTTAATGTATCTAATTCGAATCAGCAAAAGACTGACATT  
 TTATTTGTCTCTTTTCGTTCTGTTTGTTCATCTGTGCAGAGATTTCTCTGTGAAGGGCAACGCACTGCTGGCA  
 TCAAAGATATCAGTTTACATATATAACAAGTGTAAAGATTTCCACCAAGGACATCTCAAATGTTTCTTGTGTT  
 GCTTTACACTGGAAGATTTAAAGATAAAAACTTACGATAAAGCATTTTCAGGAATTTGTATTGCAATTTCTTA  
 AGATGAAAGGAACAGCCACCAAGCAGTTTCACTACTTACTGATTTCTGTGTGGACTGAGTACATTCAGCTG  
 ACGAATTTAGTTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGGCAACTTCGCAAAATATGAGACTATTTCC  
 ACTTGGGAAAAATTAACACAGCAAAAAAATAAAAAAATAA

111/615

**FIGURE 110**

MYLSRSLSIHALWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVKLDPPDITCGDP  
PETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI  
TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDL SQHTVLEI ICTEYESTGYTTNSKIIHFEI  
KDRFALFAGPRLRNMA SLYQLD TTKKLRDFFTVDLRIRLLRPVGEIFVDELHLARYFYAISDIKVRGRCKCN  
LHATVCVVDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLHCQN  
GGTCHNNVRCLCPAAYTGILCEKLRC EAGSCGSDSGQGAPPHGTPALLLLTLLGTASPLVF

1052586.011502

**FIGURE 111**

GCGTGCCTGAGCTCGCCGGGACCGCGGGCTCGCCCTCGCCCTCGCCCTCGCGCTGACCGCGTAGACCGAC  
 CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCGTCGCCCGACCGGTCCCCGCCCTTTGTAAAACT  
 TAAAGCGGGCGACGATTAAACGCTTCCCGCCCGGTGACCTCTCAGGGGTCTCCCGCGCAAAGGTGCTCCGCCG  
 TAAGGAAATGGGCAAGGTGGAGCAGCTCTGAGCCTCGAGCCGACGACGAGCTCAAAATCCGAGGTCCCTTCA  
 CCGATGTTGTCAACCAACCTAAAGCTTGGCAACCGGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTACAG  
 CACCACGTAGGTACTGTGTGAGGCCAACACGGCGAATCATCGATGCGAGGGCCTCAATTAATGTATCTGTGATGT  
 TACAGCCTTTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGTTTATGGTTCAGTCTATGTTTGCTCCAACGT  
 ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGT  
 TTGAATTGCCAGCAGAGAATGATAAACCATGTATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAGA  
 CAGAAACACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAGGTTATGGAAGAAT  
 GTAAGAGGCTGCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAACAGCAGTTCAAGGAAGAAGATGGACTGCGGA  
 TGAGGAAGACAGTGCAGAGCAACAGCCCAATTTCAGCATTAGCCCCAAGTGGGAAGGAAGAAGCCCTTAGCACCC  
 GGCTCTTGGCTCTGGTGGTGGTGGTCTTTATCGTTGGTGTAAATTATTTGGGAAGATTGCTTCTGAGAGGTAGCATG  
 CACAGGATGGTAAATGGATTGGTGGATCCACCATATCATGGGATTAAATTTATCATAAACATGTGTAAAAAGA  
 AATTAATGTATGATGACATCTCAAGGTCTTGCCTTTAAATTAACCCCTCCCTGCACACACATACACAGATACACA  
 CACACAAATATAATGTAAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACGATTGAGGGGGAAAAAAGATGAT  
 CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATAATTGTAATGTCATTTTAAACATTGGTAGG  
 CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCCTTCTCGCTGTGGTGTGCTGGCCCTTGGGGAG  
 CTGGAGCCAGCATGCTGGGGAGTGGGTCAGCTCCACACAGTAGTCCCACTGTCGCCCACTCCCGGCCAGGCT  
 GCTTTCCGTGCTTCAGTCTGTCCAAGCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAGGAA  
 TTGCACTGTGGCAGCATCAGACGTAACGTGATAGTGAAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGA  
 AATAAATGGCAGTGGTCTTGTTCACTTAAAGGGACCAAGCTAAATTTGATTGGTTCATGTAGTGAAGTCAAACTG  
 TTATTGAGAGATGTTAATGCATATTTAACTTATTTAATGTATTTTATCTCATGTGTTTCTTATTTGTCAAGAGT  
 ACAGTTAATGCTGCGTGTGCTGAACCTCTGTTGGGTGAACCTGGTATTGCTGCTGAGGGCTGTGGGCTCCTCTGT  
 CTTCTGGAGAGTCTGGTCATGTGAGAGGTGGGTTTATTGGGATGCTGGGAGAGAGCTGCCAGGAAGTGTTTTTCT  
 GGGTCAGTAAATAACAACTGTCTAGGGAGGAAAATCTCAGTAGTGACAGTCAACTCTAGTTACCTTTTTTAA  
 TGAAGAGTAGTCAGTCTCTAGATTGTTCTTATACCACTCTCAACCAATTACTCAACTTCCACGCCCCAGGTCC  
 AAGTCTGAGCCTGACCTCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTCAGAGGGTTAGAA  
 GCGAGGGCACCAGCACTTGTGGGTGGGGAGCAAGGGAAGAGAACTCTTCAAGCAATCCTTCTAGTACTACTT  
 GAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGCAACCCAGTTCGTGTTGACTATGTAGCATCTTGAAA  
 AGAAAAATTATAATAAGCCCCAAATTAAGAAA

113/615

## **FIGURE 112**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHELKFRGPFTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGII DAGASINVSVM LQP
FDYDPNEKSKHKFMVQSMFAPITDTS DMEAVWKEAKPEDLMDSKLR CVFELPAENDKPHDVEINKIISTTAS KTET
PIVSKSLSSSLDDTEVKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKT VQSNSPISALAPTGKEEGLSTRLL
ALVVLFFIVGVIIGKIAL
```

**Important features:**

**Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

10052506-033502

**FIGURE 113**

CCCACGCGTCCGGGTGACCTGGGCGGAGCCCTCCGGTCCGGCTAAGATTGCTGAGGAGCGGGGGTAGCTGGCA  
 GGGCGCGACTTCCGAAGGCCGCCCTCCGGCGAGGTGCTCATGACTTCTCTTGTGGACCA**TG**TCCGTGATCTT  
 TTTTGCTCGCTGCTACGGGTAAGGATGSACTGCCCTCTCAGCTCTACTGATTTTACCACACCAAGATT  
 TTTGGAAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGAGGTTTGCAGAAAG  
 TTGTGACTTTAGTATACATTTTCTCTTTCCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC  
 AGCCATGGCCTTCTGCTTCTGGAGACCTGTGGTGGGAATTCACAGCTTCTCTATGACACTACCTGCATTGGCCT  
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG  
 TTCTCTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTCCTACTCT  
 GGAGGACACAGATGTGGCAATGGGGTGATGAATGGTCAACACCGATGCACCTGGAGCTGCTCCTAAATTTCCG  
 AATGGAACCAAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCAACATCATGTGTGCTGCCCTGAATCTCATTGC  
 AGGAGTTCACCTTGCAAACTTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGTTGGACCAAACCTCG**TGA**GC  
 CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTTCTGCTGCTG  
 GGGAAATCTCATCAGCAGGGAGCCTGTGGAAAAGGGCATGTCAAGTGAATCTGGGAATGGCTGGATTCCGAAAACA  
 TCTGCCCATGTGTATTGATGGCAGAGCTGTGCCCAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATT  
 CTATTCCTCTGACCCATGCTTAGTACATATGACCTTTAAACCTTACATTTATATGATTCTGGGGTTGCTTCAGAA  
 GTGTTATTTTCATGAATCATTCATATGATTTGATCCCCCAGGATTCATTTTGTTTAATGGGCTTTTCTACTAAAA  
 GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCATTTACTTTACATATTCGTTTTCAATACTTGTCTGTT  
 ATGTTACACAAGCTTCTTACGGTTTTCTTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAAACAAAC  
 TCAGTAGTACAACCTAACTTGTATAAAAGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAT  
 GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAAAAA

1052536.01502  
 205710.985201

115/615

**FIGURE 114**

MSVIFACVVRVVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSABGCCDFS IHFSSFGDVACMAICS  
CQCPAAMAFCFLETLWNEFTASYDTTCIGLASRPYAFLEPDSIIQKVWHPNYVSSSOMECSLEKIQEELKLOPP  
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

1052555.01502

**FIGURE 115**

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCATGTGAAACGTGAGCGGACCCGACCTTAAAG  
 AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTGCCTGCCCTTTAAAGGCGGGCGCTCC  
 GGCAGACTGTATCTGAGCCCGAGACTGCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTTAGGCTGGGTG  
 TGGGTGCTTGGCGGCGCGGCTTCTCTCCCGCTCTGTCTCTCCCGGGCCAGAGGCACTTCGGCTTCAGTCATGCT  
 GAGCAGAGTATGGGAAGCACTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATCCACGAGAGGATCCGCGAG  
 TGTATTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTTCTGACCCGCTTCAAGAAGCCT  
 GCTGAGTTTCAACACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCCTG  
 GCAATTGCCCTGGGTGCTGTCTGTCTCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCTCTGG  
 AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTCCCCAACTCG  
 TCCCTCATCTTCTCATGCCCCTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTCT  
 CTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGTGGTGTCTAGGTATGGTGTGGGTGGCA  
 TCAGCCATTGTGGACAAGAAACAAGGCCAACAGAGAGTCACTATGACTTTTGGGAGTACTATCTCCCTAACCCT  
 TACTCATGCATCTCCTTCTTGGGGTTCTGTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCC  
 GTCACCTGGGAAGCTGCTAGTCAAGCCCCGGCTGTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG  
 GAGGCAAGCCCTGACCCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTGCTACACAGA  
 CAGGTCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG  
 GGCTACCCCTGGCTATGCTGTGCTTGTCTGGTGTGACGAGGCTGTCTGTGCTCATTTGTGGCCATCCACATCCTG  
 GAGCTGCTCATCGATGAGGTGCCATGCCCGAGGCGATGCAAGGTAACCTCTTAGGCCAGGTCTCCTTCTCCAAG  
 CTGGGCTCCTTTGGTGCCGTCATTGAGGTTGACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTCTAT  
 AGCTCTCCACTCTTCCGGAGCCTCGGGCCAGATGGCACGACACTGCCATGACGACAGATAATGGGAAGTGTGTC  
 TGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTTGGGGCTCACTCGCTTTGACCTGTGGGT  
 GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTTCTCTACAACGACAGCTTTGACGGGCTCACC  
 AACTCTGTCTGTGTAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTG  
 CCGCTGCCGCTCTCCGTTTCCCCAGGCATCTAGGAAGACCCAGCACCACTGACCTCCAGCTGGGGGTGGGAAG  
 GAAAAAATGGACACTGCCATCTGTGCCATAGGCCCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA  
 ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATAATTGCATAATCTGAGGCCAGAGTTTGGGACCA  
 GGACCTCTGCTTTTACACATCAATCTGCCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGA  
 TGTGCAATAGGGTGGGTAGGGGAGGGAAGGACTGGGCCAGGCGAGCTCGGAGATAGATTGTCTCCCTTGC  
 CTCTGGCCAGCAGAGCCTAAGCACTGTCTATCTCTGAGGGGCTTTGGACCACTTGAAGACCAAGGGGATAGG  
 GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGAAAAAA



117/615

**FIGURE 116**

MEAPDYEVLSVREQLPHERIRECIISTLLFATLYILCHIPLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA  
LGAVLLLPFSIISNEVLLSLPRNYIQWLNGLIHGLWNLVFLFPNLSLIIFLMPFAYFPTBEGGFAGSRKGVLR  
VYETVVMMLLTLLVLGMVWVASAIVDKKANRESLYDFWEYLLPYLYSCISFLGVLLLLVCTPLGLARMPFVSTG  
KLLVKPRLEEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYP  
LAMLCLLVLTLGLSVLIVAIHILELLIDEAAMPGRMGQTSLGQVSFSKLGSPGAVIQVVLIFYLMVSSVVGIFYSSP  
LFRSLRPRWHDNTAMTQIIIGNCVCLLVLSALPVFSRTGLTRFDLLGDPGRFNWLGNFYIVFLYNAAFAGLTTLC  
LVKTFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQH

10052586-011502

[illegible]

119/615

## **FIGURE 118**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDWTGSTPAYGYWFKAVTETTKGAPVAT
NHQSREVEVEMSTRGRFQLTGDDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVTYNFMNDGFFLKVTIVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHFPWGRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLNGTSLPLVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRQTETPRPRFRSHSTILDYINVVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPPEFKSSTQAPESQESQEELHYATILNFPGVRRPR
PEARMPKGTQADYAEVKFQ
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

Downloaded from www.nrjonline.org

**FIGURE 119**

CTCGCGCAGGGATCGTCCCATTGCGCGGGGCTCGGAGCGCGACCCCTTGGGGGGCTCCGGGATTTGCTACCTTTT  
 TGGCTCCTCTCGTGCAGACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTCTTGCACAA  
 GGGGGCGAGCGACGAGCAGCTTCTTGGGCTTCTGTGGCCCTGCACCGGAGTTGACGCCCCGACCCAGCAGCTG  
 GCTGTGCTGTGGGTGCTCCCCAGGCGCTTGTGCTTCTGCGGAGCAGGCGGAATCGCATCGGAGGCGCTTCTCGTGTG  
 CCGGTTGAGCTGTGGAGGAGCTGACTCTCGAGAGTGGACATGCACAGGAGGTGATATGATTGGTCTGCTTTGTGCTCAGCGAGGA  
 GGAGAACAGTGGTGGGAGTCACTGTTCGGAGCAGGGGGCTGGGGGCAAGATTGTACCTGTGCACACCGGATA  
 TGAGGCAAGGCGAGCGAGTGGACAGATCTCGGAGACGCGGGATATGATTGGTCTGCTTTGTGCTCAGCGAGGA  
 CTTGGCCATCGGGATGAGTTGGATGGTGGGGAAATGGAAGTTCTGTGAGGGACGCGCCCCAAGGCCATGAAACAAAT  
 TGGGTTCTGCGCAGCAGGGCAAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC  
 CTATAATTGGAAGGCGACGCGCAGGGTGGAGCTGTGTGCACAGGCTCAGCGGACCTGGCAACCTGGACGACGG  
 TCCCTACGAGGCGGGGGGGAAGGAGCAGGACCCCCGCTCATCCGGTCCCTGCCAACAGCTACTTTGGCTT  
 CTCTATTGACTCGGGGAAAGGTTCTGGTGCCTGCAGAAAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCAACCA  
 CAAGGGTCTGTGGTCTACTCTGCGCAAGGACAGGCGCAGTGCCTGTGGTCCCGAGGTTATGTCTGTCTGGGGAGCG  
 CTTGACCTCGGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTATGGCTGGCCAGACCTGATAGTGGG  
 TGCCCCCTACTTCTTTGAGCGCAAGAAAGAGCTGGGGGTGCTGTATGTGTAATGAAACAGGGGGGTCACTG  
 GGCTGGGATCTCCCTCTCCGGCTCTCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTGTCTCTGGGGGA  
 CCTCAACCAAGATGGCTTTCCAGATATGTGAGTGGGTGCCCTTTGATGGTGTATGGGAAAGTCTTCACTACCA  
 TGGGAGCAGCTGGGGGTGTGCGCAAACTTCAAGGTGTGGAGGGCGAGGCTGTGGGCACTCAAGAGCTTCTGG  
 CTACTCCTGTTCAGGAGCTGTGGATATGGATGGGAACCAATACCTGACCTGTGGTGGGCTCCCTGGCTGACAC  
 CGCAGTGTCTTCAAGGCGAGACCCATCTCCATGTCTCCATGAGGTCTCTATGTCTCCAGCAAGCATCGACCT  
 GGAGAGCGCAACTGTGCTGGGCGGCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAAGCTACATTCAGCTCC  
 CAGCAGTATAGCCCTACTGTGGCTCTGGACTGTGATGTAGATCGGGACAGACAGCGGAGGCTCCGGGGCGAGCT  
 TCCCGTGTGACGTTCTGAGCGGTAACTGTGGAAGAACCCAGACCCAGGCTCGGGACCTGTGGCTGGCTCAAGCA  
 CCAGCATGACCGAGTCTGTGAGACGCGCATGTTCAGCTCCAGGAAATGTCAAAGACAAGCTGTGGCCCAATGT  
 AGTGACTTGTCTCACTAGTCTCCAGACCTCGCTCCGGCTCCGGCGCAGGCTCTGCGCAGGGGCTGCCTCCAGTGGC  
 CCCCCCTCTCAATGCCCAACGCGCCAGCCAGCCAGCGGCGAGAGATCCACTTCTGAAACAAGGGTGTGGTGAAGA  
 CAAGATCTGCCCAGAGCAATCTGCAGCTGTGCCACGCCGCTTCTGTACCCGGGTACGCGGAGCGGGGCGGGGCAAGT  
 TCTGCCCATGTGATGTGGATGGGAACAACAGCCCTGTTTGCACTGAGTGGGCGAGCCAGTCATTTGGCTGGAGCTGAT  
 GGTCAACCACTTGCATCGGAGCGGCAACCCAGCCAGCCAGGCTGATGGGATGATGCCATGAAGCCCAAGCTCTGTG  
 CATGCTCTCTGACTCACTGCACTACTCAGGGTCCGGGCTCTGAGCCCTCGGAGAGAGCACTCTGTGCTGTCCAA  
 TGAGAAATGCTTCACTGTGAGTGTGAGTGTGGGAAACCCATGAAGAGAGGTGCCCAGTCACTTCTACCTCAT  
 CTTTGAACCTTCCGGATCAGCATTTGAGCACCGGAACTGGAGGTGAGAGCTGTGTTGGCCACGATCAGTGAACA  
 GGAGCTGCATCCAGTCTCTGCACAGACCGGTGTCTTCAATTGAGCTGCCATGTCCATTCGAGGAATGGCCATTCC  
 CCAGCAACTCTTCTTCTCTGTGGTGGTGGGGGCGAGAGAGCATGAGCTTGAGCGGATGTGGGCGAGCAAGGT  
 CAAGTATGAGGTACGTTTCCAAACAGGGCCAGTCGCTCAGAACTCCGGGCTCTGCCCTTCTCAACATCAATGTG  
 GCTCATGAGATGGCCAAATGGGAAGTGGTGTGCTGATACCAATGCAAGTTGAGCTGGAGGGGGGCGAGGGGCTGG  
 GCGAGAAAGGGCTTTGCTCTCCAGGCGCAACATCTCCACTGGATGTGGAACATGAGGAATAGGAGGCGCGGGGA  
 GCTGTGAGGCACTTGAGCAGCAGGAGCTGTGAGCGGCGAGGAGCCAGCATGCTGCTGTGGCCAGTGTCTCTGCTG  
 TGAGAAAGAAAGAAACATCACCTGGAATCGCGCCGGGGGACGCGCAACTGTGTGGTGTTCAGCTGCCCATCTA  
 CAGCTTGTACCGCGGGCTGTGGTGTGATGTCTGGGGCCGTCTCTGGAACAGCATGTTCTTGAGGAGTACTCAGC  
 GTGTGAAGTCCCTGGAAAGTATTTGCGGGCCAAACATCAACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA  
 TGCTTCCACAGTATCCAGTGTGTTACTTGGACCCATGGCTGTGGTGGCAAGAGTGGCTCTGTGGGT  
 CATCTCTCTGGCTGTACTGCGTGGGCTGTGTGTGTAGCATGCTGTGTGTGCTCTGTGTGAAGATGGGATTTCT  
 CAAACGGGCGAAGACCCCGAGGCGCACCGTGCCCAAGTACCATGCGGTGAAGTCTCTCGGAGAGCCGACAGCA  
 GTTCAAGGAGGAGTGAAGCAGGCGACCATCTCTGAGGAACTCTGGGGCAGCCCCGGGGGAGGGGCGCCGATGCA  
 CCCCCATCTGGCTGTGGCTGTGGCTGTGCTTCCAGGCGCAGGCAACCGCTAGGTCTTCC  
 CATGTCCAGCTGTGGCTGTGGCTGTGGCTGTGCTTCCAGGAGATGGCTGTGGATGAAGAGTGAAGT  
 GAGTGTGCTGGTGTGCTGATCAAGATTGGCAGGATCGGCTTCTCAGGGGCAAGAGCTTCCACCCCAAGAA  
 TCTTCCCAACCAACTTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGCAAGGCGCATGGGTAGGG  
 TGGAAGGGCAGGGGTGCTTGTGATGCAAGGTGGGGGAGAAGGATCTTAATCTTCTTCTTCCATACCTCTGT  
 GTAACAGGAGCCCAAGGACTGTGCTTCCCGGAAGTGCCTTAAGCTAGAGGTGGGGAGGAGGTGTGTGCTACTGA  
 CTTAGGCTGTCTCTCTCTAGTTTCTTCTTCTCTCATCTGACTGTAGTTGTGCCCATCAGTCTAGTGGTTTCGTGGT

121/615

## FIGURE 120

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWAGSGICYLPGSLLEVLLFSRAVAFNLDVMGALRKEGEPGSLFGFVSVALHRQLQRPQSWLLVGPAP
QALALPGQQANRTGGFLFACPLSLEETDCYRVIDIDQGADMQKESKENQWLGVSVRSGQPGGKIIVTCAHRYEARQRV
DQILETRDMI GRCFVL SQDLAIRDEL DGGGEWKFCGRPGGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGTV
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRLI PVPANSYFGFSDSGKGLVRAEELS FVAGAPRANHKGAVVI
LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGGWDLI VGAPYFFERQEEELGGAVYVYLNQGGHGWAGISPL
RLCGSPDSMFGISLAVLGLDNLQDGFPIAVGAPFDGDKVFIYHGSSLGVVAKPSQVLEGEAVGIKSGFYSLSGS
LMDMDGNQYPDLLVGSADTAFLFRARPILHVSHEVS IAPRSIDLEQPNACAGGSHVCVDLRVCFYSYI AVPPSSYSPT
VALDYYVLADATDRRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLR AIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDET FQPLPMDVD
GTTALFALSGQPVI GLEMLVTNLPSDPAQPADGDDAHEAQLLVMLPDSLHYSGVRAIDPAEKLCLSNENASHV
ECELGNP MKRGAQVTFYLLSTSGIS IETTELEV ELLLATI SEQELHVPVSARARVFI ELPLS IAGMAI PQOLFSS
GVVVRGERAMQSERDVGSKVYEVTVSNQGSRLTLGSAFLNIMWPHEIANGKWLLYPMQVELEGGQGGPGQKGLCS
PRPNILHLDVDSDRRRRRELEPPEQGEPEGERQEPMSWVPVSAEKKKNITLDCARGTANCVVFSCLPYSFDRAA
VLHVWGRLWNSTFLEEYSVAKSLEIVIVRANITVKSSIKNLMRLDASTVIPVMVYLDPMMAVVAEGVPWWVILLAVL
AGLLVLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNWNGSPRRRPGDAHPILAAD
GHPELGPDPGHPGPTA
```

### Important features:

#### Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 1040-1062

#### N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

**FIGURE 121**

GGCACGAGGCGGCGGGGCGAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC  
 GTGGAGGAACCTAGCACCTGCCATCCTCTCCCAATTGCCACTCCAGCAGCTTTAGCCCATGAGGAGGATGT  
 GACCGGGAAGTGAAGAGCCCTCTGGAAGCATGGAGACTGTGGTGATTGTTGCCATAGGTGTCTGCCACCA  
 TCTTTCTGGCTTCGTTTTCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCCGAGACCTGCTGCAGC  
 GCTATGATTCTAAGCCCATGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAACTGG  
 ACGATGTCGTTATCACCACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCTCTGGGTCT  
 TCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGACAGAGAAGCTTGTGGCATGACAATGGGCT  
 CTGGGCGCAAGATGAAGACTTCAGCCAGTGTGAGCGACATCATTTGGTGCCCAAGCGGATCAGCCCCAGGGTGG  
 ATGATGTTGTGAAGTCGATGTACCCTCCGTTGGACCCCAAACCTCTGGACGCACGGAACGACTGCCCTGCTCCTGT  
 CTGTCACTCACTGGTGTGGTGCAAGGAATGCCCTGCCATCTGACGGGAGGCTTGGATGGATTGACCAAGTCTC  
 TGTGGGTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGCCCTCCAG  
 GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTTC  
 CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT  
 CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCGCTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGT  
 GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTGCAAGAGGAGTATTGAAAACTGGTGGAC  
 TGTCACTTTTATAGCTCACCTAGTGTCTTCAAGAAAATTGAGCCACCGCTAAGAAAATCAAGAGGTTTCACAT  
 TAAAAATTAGAATTTCTGGCTCTCTCGATCGGTGAGAATGTGTGGCAATTCGATCTGCATTTTCAGAAGAGGAC  
 AATCAATTGAACTAAGTAGGGGTTCTCTTTTGGCAAGACTGTACTCTCTCACCTGGCCTGTTTCATTATT  
 TGTATTATCTGCTGCTCCCTGAGGCGCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAC  
 TACAAAGTTGATGATTTCTTTTATCTTTATGCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT  
 ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

123/615

**FIGURE 122**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHIE  
AILENEDWIEDASGLMSHCIALKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL  
DPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWIDQSLSAABEHLEVLREAAALASEPDKGLPGPEGFLQEQSAI

1052586.011502

**FIGURE 123**

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCGCGGGGGCGCAGCGCCCGAGCCCGGGC  
 CTCGAGACGGGACCGAGAGCAT**CATG**GGCAGCACTGTCCCGGCTCCGCTCCGCTGCTGCTTCTGCTGCTGCTCC  
 TCGCGCCGGGCCGAGCAGCCCTCCGGGGCCGAGCTCACTTTCGAGCTGCGGCAACGCCAAGCACTGCTTCCACG  
 AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT  
 ATGTAGAGGACCCCCAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCAGSTACCGGGCTG  
 AAGTCAAGGGCGTTTATCAGTTTTGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT  
 TTCAAGTGGCGATGAGCCTCCCATCTCCAGACATGGGGAAACAGGGTCACAGCTCTCACCAGATGGAGTCCG  
 CTGCGTGAACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCAGACGCATTACCGGCTGCGGGAGGCCCAGG  
 ACCGGGCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGCTCTGTTGGCGAGACGATTGCCCTGTTCTGTGG  
 TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTCACAGAAAAACGACCCATCAGCAGGGCAGTCCACT**CT**  
**AG**CCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTCACAGCCTGCTGGGCT  
 GGGTCGCGTAGCCAGGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTCCTTTTCATGCCCATGCTTGATT  
 CTTGCACCTCAGCAGCTGAAGGTCTCAGAGACCAAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGCAGCGCTG  
 AAAAGACATTTACAAGTAGGCCAGGGATTAGCCACTGTGGAGGGTGGACAGGCAATGGTTCACTGGCCTGGCTG  
 TTGGCAGGAACCTCAAGTGCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTCATGATGCATGGGTCAT  
 TTGCTCTTGGGTGCTCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT  
 GTACCTGAGGAACCAAGGCCCTGGGTGACTTTGCAGATCTGCTCACCCCTCGGTGAGCAACAGTGTGAGCCATGCA  
 AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTCTCAGGAGGTAGAAAACTGTGGGAACTG  
 TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1005236-01532



1052586 01302

**FIGURE 124**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052
```

&lt;subunit 1 of 1, 217 aa, 1 stop

&lt;MW: 24777, pI: 5.55, NX(S/T): 0

MGSTVPRASASVLLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG  
GHYDVDCVVEDPQGNITRYETKKQYDSFTYRAEVKGYYQFCFSNEFTFSHKTYVDFPQV  
DEGPEPILPDMGNRVLTALQMESACVITHEALKTYIDSQTHYRLREAQDRARAELNSRVS  
YWSVGETIALFVVSFQVLLLLSFPTEKRPISRRAVHS

Important features:

Signal peptide:

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32, 48-54, 131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

126/615

## **FIGURE 125**

GGCAGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCCCCGAGCCTCTGT  
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG  
GAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGTAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCT  
CAGGCTTCTGTCTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGACAGAGCAAACTCTTCCCCCTTCTACT  
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT  
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAACGCCCGCTGGCTGGAAC  
CCCGACCAACAGCTGCCATGTGGGCCCTGCAAAACCGTGGAGAAGGAGCGAGGCCCTGGGTGGGAGGTACCCAGGCA  
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAAATTCT  
TCCGCTACCATGGGCTGTCTCTTTGCAATCTGGGCTCGCTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG  
CCCTGGAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAAA  
AAAAA

1052586.01502

127/615

## **FIGURE 126**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHHISMGCFAFINLCILASQ

HAWAQLTFWEASQLYLLFLSLTLATVNAWLEPRITTAAMWALQTVKEKERGLGGEVPGSHQGPDPYRQLREKDPKY

SALRQNFRYHGLSSLCNLGCVLNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

105536:04532

**FIGURE 127**

GCTTCATTTCTCCGACTCAGCTTCCCACCTGGGCTTTCCGAGGTGCTTTGCGCGCTGTCCCCACCACTGCAGC  
**CA**TGATCTCCTTAACGGACACCCAGAAAATTGGAATGGGATTAAACAGGATTGGAGTGTCTTTCTGTTCTTTGG  
 AATGATTCTCTTTTITGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAA  
 TGGTTTAGAAAGAACATTAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGT  
 ATTTGTAGTCTTATTGGTTGGCTTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAGGGG  
 CTTCTTTCTGTCTGTGTGTGGCTTTATTAGAAGAGTGCCAGTCCITGGATCCCTCCIAAATTACCTGGAATTAG  
 ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TA**ACAACAAGTGAATTTGAAGACTCATTAAAAATA  
 TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTT  
 TACAGGAGTTTAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTA  
 CTCAGTGAACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAAATC  
 TTGAAGGCTATTTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCTGTTTCT  
 TTTCTTTTTATTTTGAAGCTCAGGAGCATCCATAGGCATTGTCTTTTGAAGTGTCCACTGCAATGGCAAAA  
 TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAA  
 CAAGGAAACCCCAATTTGATGATGGATTACTTTTTTTTGNCGNCAGGGCC

129/615

## **FIGURE 128**

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFPQKHMKATGFFLGGV  
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFTIRRVPLGSLNLPGIRSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

10052536-014501

[illegible]

131/615

## **FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENIVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDWLTLEDYREPLEVNLFGLLISVTLNMLP
LVKKAQGRVINVS SVGGRLAIVGGGYTPSKYAVEGFNDLSLRDMKAFGVHVSCTIEPGLFKTNLADPVKVIKKLA
IWEQLSPDIKQQYGEGYIEKSLDKLGNKSYVNMDLSFVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMFPA
LQDFLLLLKQKAEIANPKAV
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

105536-1453

**FIGURE 131**

AGACAGTACCTCCTCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCC**ATG**AAACATCA  
 TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTGGTGAAGTTTTTCAITTCCTC  
 AGAGGAGAAATCTGTGGCTGGGAGATGTTCTCAITACTGGAGCTGGGCATGGGAATAGGCAGGCAGACTACTT  
 ATGAATTTGCAAAACGACAGACATATTTGGTCTCTGTGGGATATTAAAGCGCGGTGTGGAGGAAACCTGCAGCTG  
 AGTGCAGAAACCTAGGCGTCACCTGCGCATGCGTATGTGGTAGACTCGAGCAACAGAGAGAAGATCTATCGCTCTC  
 TAAATCAGGTTGAAGAAAGAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC  
 TTCTCAGCACCAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTGGATCAGAAAAG  
 CACTTCTTCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAAGGA  
 TTCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTGGCTTTACAGAGGTCGACATCAGAACTTC  
 AGGCCTTGGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTGTGAATACTGGGTTCAACAAAAATC  
 CAGGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGAAGAAGTCGATAGATGGAATACTTACCAATA  
 AGAAAATGATTTTTGTCCATCGTATATCAATATCTTTCTGAGACTACAGAAATTTCTTCCGAAACGCGCCTCAG  
 CGATTTTAAATCGTATGCAGAAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAAT**GA**ATAAATA  
 AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAAGCTTTATTTACAT  
 TTTTTCAGTCTGATAATATTAACCAATTTGGTTGGCCTAGCAGCAGTCAAAACGAACAGATTAAATACCTGT  
 CTTCCTGTTTCTCAAGAAATATTACGTAGTTTTTCATAGGTCTGTTTTCTTTCATGCTCTTAAAAACTTCG  
 TGCTTACATAAACATACITAAAGGTTTTCTTTAAGATATTTATTTTTCCATTAAAGGTGGACAAAAGCTACC  
 TCCTTAAAGTAAATACAAAGAGAACTTATTACACAGGGAAGGTTTAAAGCTGTTCAAGTAGCATTCCAATCTG  
 TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGACACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT  
 TATCTCAACCTGGACATATTTTAAGATTGAGATTGAAAGATTTCCCTAGCCTCTTCTTTTCAITTAGCCCAA  
 AACCGTGCAACTCTATTCTGGAATTTATTACTTGATTCTGCTTCTGTATAACTCTGGAAGTCCACAAAAGTGGA  
 CCCCTATATTTCTCCCTTTTATAGTTTATATAAGATACATTATGAAGGTGACCGACTCTATTTTAAATCTCA  
 GAAITTTAAGTTCTAGCCCCATGATAACCTTTTCTTTGTAATTTATGCTTTCATATATCTTGGTCCCAGAGAT  
 GTTTAGACAATTTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAATGTACTGGCTATTACATAAGAAACA  
 ATGGACCCAGAGAGAA



133/615

## **FIGURE 132**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1
MNIILEILLILLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTYYEFAKRQSIILVLWDINKRGVEE
TAAECRKLGVTAHAYVVDSCNREEIYRSLNQVKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNILGHFW
ITKALLPSMMERNHGHIVTVA SVCGHEGIFYLIPYCSSKFAAVGFHRRGLTSELQALGKTGKTSC LCPVFVNTGF
TKNPSTRLWPFVLETDEVVRS LIDGILT NKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK
```

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

105256-07502

CTGAGCGGCGGCTGATCATTTAGGGGGGAGATGAGTGGCGGGTGTCTCGGGCTTTGTGCTCGCGCATCGCTTT  
 CCAGACGCTTCAACACGCGACTCGGACCGAGGAGTTTCTTCTGGGGAGGTAAAGGTGGAAGCAACAGACAT  
 TACTGTATCCCAAAATGCGATGCTTTGAAGTTGTTATGACAATTGACATTCAGAAATATATTCCATGCTTCAAGCT  
 TTTTAGCTTTTATAATTCTTCAGGCGAGTAATATGAGCAAGCATGAAGAAATATTACAAATGCTAAAAAG  
 TGTGTGAGTTGTTGATCAAAATTCCTGCTCATTCAGATCAGCATCATGACGTTTAGAGATGAGGCTGCTTCACAAAA  
 TTTCTGAGAGCATTTTCAAACCAAGCATCTGTTTCTGCTATTACCAACCAAGTATATAAACAGAGGCTGCTC  
 TACTCATCGACTGGAACATCTCTTATATAAACTCAAAAAGGACTTTTTCAGGGTACCTTTAGTGTGTGCCAA  
 TCTGGCATGTTGTAACACCTGGGTTATAAACTCATGAGTTTCTGTATGTCCTCATGTTTAGCCGCTTTAGCCGAGT  
 ACAAACACACAGCTCTAAATTTTGAAGAGAGTGTGCTTTAAAGGGGTTACATAGATTAATGAATGAATGATGCT  
 TTTCAATCAAGAGGAAATTAAGAGGATATACGAAAAAGGTGGAAGAGGATGACAGCATGATGAATCAATGATGAA  
 GGATGTAAACAGATTAACACGAGAAATTTGAGAAAGGAGAGGAGCAGCAGGTTGAGGCAACAGAGAGAGACAT  
 CCAAAAGAGACCTTCAGGAGAACATTTTCTTTCTGAGGCATTACGGACCTTTTTCCAAATTCGAAATTTCTTCA  
 TTTCAATGTGTATGCTTTAAAAAATAGACATGTTTCTAAAAAGTAGCTGTAACTACAACACCATCTCGATGTAGT  
 AGACAACTTCGACCTTAATGTGATGAACACATCTGACATCTCGTAGGTAGTGTCCAGTATGACACCAAAATCAATAA  
 GCATAAGGCTTTGAGATGTAGATGACAGATGGCAATTCGAAGTAGTCTCGGTTGTAGATACACAAGACCAAGATC  
 TAAAGCAAGATCTCGTGTAGTAGTAAACAAGATAAGACATCCAAATGAGCAGCCCAAGAACAGATGAAGAAATGGA  
 AAGATGAAGGTTTGTGGTAGAATTCACGGTCTCTACATTTGTAATCTTTAACTCTTAACTCTACAAGGAGTTTT  
 ATTTGGCTGTGGGTAAAGGCCAAATCTTCTATGTTTTTCTATGTTGAGCTGCTGCGATAGTCTATTGTT  
 TTTACTATGTTCCAGCTGTTTCAGTAGTAACACAGATAACTCTATGTCATTACTTCAACAAGTACTTTTCAA  
 CATCAGATGCTTTTATTTCAAACCTTTTTCACCTTTCTCATAGTTGTGGAGGGAAGGCTTACACAGACAT  
 TCTTTTAGATTTGAAAGGTGAGGACAGGACACGCTGACCTGTAATCCGACATGTAGGAGAAACAGTCA  
 AGGAGGATGCTTGAAGCTAGGAGTTAGACAGACCGCTGGGCAACGTTATGAGACCTGCTCTATAAAAAATAA  
 ATGGAAGATGCAAGATAGCTCTATTCAAATATGGAAGAAATTTATGAAATTTATCTGAGTATTAAAA  
 TCTCTCTTAAGTGATATCTTTTGAAGATCATTTGCTGTAGGCTGACGATGCCAGATAAAATGCTGGATATCATGCAAT  
 AAATTTGCAAACTCATCTTAAATTTTAAAAAATAAAAAAATAAAAAA

135/615

**FIGURE 134**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEGVKGEAKNSITDSQMDDEVVVYITIDIQKYIPCYQLFSFYN  
SSGEVNEQALKKILSNVKKNVVWYKFRRHSDQIMTFRERILLHKNLQEHFSNQDLVFLLLTPSIITESCSTHRLE  
HSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVOTHSSKFFEEEDGSLKEVHKINEMYASLQEE  
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS  
LKNRHVSKSSCNYNHHLVDVNLTLMVETDIPASPASTPQIIKHKALDLDRAWQFKRSRLLDLTQDKRSKANTG  
SSNQDKASKMSSPETDEETEEKMKGFGEYRSPTF

135/615

**FIGURE 135**

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC  
 CAAGCAGCGGCGAGCGAAAGCCGCGCGCCGAGCCACCCCTCTGTCGGTCCCCCGGGGGCTGCCACCCCTCCCTCC  
 TTTCCCGGCTGCCCGCTCGCCGCGCAGTCACTTGGCCGGTTTCGTCGCCCGGAAACCCCGAGGTCAACCGC  
 CGCGCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTCTCTCTCCCTTGGCCCGGCGCTGGCACCCGGGG  
 ACCGTTGGCTGAGCGGAGGCCAGCTCTACTTTTGGCCCGCGCTCTCTCCGCTGCTCGCTCTTCCACCAACT  
 CCACTCTCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGCCCGCTGCCGTAGCGCCG  
 TTCCGCTCCGTTCCAAAGGTGGGAACCGCTCCGCCCCGGCCCGCACCATGGCACGGTTCCGCTTGGCCGCGCTT  
 CTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTCGA  
 CGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATC  
 TGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAGTACAGCTGCAAAAGTAAAGATGATTTCAAA  
 AGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGCTTTTGCTTCAAGTACAGAAAGTTGATGAATCTCT  
 AAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTATACATGCAA  
 AATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGTGGGAAATGTGAACCTGGAAGAA  
 ATGCTAAATGACTTCTGGCTCGCTCCTGGAGCGGATGTTCCGCTGGTGAACTCCCAAGTCCACTTTACAGAT  
 GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTCCGAGATGTCCCTCGCAAAATGAAGCTC  
 CAGGTTACTCGTCTTTTGTAGCAGCCGCTACTTTTCGCTCAAGGCTTAGCGGTTGCGGGAGATGTGCTGAGCAAG  
 GTCTCCGTGTGAACCCACAGCCAGTGTACCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGGT  
 CTCGTGACTGTGAAGCCATGTTCAACTACTGCTCAAACATCATAGAGGCTGTTTGGCCAAACCAAGGGGATCTC  
 GATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGGGCTAGAGGGTCTTTCAACATTGAA  
 TCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGGTGCT  
 CAGAAGGTTTTCAGGGATGTGGACCCGCCAAGCCCTCCAGCTGGACGAATTTCTCGTTCCATCTCTGAAAGT  
 GCCTTCAGTGCTCGCTTCAGACCACTACCCCGAGGAACGCCCAACCAAGCAGCTGGCACTAGTTTGGACCGA  
 CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCCTTCCGAGCAACGTTTGGCAAC  
 GATGAGGGATGGCTGCAGGAACCGCAATGAGGATGACTGTGGAAATGGGAAAGGCAAAAGCAGGTACCTGTTT  
 GCAGTGACAGGAAATGGATTAGCCAAACAGGCAACCAACAGAGGTCCAGGTTGACACCCAGCAAAACAGACATA  
 CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGATGCATACAATGGGAACGACGTG  
 GACTTCTTTGATATCAGTGATGAAAGTAGTGAGAGAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCTTCA  
 GAGTTTGATCTACAATGCCATGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACGTCTGGTCTCCGCTCT  
 GGGGCACAGGCTACCTCTCTACTGTCTTCTGCACTCTGTTCTCGTGTATGCAAGAGAGAGTGAAGATTAATTCTCA  
 AACTCTGAGAAAAAGTGTTTCATCAAAAGTTAAAGGCCACAGTTATCACTTTTCTACCACTCTAGTGACTTTGC  
 TTTTAAATGAATGGACAACATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTC  
 TCAATCACTTTTGGAGGAAAGGCACTGTGCAITGAGTTGGTCTCTGCTCCCCAAACCATGTTTAAAGTGGCT  
 AACAGTGTAGGTACAGAATATAGTTAGTTGTGCAATTTGATTTTATCACTCATATTTTGTATGTTTATGTTT  
 TTCTCATTTTGTGTTGGGTTTTTTTCCAACTGTGATCTCGCTTGTTTTCTACAAGCAAAACAGGGTCCCTT  
 CTGCGACGTAAACATGTCGTAATTTCTGAAATATTAATAGCTGTACAGAAGCAGGTTTATTTATCATGTTATC  
 TTATTAAGAAAAAGGCCCAAAAGC

137/615

**FIGURE 136**

MARFGLPALLCTLAVLSAALLAABLKSKSCSEVRRRLVSKGFNKNDAPLHEINGDHLKICFQGGSTCCSQEMEEKY  
SLQSKDDFKSVVSEQNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSELFKDLFVELKRY  
VVGNNVLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQGDVPRKLLQVTRAFVAARTFAOGL  
AVAGDVVSKSVVNPTAQCTHALLKMIYCSHCRLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLVVAE  
RLEGPFNIESVMDPIDVKISDAIMNMQDNSVQVSQKVFGCGGPPKPLPAGRISRSISESAFSARFRPHHPEERT  
TAAGTSLDRLVTDVKEKLKQAKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGSRYLFAVTGNGLANQGNNPEV  
QVDTSKPDILILRQIMALRVMTSKMKNAINGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE  
KADSAGVRPGAQAYLLTVFCILFLVMQREW

20250528.011502

CGGGCTCTTGACGGGGCTCGAGTGGCTGCTCGACGGGACGAGGAAGCGAGGCTCTCGGTTCTCTTCAGTGGCGA  
CTCTTGACGGCCCGAGTGGGGGGGGCCCCCTTGGCGCGTGGCAGCACTGATCATGTGATCATGACACCGCCGCGCGGCT  
CGGCCCTCATCGGGACCTTCATCTCGGTGAGCTGTGAGTCTTTGGCAGAGGATATGACAACAGCAGAAGTTGGCGCGCG  
GGCTCTGTCTGGAGGAAATTGGAAAGCACTGTGAGATTGACGGGAAATGATTTCTTCTCTTCTGCTTTCT  
GCTTTTCTGTGATCTCTCTTCTATCACTAATCTTGCTGACAAATTGGAAAGCTCTGGCTTTCAGGCTTGAAGGAAAG  
GACAGAAGTTGGGCCAGAAATTTGTGGTTTAAACACGCAATACCCGCTCTTACAGCTCTCTCAGAAGCGGAGA  
CCAGCAACCTGGAAGATCTCTTGACATTTGTCTACAGAAGACACAAGAAGCACTCCAGCGGGGACCACTCACT  
CAGATTTAGACCCCAAGSCAACACTTGAAGATGGGACACAGGAGAGGCGCAAAAGGCAAGGCCCTCT  
GGATCCCCCGCGAAGAGGATCCGCGAGAGGACAGTCTACAGCTGGAGGGGGAGCGGTGATCGAGCTGAGCAGSG  
CACAGAGCTCCCTTCAGAAGAGCAGAGATGGCCACAAGCTCCCTCTCCACCGCCAGGACACAGGGGACAGCG  
AGTGCATCTGAATCTTCGCGCAAGGCGGGTGATTGATGCTGTCTCTGATGATCGAAGGAAGTACCGCAAGTTGG  
ATGGGGCATCGAGCGCTGAAGGCTGTGTCAGGAGTCTCTCAGTGAGTGTTGGTGGCTCGGTCTTCACTATGATGAC  
CGCGCTGGAACACTGTGATTTCTGGGTCTTGAGGAAGAAGTTTGAAGGAAGCAGGAAGTGGGTGTCTGAAGAAGTT  
ACACTTTGAAAAGAGCGTGGACGTCAACCTTTTGAGAGCAGATCGCATCTGGCGGGGGGCTCTGTAGTGCGCTTA  
CCACTGTCTGGGAGCAGCTCTTCTCGAGGAAGTCTGAGGAATTTGGAATTCGCGTACGCTGCTCTCAGAAAC  
ACCATTCAGGATCTCTTCTCGATTGTGAACATCGGTATCGGATCTGGAGCTGCCACCAGCCAGCGTGAACCTCCGACAG  
CACTGTGCGCGAGGTTGACACAGCACTTCAGTGGAGTTTCGGGAGGCTCTCCGCTCTCACAGGGGATAAGAAGTTTCA  
GGAGCGAGCTGGAGAAGGTTGACACAGCACTTCACGGCGCTGTCTGGAAGAAGGATGGGCTGTGCTCCATTTCTCAT  
CAATACCACTGAGCTGGCTCTTCTACCCACTCGGCGGTATTACGCTGGGCGCAGGGCGCGACAGCTACTAGTAACT  
CTGTCTGGAAGCAGTGATTCAGGGCGGGAGCAGGAGGACAGCTGTCTGGAAGATCACTGTGGAAGCACTCGAGGG  
TGTCAAGACGCACTCTGTCGGCATCTCGAGGCGAGTAAGCTCACTTTGGGGGGAGCTTGCCCTCGCGCTGTT  
CAGTGCAGGAATGGACACACTGTTGTGCTTCTGCGGAGGACGCTGGCTCTGGGCGCTTACCTACGCGCTCGCCGC  
GAGCAGCACTGAGAGCTGGCCCGGAGGCTCATGAGACATTTGTTACCGATGAACCGGACAGTGGAGACGGGCTGAGT  
TCCCGAGATCTGTGCGCTCAACCTTTACCCCAAGCGGGCGCTGCGGAGCTGGAGGTTCAAGCAGCAGACAGGACA  
CAACTCTGTGCGGCGAGAGACGCTGGAGAGGCTGTGTTACTCTTACCGCTGACAGGGGACGCAAACTACAGGA  
CTGGGCTGGGAGATCTCGAGAGCTTCAGCGGATTTCAGACGGGTCCCTCTGGGTGGCTATTTCTTCATCAACAA  
TGTTCAGATCTCTCAGAAGCCGAGGCTTAGGGAAGAATGAGAGGCTTCTTGGGGGAGAGCTCAAGTATCT  
GTCTTGTGCTCTCTTCGATGAGCCAAACTGCTGACGCTGGACGCGCTACGTGTTTCAACACCGAAGGCCCACTCTCT  
GCTATCTGTGACCCCTCGCTAGGTTGGATGGCTGTGTGTGTGGGGAATCTCGGTTGGGACAGAGCACTTCGTGGG  
TCTGTGGCAATTTTCAAAGGGGCGACGTGACAGCGGACCGGACAGGTTGGCCCGAGGCTCTGAATCTGTGCTCTGGGCT  
CTCTCTGCTCTCTGCTTTTAACTCAGGACACGCTGAGGACAGTGAAGGCGCTCAGTCTTGGTGTGCTGGGGGTGGG  
CTGGCGCGCTGGAGCTCTCGCCTCTCTCTTCAAAGAAGACAGGAATCATGATCAGCAATTGTCTGAAGCTCTGAGACG  
GTCTCTGCGGCGACCAAGAGGGGGCTTCGAGTGTGTCCTGGTACTGGGGTGACCAAGGTGACAGCCAGCGGCT  
CGAGCTCTTCCGCCGGCTGTGTAAGCCTCAGATCTCCCAATCAAGGGGTCTGGAGGGGCTGCGCTGCTCTCAGAG  
GCTCTAGGCTCCAGGCTGGCTCTGTGTTTAAAGCTGTGACTCAGGAGTCTCTCTGGCCGCGCGAGGGGCT  
TGGAGGGCTGAGCGACAGTCTGCTCTAGCTCTACGGGCCCTCTCAGTGGAAATGGTCTTTTCGGTGGAGATAAAG  
TTGATTTGCTCTGCCCAACAA

139/615

## **FIGURE 138**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMVYPPPPPPPHRDFISVTLSPFGESYDNSKSWRRRSCWRKW
KQLSRLQRRNIFLLAFLFLFCGLLFYINLADHWKALAFRLLEEQKMRPEIAGLKPANPPVLPAQKADTDPENLP
ETSSQKTQRHIQRCPPHLQIRPPSQDLKDGTEEBATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTETLPSRR
AEVPTKPPLPPARTQCTPVHLNVRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSFEWFGGLGLTLIDALDTMWI
LGLRKEFFEARKWVSKKLHFEKDVDVNLFESTITRLGGLLSAYHLSGDSLFRLKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAHPPRWTSDSSTVAEVTSIQLEFRELRLTGDKKFQEAWEKVQTHIHGLSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRTHLLRHSEPSKLT FVGELAHGRFSAKMDHL
VCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPEIVHFNLYPQGRRDVEVKPADRHNLRLPET
VESFLFYLRVTGDRKYQDWGWELLQSFSSRFTRVPSGGYSSINNVDPPQKPEPRDKMESFFLGETLKYLFLLFSDD
PNLLSLDAYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

139/615: 011502

**FIGURE 139**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC  
 CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG  
 CG**AT**GAAAGTTCTAATCTCTTCCCTCCTCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA  
 ATCCAGGGGTCCGCGAGGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT  
 GTGAGTGCAAAGATTGGTTCTCTGAGAGCCCCGAGAAGAAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGT  
 GCCCCTGTGATCATTTCAGGGGCAATGTGAAGAAAAACAAGACACCAAAGGCACACAGAAAGCCAAACAAGCATT  
 CCAGAGCCTGCCAGCAATTTCTCAAAACAATGTGAGCTAAGAAGCTTTGCTCTGCCCTTTG**TA**GGAGCTCTGAGCGC  
 CCACTCTTCCAATTAAACATTTCTAGCCAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTC  
 ACTCTCCCACTGTACCCACCCCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTGTTGT  
 TGCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTTAATTAC  
 CTGAAAGATTCCAGGAAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAAC  
 AGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAAAAA

105256.01502



141/615

**FIGURE 140**

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECCKDWFLRAPRRKFMIVSGLPKKQC  
PCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

105235.01501

**Index**

**AATGGCTGTC**TTAGTACATTCGGCTGACAGTGTGTCCTGGAGAGCTGCTTGTCTTATTCTGACCCGCTATGCGAGACGA  
 CAAACGACACGAGCGACGACGACGACGACGACGATCTGGGCAAGACGCCAACGACGACTCCCAAAATCTCTAAG  
 CTTCTTGGGACGACGAGATCATGTGAAGATCGAGTCGAGTTCATCTCCGCTCATTGTCCAGGAGCGACGAGATTTAT  
 GGAATTTGATGATAATGAAGGAAAAATTATCAAAAG**TGA**CATCTCCAGGACACACCATCTGGCTCTGCTTATG  
 TCCAGAGCGCAGCCAAATCTCGTCTTTCCAGTTGGGTCACAAATCTCTCCAGACGACGCCCTCAAGAGAACTG  
 CAACGAGTCTCCAGGATTCAGGCTCTGGCTTCACCAACCAAGACTCATTTTGAACACGCTGACTGGCTTTTGGC  
 TTTTAGAAGATTTAGATAAAATATGGCCGCTTTGGGATCACAATGTTGATGGAGGGGAAAAAAAAAAAAAAAAAAAA  
 AAAAAAATAAAAAAAAAAAAAAAAAAATA

143/615

**FIGURE 142**

MAVLVLRLTVVLGLLVFLTCYADDKPKPDDKPDGSGKDPKDFPKFLSLLGTEIENAVEFILRSMRSTGFM  
EPDDNEGKHSSK

1052586.011502

144/615

**FIGURE 143**

GGAGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG  
CCA**TG**GACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTACCTGCCCCCTGCACCTCATGGCTCTGC  
TGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA  
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC  
TGGAGCTGGGCTGCGGAACCGGAGCCAACCTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCTGAGCCCAA  
ATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGTGG  
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACCTCTGGTGCTGTGCTCTG  
TGCAGAGCCCAAGGAAGGTCTGCAAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGC  
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACTGGAAACACATTGGGG  
ATGGCTGCTGCCTCACAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGGAAACGAC  
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCCAAGCT  
CCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAAACAAGCCACCCACAGCCTATCTATCTTCCAAGTGA  
GAGGGACCT**TAG**CAGAAATGAGAGAAGACATTTCATGTACCACTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCACTTCTACGCTGACCAGGGAGGAAACACTAGG  
ACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTCCCTTTCCTT  
CGTTCCTATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG  
TCATGGTGCTGCATCCCTGCCAAGCCCCCTGACCTCTCTCCCCACTACCACTTCTCTCTGAGCTGGGGGCA  
CCAGGGAGAATCAGAGATGTCTGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTT  
TAATAAATAGACGAAACACG

105256.01501

145/615

**FIGURE 144**

MDILVPLLQLLVLLLTPLHLMA LLGCWQPLCKSYFPYLMAVLTPKSNRMESKKRELFSQIKGLTGASGKVALL  
ELGCGTGANFQFYPPGCRVTC LDPNPFEEKFLTKSMAENRHLYERFVVAPGEDMRQLADGSM DVVVCTLVLC SV  
QSPRKVLQEVREVL R PGGVLF FWEHV AEPYGSWAFMWQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQ  
PPPLKWLFPVGP HMGKAVKQSPFSSKALICSPFSLQLEQATHQPIYLPLRGT

2025.07.15 10:55:56

**FIGURE 145**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGGCAGATGTTGGGGC  
 TTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA  
 AGATGTCATTCCGTAAAGTAAACATCATCTCTGGTCTGGCTGTGTCTCTCTTCTTACTGGTTTTGACCATA  
 ACTTCCTCAGCTTGAGCAGTTGTTAAAGGAATGAGGTTACAGATTCCAGGAATTGTAGGGCTCAACCTATAGACT  
 TTGTCCCAANTGCTCTCCGACATGCGATAGATGGGAGACAAGAGGAGATTCTCTGGTGCATCGCTGCATCTGAAG  
 ACAGGCTTGGGGGGCCATTGCGAGCTATAAACAGCATTGACACAACTCGCTCCAATGTGATTTTCTACATTG  
 TTACTCTCAACAATACAGCAGACCATTCTCCGGTCTTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA  
 TTGTCAATTTTGACCCCTAAACTTTTGGAAAGGAAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT  
 TAACCTTTGCAAGGTICTACTTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA  
 TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTTCAGAAGATT  
 GTGATTCAAGCTCTACTAAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA  
 AAAAGGAAAGAAATTCGTAAGCTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAACC  
 TGACGGAATGGAAACGACAGAATATAACTAACCACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGACTGT  
 ATAGCAGAACCCTGGCTGGTAGCATCAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG  
 ATCCTATGTGGAATGTCGCCACCTTGTTCCAGTGCTGGAAACGATATTCACTCAGTTTGTAAAGGCTGCCA  
 AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT  
 ATATTCAGACCCAAAGGCAATTAACCTAATCCGAAGATATACCGAGATCTCAAAACATAAAAGTGAACAGAA  
 TTTGAACGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAAGATAGCTGCATGGGAAGTAAACAGTTGCTAGGCTTC  
 AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCACTAGGTAAAGATGACAACTGCCCTGTCTGGCAGT  
 CAGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTCAACAGTGTTTTCTTACTACAATGCTG  
 AATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATCAAACTGCTGTGGTTTTTA  
 ATTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTT

1055256.01501  
 20510.02501

147/615

**FIGURE 146**

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVFNALRHAVDGRQEEIPVVIAASED  
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKVKEDPDQGSMKPL  
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYK  
KERIRKLSMKASTCSFNPGVFVANLIEWKRONITNQLKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTID  
PMWNVRLGSSAGKRYSPQFVKAALLHWNGHLKPGWGRRTASYTDVWEKWYIPDPTGKFNLIIRRYTEISNIK

202510-08225001

**FIGURE 147**

GTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCACTTCCTCCAAGCA  
 AGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTGTCATCTGTTTGTATAA  
 ATGATGTTGACACCTCCACCGAAATTTAAGTGAATCATGTGCGGAAGAGATACAATCCTTGGCCTGTGTATCC  
 TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCACTACCACCCTTCTGGTTCACATTTTCATTT  
 CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTATGTGTGCTGTATTATGACTATACCAACGACCTCA  
 GCATAGAATTGGACACAGAAAGGGAAAAATGAAAGTGCCTGCTGGGTTTGCTATCGTATCCACAGGCATCACGG  
 CAGTGTCTGCTGCTCTTGATTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAATCAGAAATA  
 AAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTGCCCATCCTCATTTTCTTCTGGGTCC  
 TCTGGGTGCTGTGCTGCTGAGCTGGGAACTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAAATATA  
 AGCCCCCTTCGGGCATTTCGGTACATGTGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG  
 CGTGCCAGCAAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCACAGAAAGTAAAAATGATCCTCCTGATC  
 ATCCCATCCTTTCTGCTCTCTCCATTCTCTTCTTACCATCAAGGAACCGTTGTGAAGGGTCATTTTAAATCT  
 CTGTGGTGAGGATTCGAGAAATCATTTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATGT  
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAAATG  
 CATATACTACAACCTGCTATTAAATGGGACAGATTTCGTACATCAGCAAAAGATGCATTCAAAATCTTGTCCRAAG  
 ACTCAAGTCACITTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTTCTAGGAAAGGTGTTAGTGGTGTGTT  
 TCACGTGTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTGTTATGG  
 TAGCTTTTTTGGCCTACTTAGTAGCCCATAGTTTTTTATCTGTGTTGAAACTGTGCTGGATGCATTTTCTGT  
 GTTTTGTGTTGATCTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAAATTTCTGAGTT  
 TCGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAGCACTCATTAAGGAATGAGGAGGGAA  
 CAGAACTCCAGGCCATTGTGAGATAGATATCCCATTTAGGTATCTGTACCTGGAAACATTTCTTCTAAGAGCCA  
 TTTACAGAATAGAGATGAGACCCTAGAGAAAAGTTAGTGAATTTTTTTTTAAAGACCTAATAAACCTTATTC  
 TCCCTCAAAA



149/615

**FIGURE 148**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDLSIELDTERENMKC  
VLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFAILFFWVLWVAVLLSLG TAG  
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY  
HQGTVVKG SFLISVVRIPRIIVMYM QNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQ NAYTTTAINCTDFC  
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRA FQVWAVP LLLVAPFFAYLV AHSFL  
SVFETVLDALFLCFAVDLE TNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

2025-10-26 09:55:00

[illegible]

151/615

**FIGURE 150**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVYG  
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVITYPSAL  
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVVTLMOQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQE  
MDLWSTATYTSSQNRPRADPGIQRODPSGAAPQKPVGADVSLGLVPKEELSTQSLFPVSLGDPNCKIDLSEFLIDG  
STSIGKRFRFRIQQLLADVAQALDIGPAGPLMGVQVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRA  
ISFVTKNFPSKANGNRSGAPNVVVVVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAV  
CRTNGFYSLHVQSWFGLHKTLPVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVTLQFVTNLTKF  
EISDSTDTRIGAVQYTYEQRLFPFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKSKPNKRKLMILI  
TDGRSYDDVRIPAMAAHLKGVITYAIGVANAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

1052536-24502

**FIGURE 151**

CAGGATGAACCTGGTTCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCT**ATG**CCTTTCCGGCT  
 GCTCATCCCGCTCGGCTCCTGTGCGCGCTGCTGCTCAGCACCATGGTGCGCCAGGTC CCGACGGCTCCGCGCC  
 AGATCCCGCCACTACAGTTTTTCTCTGACTCTAATTGATGCCACTGGACACCTTGTCTGATTTTGGGGAATGTC  
 AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGA  
 AACAAACATTTCGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAAGTAGAGGC  
 TGGATGGCCCTGTTCCGGGCTCTCTTGAGAATGGCTGAGGAGGCGGCCGAAACTCCTCCAGCCTTTTCAGAC  
 CCCACTGGCATGCCATATGGAACAGTGAACCTTACTT CATGGCGTGAACCCAGGAGAGACCCCTGTCACTGTAC  
 GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGT  
 GGCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGTTCGGCAACCACTTGTATGTGCT  
 CACTGGCAAGTGGGTGGCCAGGACGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAGG  
 AGCCATCTTGCTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAGCCATCCGGAACCTACACCCG  
 CTTGATGACTGGTACCTGTGGGTTGAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCAGTCTTGGAGGC  
 CTACTGGCTGTCTTCAGAGCCTCATTTGGAGACATTGACAAATGCCATGAGGACCTTCTCAACTACTACACTGT  
 ATGGAAGCAGTTTGGGGGGCTCCCGAATTCACAACTTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA  
 CCCACTTCGGCCAGAACTTATTGAAAAGCGCAATGTACCTTACCCTGCCACGGGGGATCCCACTCTTGAACCT  
 CGGAAGAGATGCTGTGGAAATCCATTGAAAAATCAGCAAGGTGGAGTGCAGATTGCAACAAATCAAAGATCTGCG  
 AGACCACAAGCTGGACAAACCGCATGGAGTCGTCTCTCTGGCCGAGACTGTGAAATACCTTACTCTCTGTTGA  
 CCCAACCAACTTCATCCACAACATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGATCCTGGG  
 GGCTGGGGGTACACTTCAACACAGAAGCTCACCCCATCGACCTTCGCCGCCCTGCACTGTGCGCAGAGGCTGAA  
 GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAAGGAGCAGGTGCAAAATTCAGAA  
 AAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTCTCACCAGAAAACCATGACCA  
 GGCAAGGGAGAGGAAGCCTGCCAAACAGAAAGTCCCACTCTCAGCTGCCCCAGTCAGCCCTTCACTCCAAAGTT  
 GGCATTAATGGGACAGGTTTCTTAGACTCTCAT**TAA**CACTGGATAATTTTTTATTTTTATTTTTTTGGAGCT  
 AAACATATAAATTCCTTTTGGCTATCATAAA

153/615

## **FIGURE 152**

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN  
ASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPAFOTPTGMPYGTVNLLHGVPNGET  
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWWAQDAGIGAGVDSYFE  
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWQMYKGTVSMPPVQSLWAYWPGLOSLIGDIDNAMRTFL  
NYTYVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECGFAT  
IKDLRDHKLDRMESPPLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC  
CQRLKEEQWEVEDLMREFYSLKRSRKFQKNTVSSGPWEPPARPGLTFSPENHDQARERKPAKQKVPLLSCPSPQ  
FTSKLALLGQVFLDSS

1052586.011502

**FIGURE 153**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAAAAGTGAAGAAAAACA  
 GAAAAGGAGAGGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAACCGATCAGGCATGGAACTCCCTCTCGT  
 CACTCACCTGTCTCTGCCCCCTGGTCTTCTGACAGGTCTCTGCTCCCCCTTAACTGGATGAACATCACCCACG  
 CCTATTCGCCAGGCGCACCAAGCTGAATTGGGATACAGTGTCTTACACATGTTGGGGGTGGACAGCGATGGAT  
 GCTGGTGGGCGCCCCCTGGGATGGGCCCTCAGGCGACCGGAGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC  
 CCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCTCTGTGAATAT  
 GCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGATTTCATGGTGAGCTAAAGGAGAGGGGTGGTGGCAG  
 TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAAGTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGT  
 TAAAAACCTAGAAAGCAAAAGGTAGGTAAATGTGAGGGAGTAGTCTTCATGCCTCCTCAACTGGGAGCATGTTC  
 TGAGGGTGCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT  
 TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCGTGTGGATGCTTCATTCACGCTCAGGGAAAGCCTGGCA  
 CCCACTGCCCAAAGTGAAGCCAGAGGAAGGCTGAGTACTTGGTTCCAGAAAGGAGATACTGGGTGGGAAAAAGATG  
 GGGCAAAGCGGTATGATGCTTGGCAAAGGGCCTGCATGGCTATCCCTCATTTGCTACCTAATGTGCTTGCAAAGCT  
 CCATGTTTCCTAACAGATTTCAGACTCTGGCCAGGTGTGGTGGCCACACCTGTAATTCAGCACTTTGGGAGGC  
 CAAGGTGGGCAGATCACTTGAGGTGAGGAGTTCAGGACCAAGCCTGGCCAACTGGTGAACCTCCATCTCTACTAA  
 AAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA  
 GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTGCGGTGAGCCAAAGATTGTGCTCTGCACTCTAGCGTGGGTG  
 ACAGAGTAAGCGAGACTCCATCTCAAAAAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTG  
 GCCTGGCACAGTAACTCATGCTGTAAATCCCAACATTTGGGAGGCCAACGAGGAGGATTGCTTGAGGTCTGGA  
 GGTTGAGACCAGCCTGGGCAACATAGAAAAGACCCATCTCTAAATAAATGTTTAAAAAT

1055356.1150

155/615

## **FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039  
><subunit 1 of 1, 124 aa, 1 stop  
><MW: 13352, pI: 5.99, NX(S/T): 1  
MELFFVTHLFLPLVFLTGLCSPPFNLDHHPRLPFGPPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGDRRGDVYR  
CPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFVMS

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

10052586.011502

**FIGURE 155**

GCGAGCTCCGGGTGCTGTGGCCCGGCTTGSCGGGGCGGCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC  
 AGCGTCCCCGCCGCCCTCTCGGGAGCTCTGATCTCAGCTGACAGTGCCTCGGGGACCAAAAGCCTGCGCAGG  
 GTCTCATCTTTGTGCCCGGCTGGAGTTCACTGCCATGATCATGGTTTACAGGCTCTGACCTCCTGGGTCAA  
 CGGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATAGAGATCAAAATGGGAAAATATGCTGCTTTGGTTGAT  
 ATTTTCACCCCTGGGTGGACCTCATTTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT  
 ACCCCGGATTGTCACTGAAAGGACTTTCCATCTCACAGCCCGCATTTGAGGCAGATGCTAAGATGATGGTAAA  
 TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGCCTTTCTGAATTTGGAGGATTATCTTTCTCA  
 TGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGTTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA  
 AAATATCAACCAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAAGCATCTT  
 GGACAAAAGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTCCACGGGCTGTAGTGGCATTCTCAT  
 TTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAGGACTATGTCAAAAGGAGTAAAAAGCT  
 AAGGTTAGGTTGTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA  
 AGCTAGTGGTGGTACCAAGAGAGGGTACAGAGAGCATCTCGAGAGAGAGCGAAGGTTGGGAGAGAGAGAAA  
 AAAATCTGGCCGGGTGAGAGGATTGCCAAGGGAGGCTTCCCTTTCAGTGGACCCGGGTCAAGAAATACCCACAT  
 TCCGAAGGGCTGGGCACAGGAGGCGATGGGGGACGCTACCTTGGACTATGACTATGCTCTCTGAGCTGAAGCG  
 TGCTCAAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAATGCCTGGTGAATGATCCACTT  
 CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTCAGTGTGTCCGACGAATCCAATGATCT  
 CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCAACGGTTTCGGGGTCTATCTGCGCTCTGAAAGATCCAGACAA  
 AAGAATTTGAAGCGCAAAATCATTTGCGGTCTACTCAGGGCACAGTGGGTGGATGTCCAACGGGTTTCAGAAAGA  
 CTACAACGTTGCTGTTTCGATCACTCCCTAAAATACGCCAGATTGCTCTGGATTCAACGGGACGATGCCAA  
 TTGTGCTTACCGCTTAAACAGAGCCTGAAACAGGGCGGTGTATCATTAATCAGAGAAAACAGCTCTGCTTCA  
 CCGTAGTGAGATCACTTCATAGGTTATGCTGGACTTGAACCTGCTCAATAGCAATTTCAACATTTTTTCAAAATCA  
 GGAGATTTTCTGCTCATTTAAAAATGTATAGGTGCAGATATTGAACTAGTGGGCACTTCAATGCCAAGTATAT  
 ACTCTTCTTACATCTGGTGATGATTTTATTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTTAA  
 ACCTTCAAAACAGCTATTATAAATAACATGTGACTCCTTAATGGACTTATCTCAGGGTCCTACTCTAAGAGAAAT  
 ATTTGTGTATCTGTTGGGTCTGGGACATTTAGTTTATGTTTTTTTGAAGAAATACAAATCAGAAGAAAAAGCAGC  
 ATTATAAACAACAACTAATACTGTTTTACTGCTTTAAGAAATAACAAATTACAATGTGTATTTTAAAAATGGGA  
 GAAATAGTTTGTCTATGAATAAACCTAGTTTGAAGAAATAGGAAGCTGAGACATTTTAAATCTCAAGTTTTTAA  
 TTTAACTAATACTCAAAATATGGACTTTTTCATGTATGTCATAGGGAAGACACTTACAAATTTATGAATGATCATGT  
 GTTGAAGCCACATATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAAATCTGTAA  
 TCTTTTTCAAGAAAGAGTCTTTTTCTCCTTGACAAAATCAGCTTTTGTATGAGGACTATAGGTGAATTTCTCTG  
 ATTAGTAATTTTAGATATGTCTTTCTCAAAAATGAATAAAATTTATGAATATGA

105256.01502  
 2014.01.15



157/615

## **FIGURE 156**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFPTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL  
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNTITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFFPSTAVKL  
STGCSGILISPOHVLTAAHCVHDGKDYVKGSKLRVGLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQE  
RAKGGRRRRKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMDATLDYDIALLELKRAHKKKYMELGISPTIK  
KMPGGMHFGFDNDRADQLVYRFCVSDESNDLLYQYCDAESGSTGSGVYLRLLKDPDKFNWKRKI IAVYSGHQW  
VDVHGVQKDYNAVVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

157/615

**FIGURE 157**

GGGACCCATGCGGCGGTGACCCCGGGCTCCCTAGAGGCCCCAGCGCAGCGCGGACAAAGGAGCATGTCGCGG  
 CCGGGGAAGGCCGCTCTCCGCGCCGCATTAAGGCTCCGGTGC CGCTGGGGCCGCGCGCGCTCTGCGCGCCG  
 GGCTCCGGGGGCGCGCGCTAGCGCAGTGC CGCGCGCTGCGCCCGCAGGCGCCCGGGCCGCGACGATGAGGCCACCC  
 GGAACCGCGCGGCGCGCGCGCGCGCGCTGTGTGCTGCGCTCTCGCTGTAGCGCTGCTCGCGCTGCTGGGA  
 GCGCGCGGCGCGCGCGCGCGCGCGCTGCCCGCGCGTGAAGCAGCATGGCGCGCGCGCGAGGGGCTGGCAGG  
 GCGCGCGGCGCGCGCGGAGGCAAGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCTCTGCGCCGACATCTG  
 CCGCAACCGCAGCGTCAACCTGATTCTGAGTAAACAATAAGATATCCGAGCTGAAGAAATGGCTCATTTTCTGGGTTA  
 AGTCTCTTTGAAAGATTGGACCTCCGAAAACATCTTATTAGTAGTATAGATCCAGGTGCCCTCTGGGACTGTCA  
 TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAAT  
 CTGGTTCCGCTAAACCTTTCCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTGCGTCATTA  
 CGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTACTGTAACTACTGTGGATGCATCGCTGGGTAAAGGAG  
 AAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACAGTACAGGCGTGAAG  
 CAGGAGCTGTGTGACATGCGACCTCCGCTTGAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTG  
 TTTGAAGGAGACAGCCTTCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAG  
 GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTGAAAGAACATGATTCAACAAGTCTCTTG  
 ATTGCAAGTGCCTTAACCATTTCTAATATTACAGGCTGGATCTACTGGAAATGGGGCTGTCTGTCCAGACCAAA  
 CGTGGAAATAATACAGGAGCTGTGGATATTGTGGTATTAGAGAGTCTGTCACAGTACTGTCTCCAGAGAGGGTG  
 GTAAACAACAAGGTGACTTCAGATGGCCGAGAACAATGGCAGGCATTACTGCATATCTGCAGTGTACCGCGAAC  
 ACCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAGCTTGGCGCAGATGTGATAGAGGTGGC  
 TTTTGGGCAGATGATGATTATCTCGCTGTCAGTATGCAAAATGATGTCTACTAGAGTTCCTTTATATGTTTAAATCAG  
 ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTGCAAGTACTGTGCTTCACTGTGGAGCAGCCACAATT  
 TCTGACAAAATGGATGTATATTCTGTGGCAGAAATGATTGAAAATTTGGAAAGATTTACCAAGGAGCAAAATCA  
 AAAGAGCTAGGTGACGTGATGGTTGACATTTGCAAGTAACTCATGTGTGGCTGATGAACGTGTCTGTGGCTGGCG  
 CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCACTCTCTCAGCGCAATTGCTACTACCGGCTAGCGGTGGG  
 GCTCACGTTTATTCACCAATTTACCCCAATATTGCTCTGGAAGCTTATGTATCAAGTCTACTGGCTTACGGGG  
 ATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGGACTTTCCGATTATGGGAGCGCGGATCCA  
 GAGGGAACCTGGATTAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTTCAGTCTGGCCTAAAGGTA  
 TGTACACTCTGCAATCATTTAAAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA  
 CCTTATTTAAAGATTTTCTTGGAGGAGATAGGTATTTGCTTTTGGTACTGTTTAAAGAAAACTAACCG  
 GAGAACTGCATTAACGACTTTCAAGGGCCCTAGGCATTTTGTGCTTGTATTCCTTCTCACATAAAATATCA  
 TAAAGCTTTATTTATTTGTTTCTTGTCTCTGATTTTAAAGACAATAAGATGTTTTCATGGGCCCCATAAAGTATC  
 ATGAGCCTTTGGCAGCTGCGCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAAGGTGTTTAAATCAAGCAAGC  
 TGATATACAAATTTTGGCAGAAAACACAAATATGTCATATATCTTTTAAAAAAGTATTTTCATTGAAGCA  
 AGCAAGGATGAAGCATTTTATCTGATTTTAAATTTGGTCTTTAGATATATTTGACTACACTGTATTGGAAGCA  
 ATAGAGAGGGCACACTCCAGCACCTTAATGGAACCAATTTTTCACCTAGCTTTCTGTGGGCATGTGTAAAT  
 GTATTTCTGTGGTTTTAACTCAGCACTTTTATTTCTGCTGTGTCCTCAATAATATCACAAACAATATCC  
 AGTCATTTAATGGCTGCATAATACTGATCCAAAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCAGTCAATAAA  
 TATTGAATGAATGAACGAAAAAATAA

1055236-011502

**FIGURE 158**

[illegible]

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

**FIGURE 159**

GGGGAATCTGCAGTAGGCTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTCT  
 CTCTGCCCTCAGCGCAGGGCCGCGCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTATTAGGACCAATTAACAGG  
 TCTTTGGAGAATTACGAACCATGTTCAAGTCAAAACTGCAGCTGCTACCATTGGTGTCTATAGAAGAGGATCTAACT  
 CCTTTCCGAGGAGGCATCTCCAGGAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCCACTATCAGATC  
 ACTAAGAAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAGGTTGTAGTGGTGTGAGCACTTTATTTTG  
 GAAGTGTATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCAGGTTTCTAAATGGATG  
 GAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCCTGCTTGGACATTT  
 TGGGAAGGGGACCTGCTGTTTGGCCAAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG  
 GTAAGGTGAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAAGTCCA  
 GAACGAGATCCTCTCATTTCTCTGCTCGGAAAAACCCAAAACCTTGTGTATGCAGAATACACCAAAACCAGGCC  
 TGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCATCTTGTGGATCACTGCAAAATACAAG  
 TATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCTGTGTGGCTCACTTGTTTTC  
 CATGTTGGTGTAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCACTCAAAACA  
 GATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG  
 GGAAGCCAGTTTATAGGAACCAATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATAC  
 TCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAATCCCAAAATGTTGAAAACTGAA  
 CTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAGCCTACC  
 ATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCCTTATCATGCTGCACCCAG  
 AGCAACTCTTGAGAAAGATTAAAATGTGTCTAATACACTGATATGAAGCAGTTCACCTTTTGGATGAATAAGG  
 ACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATCACAGCTTGTGCC  
 TCAGATCATCCACCTGTGTGAGTCCATCAGTGTAAATGACTGTGTCATGTATGATGATGCCCTTTGTGCCATTA  
 TTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTCATTGTGGAAATTTGGAATTAATTCAGGCGTGTATC  
 TCTGTCACTTTATTTTAATGTAGGAAACCTATGGGGTTTATGAAAAATCTTGGGGATCATTCTCTGAATGGTC  
 TAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTCTCTTTTGTAAAACCATAACTCTGTGTAATCAGGA  
 GGTTCCTATAATGCCACATAGAAAGAGGCCAATGCATGAGTAATTATTGCAATTGGATTTCAGGTTCCCTTTTT  
 TGCCCTCATGCCCTACTTCTTAATGCCTCTCTAAGCCAAA

161/615

**FIGURE 160**

MEWASSPLRLWLLFLLPSAQQROKESGSKWKVFIDQINRSLNVEPCSSQNCSCYHGVIEEDLTPFRGGISRK  
MMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPDMEMVINVRDYPQVPKWMPEAIPVFSF  
SKTSEYHDIWPAWTFWEGGPAVWPIYPTGLGRWDLFREDLVRSAQWPWKKKNSTAYFRGSRTSPERDPLILLS  
RKNPKLVDAEYTKNQAWKSMKDTLGKPAKDVHLVDHCKYKYLENFRGVAASFRFKHLPLCGSLVFHVGDEWLEF  
FYPQLKPWWHYIPVKTDLSNVQELLQFVKANDDVAQETAERGSQFIRNHLQDDITCYWENLLSEYSKFLSYNVT  
RRKGYDQIIPKMLKTEL

10052500-011500

**FIGURE 161**

CCGAGCA CAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA  
 CCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTTCAACAAGATCTGAGTGTTTTAAATTAAGCATGGAATACAGAAAA  
 CAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT  
 GGCCTCTTCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAAACCTTCGGCTCG  
 CGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCCCTC  
 AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTCTTTTGATGATGGTACCTCAGCCTTCCCCACTACAATGTG  
 ATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACCTTCACACTTCGA  
 GAGCATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCCAACCTTCAGATGTGAAGGCC  
 AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTTATTA  
 GGCCAGAGGGCTGAAAAGGAAGACAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA  
 ATCCGACAAGATTTTTTAGACACATAAATAAACCCTGACCTTGAAAACCATTAGGCATTCAAGTGGGTAACTGAG  
 TTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTCAATCAATACTGGCAATTTAGTGAAGTAT  
 CTTTAAACCTAAACCACTCAGAGAAGTTTTTTCACAGGTTATCCTCTAATTGATAATTATCTTATAGAGGATTT  
 TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTCCCTCCATCTCGAGTGGGTTGGGTTAT  
 ATAATGTCCAGAGATTTGGTGCCAGGATCTATGAAATGATGGGTCAAGTAAAAACCCATCAAGTTTGAAGATGTT  
 TATGTGCGGATCTGTTTGAATTTATAAAAGTGAACATTCATATTCCAGAGAAGACAAATCTTTTCTTCTATAT  
 AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCATGGCTTTTCTTCCAAGGAGATCATCACT  
 TTTTGGCAGGTCATGCTAAGGAACACCAATGCCATTATTAACCTTCACTTCTACAAAAGCCTAGAAGGACAGG  
 ATACCTTGTGGAAGTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGGAGGTCAGTGTGCTGGCTTACACT  
 GAACCTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATAGTCAAGGCCCTTCAA  
 GATGATATGTGGAGGAATTAATATAAAGGAATGGAGGTTTTTGTGTAAGAAATTAATAGGACCAACAAATTTG  
 GACATGTCACTCTGAGACTAGAATTTCTTAAAGGGTGTACTGAGTTATAAGCTCATTAGGCTGTAAAAACAA  
 AACAAATGAGAGTTTTATTATGAACAATGTAGTCACTTGAAGGTTTTGTGTATCTTATGTGGATTACCAAT  
 TTAATAATATATGATGTTCTGTGCAAAAACTTCTTCACTGAAGTTATCTGAAACAAATTTTACCTGTTTTG  
 GTCACTTTATAAGTAGTCTCAAGATGTTGCAATTTTCAAGTTATTATTTTAAATTTAATTTCACTTCACTTTGTTG  
 TTTAAATGTTTTGACGATTTCAATACAAGTAAAGGATAGTGAATCATTTTACATGCAAAACATTTTCCAGT  
 TACTTAACTGATCAGTTTTATTATGATACATCACTCCATTAATGTAAAGTCATAGGTCATTATTGCAATACGTA  
 ATCTCTTGGACTTTGTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAATCTGAATA

163/615

**FIGURE 162**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERNWMMFYEYEPYRQDFHFTLREHSNCSH  
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTPFLLGQEAKEKDKMLALSLEDEHLLYGDIIHQDFLD  
TYNNITLKTIMAFRWVTEPCNAKYVMKTDTDVFINTEGVLVYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS  
YQEYPFKVFPYPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDVC  
QLRRVIAAHGFSSKEIITFWQVMLRNNTTCHY

10052586.011502

**FIGURE 163**

CATTCTGAAACTAATCGTGTGAGAAATGACTTTGAAAAAGCATTGCTTTTACAGAAAGTATATTAACCTTTTATAGG  
 AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG  
 TCCTAGTATTAAATTTCTATTGCTTACTGATTTTTTTCAGTTAAGAGTTGTATATGCTAGAATATGAGGATGTG  
 AATATAAATAAGAGAAGAAAAAGAAATAAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAAGAACTGGTT  
 TGTTTACATGCAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG  
 TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCACTACCTTGCAGCTAGAGCACTTCAGATTCCGTTGCCAA  
 CTCGTCCCATTTGGTTTCTCTTTTTGGTACTACAGAAGAGGAAAATCCAGGAAAATCTGCATAGAAAACACTTAGGC  
 TTTATACCAGAAAAAGCCAAACTATGAATTACTGGAAAAAGAAAGTAGAAAAAGAAAAAGTAGCCCTTACAAGAAG  
 CCAAAATTAAGAGCAAGGGATTGAATCCGGATGGAATCCAGCCCTTTCAACCCCTGGGTGGATTTTCTCCAGCCT  
 CCAAGCCATCATCACCAAGAGAAAGTAAAAAGCTGAAGAGAAATCACCAATCTCCATTAAATGTGAAGACAGTCAAAA  
 AAGAACCCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA  
 ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAAACACGATCACGTTCTAGATCACATACTCCAAGAAGACATA  
 ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC  
 GAAGACATCATATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACAGAGATGATTTAAAAAGTTCAAAACAGAC  
 ATGGTCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGACGCCAAGAAAC  
 ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAAGCAAGC  
 ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACCTTTCTCTCTTTCAGCCTGCATCAGTCTCT  
 TGGTTTTCGCTATCTACAGTGTGATGTATGGAATCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTT  
 CTTGAAACCCCTCTAGGTTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAAGAACTATGTTAATTTTTTGCACAT  
 TAAAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCATTTGACTTTATTTATAGTTTGTGATTGTTT  
 ATTGCTATAAGAACTGAGCGTGAATCTGTAAAAATGTATCTTATTTTATACAGATAAAATTGCAGACACTGT  
 TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATT  
 TTTACAAGGAAATAAATAACAACTCTGTGTTTTTCTAAAAAAGAAAAAAGT



165/615

**FIGURE 164**

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE  
VEKRRKVALQEAALKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN  
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSRSRSTRSRSHSESPPRRHHNHGSPHLKAKH  
TRDDLKSSNRHGHKRRKRSRSQSKSRDHSDAAKKJHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRGHGRHR

2025-03-01 15:02

**FIGURE 165**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAACTGGGCTTA  
 ATCTGAAGSTTCTCAGTCAAATTTCTTTGTGATCTACTGATTGTGGGGGCGATGGCAAGTTTGGCTTAAAGGAGCTT  
 GGCTGGTTTGGGCCCTTTGAGCTGACAGAAGGTGGCCAGGGAATGCGACACACTGCTTCGAGAGATTGAAGGCGC  
 TTCTGTTGCTGGTCTTGCCCTTGGCTCAGTCTGCTAACTACATTGACAAATGTGGGCAACCTGCATCTCCTGTATT  
 CAGAACTCTGTAAAGGTGCCCTCCCCTACGGCTGACCCAAAGATAGGAAGAGGGCGCTCACAAGATGGCTGTCCAG  
 ACGGCTGTGCGAGCCTCACAAGCCACGGCTCCCTCCCAGAGGTTTTCTGCAGCTGCCACCATCTCCTTAATGACAG  
 ACAGAGCTGGGCTAGACAACCTCGCTACGTGTCTCGGCAGAGGACGGGCGAGCCAGCAATCAGCCCATGGACT  
 CTGGCCGGAGCAACCGAACTAGGGCAGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA  
 ATCGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCGCAGCCAGGGCAGGGA  
 ATTCTGAAAACCACTGCCCTGGAAGTCTTTCCAGGTTGTACCACCTGATTCAGATGGTGAAATTAACAGCA  
 TCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC  
 ATATCATTTACCAACACATTTATCGTGATGGGGTATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC  
 TAAAGGTCAAAGGATGGACATCAGCAATGTCCCTCAACAACCTGCTGCGCTCTCTCGCCGAGCCCTGCCAGG  
 TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGCAGGAAACATGGAACAGGCCCGGATGCCCTACAGAC  
 CCCGAGATGACAGCTTTTATGTGATTCTCAACAAAAGTAGCCCCAGGAGCAGCTTGGAATAAAATGGTGCGCA  
 AGGTGGATGAGCCTGGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG  
 AGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGCGAGCCAGAAAGTGGCGCTCATCTGATTC  
 AGGCCAGTGAAGAAGCTGTTCACTCGTGTGCTCCGCGCAGGTTGGCGAGCGGAGCCTGACATCTTTAGGAAG  
 CCGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGGAGGAGCAACTCCCAAGCCCTCCATCCTA  
 CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCGGATGACCGTCCGAGGG  
 GAGCATCACATAGAGAATGGGATTTGCCATCTATGTATCAGTGTGTGAGCCCGAGGAGTATGAAGCAGAGATG  
 GAAGAATAAAAAACAGGTGACATTTTGTGATGTGGATGGGGTGCAGCTGACAGAGGTGAGCCGAGTGAGGCAG  
 TGGCATTTTGAAGAAGACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAGAGTATGAGCCCCAGGAAG  
 ACTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCCAGGTGACTGGTCCCCATCTGGGTCA  
 GTTGTGCTGGAATTAACACGGTGCTGTGATAACTGTAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG  
 GCTTCTGATTTGATAGGAGTTATGAAGAATACAATGGAACAAACCTTTTTCATCAATCCATTGTTGAAGGAA  
 CACCAGCATCAATGATGGAAGAATTAGATGTGGTGATTTCTTCTTGTCTGCAATGGTGAAGTACATCAGGAA  
 TGATACATGCTTGTCTGGCAAGACTGCTGAAAGAACTTAAGGAAGAAATTAATCTAACTATGTTTCTTGGCCTG  
 GCATTTTTTATAGAATCAATGATGGGTGAGAGGAAACAGAAAAATCACAATAAGGCTAAGAGTGAAGCACT  
 ATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAA  
 TGAAGGCCAGTTACACCTCAGAAAAATATGATTTCCAAAAAATTAAGCTACTAGTTTTTTTTCAGTGTGAGGAT  
 TTCTCATCTACTCACAACTTGTTTATATTTTTTCTATTCAATAAAAGCCCTAAAAACAACTAAAAATGATTGATT  
 TGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTGTGCCAAGGGTACATTAT  
 GGCCATTTTTTAATTTACAGCTAAAAATTTTTTAAAAATGCATTGCTGAGAAACGTTGCTTTTCATCAACACAGAA  
 AATATTTTTTCAGAGTTAA

167/615

**FIGURE 166**

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPPEVSAAATIS  
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTTRARPFFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ  
GRENSENTTAPEVFPRLYHLIPDGEITSIKINRNDPSESLIRLVGGSETPLVHIIHQHIYRDGVIARDGRLLPG  
DILKVNMGMDISNVPHNYAVRLLRQPCQVLWLTVMRECKFRSRNNGQAPDAYRPRDSSFHVLNKSSPPEQLGIK  
LVRKVDPCGVFI FNVLDGGVAYRHQCLEENDRVLAINGHDLRYGSPESA AHLI QASERRVHLVVSQRQRSPDI  
FQEAGWNNGSWSPGPGERSNTPKFLHPTITCHEKVNIQKDFGESLGHTVAGGASHREWDLPYIVISVPPGGVI  
SRDGRITGDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP  
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPPFIKSIVEGTPAYNDGRIRCGDILLAVNGRS  
TSGMIHACIARLLKELKGRITLTIVSWPGTFL

2025.07.15 10:25:36

**FIGURE 167**

GGGAAAGCCATTTGAAAACCCATCTATACAAACTATATATTTTCATTCTCTGCTGCTAGCTGCCTGGGCCTCAC  
 AATTTTCATTCTGTTTCTGACTTCAAGTTATATACCGTGGAA**TG**GAGTTGATCCCAACCATACATCGTGGAG  
 GGTTTTAAATTTTGGTGGTAGCCCTCACCCAAATCTGGTGTGGCTTTCCTTTCAGAGGATTCCACCTTCAAAATCA  
 TGAACCTCTGGCTGTTGATCAAAAGAGAAITTGSAITTCIACCTCAAAAGTCAATATAGGACTTGGCAAAAGAAGCT  
 AGCAGAAGACTCAACCTGGCCTCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACATCAA  
 CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAACCCACAGAACAGCATTT  
 CTGGGCCAGGCTG**TAA**TCAAGATTGTGTCGTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAAACATTT  
 GTGGAGAAGTGATGATACCTCTCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT  
 AAACCTTGACGAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTT  
 CCTGTATCATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

169/615

**FIGURE 168**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSQYRTWQKLAEDSTWPPINRTDY  
SGDGKNGFYINGGYESHEQIPKRKLKLGQQTQHFWARL

106256.01502

**FIGURE 169**

CGCTCGGGCACCAGCGCGGCAAGGATGGAGCTGGGTTGCTGGAGCGAGTTGGGGCTCACTTTTCTTCAGCTCCT  
 TCATCATCTCGTCTTGGCCAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGAATAATCATGTG  
 TCGGGAGTGGTGAATATGATCAGATTGAGTGCCTCGCCCGGAAAGAGGGGAAGTCGTGGGTTATACCATCCC  
 TTGCTGCAGAAATGAGGAGAATGAGTGTGACTCTCGCTGATCCACCAGGTTGTACCATCTTTGAAAACTGCAA  
 GAGCTGCCAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCTG  
 AGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTTGTGGA  
 AAGCTATCCCCATAATGCTCACTGTGAATGGACATTATGCTAAACCTGGGTTTGTCTCCAACTAAGATTTGT  
 CATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGACAACCGCATGG  
 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCCTCACTCCACGTCCT  
 CTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATC  
 CCCTTGTTTCCATGACGGCAGCTGCGTCTTGAACAAGCTGGATCTTACAAGTGTGCTGCTTGGCAGGCTATAC  
 TGGGCAGCGCTGTGAAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGCCAGTCAATGGGTACAGAA  
 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCCATGCTAAAAATGGCACCGTGGTGTCTTTTGTAAACAA  
 CTCCTATGTTCTTAGTGGCAATGAGAAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGGAAACAGCCCATCTG  
 CATAAAAAGCCTGCCGAGAACCAAGATTTTCAGACCTGGTGAGAGGAGAGTTCCTCCGATGCAGGTTTCAGTCAAG  
 GGAGACACCATTACACCAAGCTATACTCAGCGGCTTCAGCAAGCAGAAACTGCAGAGTGCCCTACCAAGAAGCC  
 AGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCACTTCACC  
 CTTCTACCGCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGGGGGGCACCATCTG  
 CATCCCTATCTGCGGGAAAAATGAGAACATCACTGCTCCAAGACCCAGGGTTGGCTGGCCGTGGCAGGCGAGC  
 CATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCTACACAAGGAGCGTGTTCTCGATGTGCGAGCGGTGC  
 CCTGGTGAATGAGCGCATCTGGTGGTGGCTGCCCATGCTGTGTACTGACCTGGGGAGGTCACCATATCAAGAG  
 AGCAGCACTGAAATTTGTTTGGGAAAAATCTACCGGGATGATGACCGGGATGAGAGACCATGGCATCCGACTTACA  
 GATTTCTGCTATCATCTGCATCCCAACTATGACCCCATCTGCTGTGATGCTGACATCGCCATCTGAACTCTTCCA  
 AGACAAGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCATCTTCCTTCCA  
 GGAGTCCCACTCATCTGGCTGGCTGGAATGTCTGCGAGAGCTGAGGAGCCCTGGCTTCAAGAACAGACACAT  
 GCGCTCTGGGGTGGTCAGTGGTGGACTCGCTGCTGTGTGAGGACAGCATGAGACCATGGCATCCCACTGAG  
 TGTCACTGATAAATCTTCTGTGCCAGCTGGGAACCATGCCCCCTTCTGATATCTGCACTGCAGACAGGAGG  
 CATCGCGCTCTGTCTTCCCGGAGGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG  
 CTATGATAAAACATGACGCCACAGGCTCTCCACTGCCCTTCAACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAG  
 AATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTTCTGATATCCGCTCTGACGTGTGTCTATGGC  
 TGAAGCATGTGGGCTTGAAGTGTGATTGGCCCTGTGAACCTTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAA  
 ACTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCACTACTAGGACAGCCAATTGGAA  
 GATGCCAGGGCTTGCAAGAAAGTAAGTTTCTTCAAAGAAAGCCATATACAAAACCTCTCCACTCCACTGACCTGGT  
 GGTCTTCCCCAATCTTCACTATACGAATGCCATCAGCTTGACCAAGGGAAGATCTGGGCTTCAATGAGGCCCTGT  
 TGAAGCTCTCAAGTTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGATGCTCTT  
 GTGTACTGGGCCACAGTACAGCTGTGCTCTTTCCTTCCCCTCTCTTGTACACATTTTAATAAAATAAGGGTTG  
 GCTTCTGAACTACAAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

171/615

**FIGURE 170**

MELGCWTQLGLTFLQLLLISLPREYTVINEACPGAENIMCRECCBYDQIECVCPGKREVVGTYTPCCRNEENE  
CDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRGQVLRAPKGQILLESYPLNAHC  
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKN  
FDGFHAIYEBITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI  
NGRHAKIGTVVSPFCNNSYVLGNEKRTCQONGWNSGKQPICIKACREPKISD.VRRRVLPQMVOVSRETPLHQLY  
SAAFQKQKLQSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKNSGRAPSCIPICGKIE  
NITAPKTQGLRWPNQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLG  
KFYRDDDRDEKTIQSLQISAILHPNYDPILLDAD IALLKLLDKAR ISTRVQPICLAASRDLSFSQESHITVAG  
WNVLADVRSPPGFKNDTLRSGVSVVDSLLCEEQHEDHGI PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSPPG  
RASPEPRNHLMLGLVSWSYDKTCSRHLSTAFTKVLPFKDWIERNMK

2025.04.15.07.00.00

ATGCTGCTCTTTGCTCAGGACGCTGCTCGCCATCGGCTCGAGTGCTCTTACAGCTGTTCCTCAGGTGAGGCTCTTAA  
 ATCGCTGTCCACCAACAGATCTTCTCGCTGGATGATTCCTCTGTAAAGACAGTGCCTGCC**ATG**CAGCAGACGCTGAACCTG  
 CACCACCATCAACAACACACAGCAGCTCATCTCGGGGCTCGGGGTCGCCCATGATCGTGGAGGTCCTCCCTCGGGCCCTG  
 GACGACGCCCTGGGTCTCTCTCGCTGCTGACGTGTGTCTGATCTGCGTGGGCGCTTCTCGCTGTGTGCTACAGCT  
 GGCGCGCTCGGACGGGGTGCATGG8ACATGTGTCAGATTTACCTTACCTGTGCTTCTGCTTCTCCGTGACCTTACATCA  
 CTTCTCATGTGTG8AGCTGTGCGGGCTCGAG8CCGGCTTCCCTCGTCTTCTGGGCACTTCCCATCATGCTTCGCTCT  
 CTATGTGCGCCCTCTTTCTGCTCTCTGCGCTCGCATCATCTACCCCAACACTATGTGTCAAGTTCTGTGCCACGGGCT  
 TTGGCGGGACACGCCATCGCGGCACCTCTTCTCTCTCATCGGTGTGTGGGCTTACGCCACCGAATGGGCTCTG  
 GACCGCGGCGCGCGCGGGGAGATCACTGGCATATGGCCACCTACCGCGGGCTGTGGAAGGTGTGTGGAGACTT  
 CGTTGCTGTGCATCATCTTCGCTTCTCAGCAGCCACCAACCTGTACGACACACGCGGCCCTGGAGTGTGTGGCT  
 GCGGGTGTGACGCATCTGTCTCATCTAGCGGCACTGCGCATCTGTGACCTGGGGAGTGCAGCAACGTGCTCT  
 ACCATACCCCTTCCCGAGCTTCTGTGGGGCTGGGCTGTGCTTGTGCTCTCTCATGTCACGCCCTTGTCTCT  
 TCGGCCCTTACACAGTTCGATGAAGAATATGGCGGCCACCTCGCGCTCTCGAGAGATGTAAAGCTGTGACGCCGAG  
 CCATGCTCTACAGTGTGTGCTCTGGGACGCCGACCTGCGTGTGGCCATCTGAGCGGCCATCAACCTATCTGCGGTA  
 TGTGGCTGACCTGTGTGATCATCTGCCACCTGTGTTTTCGAAGGT**CTA**AGACTCTCCAAAGAGGCTCCCGTTCCT  
 TCTCCAAACCTTTTPTTCTTCTCGCGGACGTTTCTTATGGAAGTACTCTTTCTCTCGCGCTTCTCTCTGTTCCT  
 TCTCTCTGTCTCCCTCCCTCCCAACCTTTTCTCTCTCCCAATCTGTGCATCTAACACAGTCTGTGAGTG  
 ATCTCTCTCTCTCCCTTCTCTCTGTGCTTCTCTCTGTGTGTTTGTGTGGCCACATCTGTTTCTTCAACCTG  
 AGCTGTCTCTTTCTTTCTTTCTTTCTTTTCTTTTCTTTTAAAGAGGATCTCACTCTGTGGCCAGGCTG  
 GAGTGACGTGTGCGATCTCAGCTCACTGACCAACCCCGCTCTCTGGGTTCAAGGAGATCTCTCTCCGCCAGCTCC  
 CAAGTAGCTGGGAGACAGGTGTGAGCTGCGGACCAACGCTGTTTCTCTTTTCCATCTCTTTTTCATCT  
 TCTTTTCTGGGTGCTCTGTGGGTTTCTATCTGCGCTTGTGCAAGACCTTCTCTGTGTGCTTGGGAGCCCT  
 GAGACTCTTTCTCTCTGCTCCACCAACCTCAAAAGTGTGCTGAGCTCACATCAACCCCTTGGACCGCTCG  
 ATGGCACAGCGCCGAAGAGGGCCCAATTGCGCAAGACAGCTCGCCACCTCTCGCTGTGCTTATGTCAGTGTGTAA  
 GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGTGAATGCTGGGATTTGGGCGCTTCTTCCAGTGTGAAGAA  
 GGTGTGTCAGTGATCTCCCTTTTAAATTTAAAAACAATATATATATATTTAGAGTGTGAGCTAAATTTCTCAATGG  
 CGGGGAGAGATTAAGACAGCAGCTCGGGTCTCGAGGCCGCTGGGCATCAGCCTTGGCAGAGATTTGGCTCAG  
 AATTTTGGCAGGCTTACAGAACCACTAGCTGCTAGAGGCCATCTTAAAGGAAGCAGGGGCTG8ATGCTTTCAT  
 CCGCAACTCTCTGTGGTATGAAAAAG



173/615

## **FIGURE 172**

```
</usr/seqdb2/seq/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTTRTTITTTTSSGLGSPMIVGSPRALTQPLGLRLRLQLVSTCVAFSLVASVGAWTSGMGNWSMPTWCFC
FSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLASIIYPTTYVQFLSHGRSRDHAIATFFSCIAQVA
YATEVAWTRARFPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALEWCVAVYAICFILAAIAILLNL
GECTNVLPPIPPPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV
```

### **Important features:**

#### **Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

#### **N-glycosylation site.**

amino acids 66-69

#### **Glycosaminoglycan attachment site.**

amino acids 18-21

2025-10-01 10:00:00

AAGCTGCGCCACCATGCCCTCTAAATTTTCTGATTTTGTAGTACAGACGGGGTTTCCACATGTGTGCCAGGCTGTGCT  
 TTAAGCTGTGACCTCATGATCCGCTCACTCGGCTCCCAAAGTCTGGATTACAGGACATGAGCCATGAGCGC  
 CTGGCCAGCCTATGCAATTTTAAAGAAATTATCTGTAATAGGTGCTGTCAAAACATTTGGGCATCATAGTGACCA  
 AAACACAGCTGAATTTCCCAAGACGCAAAACAGTGGAGGAGCAACAAGAAACAGGAATGCAAAAGAGACACA  
 TTTATTCATCATTTAGATAGGGTGACAAATGGGTTACGTTGTATGAGAGCTGATTTGTTAAGAGACTACAGAGGG  
 AGGACAGACTACCAAGAGGGGGGCGGAAAGCTCTCTGACAGAGTGTGATTTTCAGCCNAATGGAGAGATGA  
 GAAGAGAGCTACCGCCAGCTACCAATAGTCTCGAAGAGATGGGGAGCACTACACTACCTACCTATTTGGCTCGAGAA  
 AATAGCATGGGATTTGGAGGAGGCTGGGGGAAACCACTTTCTGCGCCACCTGGGACAGGAGCAATTGAGGCTTTGAGA  
 AAGGCGCAATGCGATAGCATGAGAAGAGACAGGTTAGGACAGGAGGACTTTTCAGGTGGAAATTAATAGGTTCTTAT  
 AACAGATATTTGGGCAAGCAAAAGCAGGGGAGAAATGATGTTATAGTGAAGTTTGGAGCGAGCTAGATGGGACAG  
 TGTGTGGGTGATGCAAGGAAAGAGTGCAGGAAGCAGGCGACAGCTGGGAGAGAGGTTGGGGGTTTGGTTTCCA  
 TCTTCTCGGAGATTCGCGGAATGTGGATGGGAGAACACAGAGAGGAGGACAGGGGCAAGGGGAAGGAAATCTTAA  
 AGAAGTCTGTGATGACCACTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 TCTCTCGCTCGCTCCCTCATCTCTCTGTTGCTGGTGAAGGATTAAGTGAAGTTTGTGCTTCTCGGGGCTGT  
 TGTGAATCTCATTTGCTTCTCGGAGGACATATTAACCTGTCTACGTTCTTATCATCTTCAITTCATTTCTGTTAG  
 CCACTGGGACATGATTTGGTTGTTCTTCTCTAGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAT  
 GGGGAAAGTTCATTTGCTCAGAGGGGCACTGACTTCTTAAATGTGTTTACCCAAGGTGAATTTGGAGACAGTCT  
 GCGATGTGTCGCCAATGTCGCGGACGCCCTAACTATCCAGAGATGCTGCTGCTGGCAGGTCTCCCTCTGATCTGAT  
 ATGACGCCCTTCCATGTTTCTGGCAGCTTTGTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 TGATGATCATAGCTGGGGTCTCCCTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 ACATGGATCTCTAAGTACTGCCACCTCTCCACTTCTCTGACCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 TCCACCTTCCCTCATCTCAGGATTTTCCAGGTGGTGAAGGACCAAGTGTGACCAAGCTCATCGCCATCGCCACATGGCCCGG  
 CGGAGTGGCTCACTTCAATGATGGAAGGGCTGGAGCAAGCGAGTGAATCACTCTGCTGCTCTGGAATCAAGCTTCAAGCT  
 TTTCTCTCTATTACAGCTTACGAGGCGGCAAGATAGGCTCGTTTTCGACAGAGATGTGCTGACGAGTTTGTGCTTGTGCC  
 TCGCGAAGCCAAAGCTCCGAGATGGTCTTCGCTGGTGGGAGGAGGACTCACTAGATCTCATATGATGAGGACT  
 TGCTGGGGGAATGGACACAGACATGCTGTGGGCAAGCTGCCCTTGGGGCGCATCTCAGAGACCTGTTCACCGGCC  
 ACGGTTTCTCCGGCTCTGTGCGCAGGCTCTCGTGAGCTGTGAGACAGACTGTCAAGAGCTGTCCCGACACA  
 CACTGTGCTCTAGTCTGTGACAGCTTGAGAGTGGGTTGTGGGCTCCCGGCGGCTGTGACTCTCCAGCTCTGCTG  
 CGATGAGCTGCTTCTCGCAACTGCCCCCAGCCGGAATGTGCTTCCGACAGTCTGAGGCCATCGACAGAGCTCCGAGAC  
 AGACTCACTCTACAATCTGCCCTTCACAGATCTCTGCTTTCCCCCGCGAGAGGAGGACGAGCCCTCTCAAGG  
 ATCTCCGACCACTCTGCCACACTAACCGGCACTGGGACCGCAGCGCTGAGCTCTGACCTGGCTCTCTGT  
 GGTGTGTCTCTAGATGAGGATGAGGACAGGACAGAGAAACAGTGAACCACTCATGCTCTGACATGGATGATGCA  
 TCCCCCGGCTCTGCGAGGGGACAGGCTCTGTGCCCAAGTGTGGGCTCAAGGCTCCAGACAGAGCTCCAGCGC  
 TAGAGGCTCTGTGGAGGCTGCTCTCTCTGTTGTGTTTGTATGAAGTGTGGTAGGAGAGGACGAGGCGTG  
 GCTCTGGGGCGACATCTGCTGCCCACTCCCGGAGGCTGCGCGGGGTTCGCCGGGCTCTGGGCGATGGCTCA  
 CTTGTGGGCGACAGTGATGTTTCACTGTTTAAATGCCACACAACATTTCTCTCGGATATGATGAACACA  
 ATGGGGTTGTGACTGGGGTGTGTAGAGGTGGGGTGGGAGGGGGCCAGCAACCCCCACCTCCCTCACTGCTCTC  
 TCTCTCTGCTTTTCTTCTCACTTCGAGTCTCATGTGAGTGTGATGATGAAGATACCCCCCACTGGAGGGGCTG  
 CTCTCTGCCCTCCGAGGCTATGGGTTGCTGCTCTCTTCAAGGGCCCTGCCACGCTGGGCTCTGTGCTGTGCTTCT  
 ATTCACTCTCTCATCTTCTCTAAATTTCTCTCTTTTCTCTTAAAGACAGAAGTTTGTGGCTCTTCTTTTCACTG  
 GGATCTTCTCTCTCTGGAGGCTTTGGAATGATGAAGACATGTACCTCTCCACCTTTTCTGGCGCTCAATGG  
 GCGCTTGGGCGCTTTCCCAACCCCTCTAGATGATGCGGGCATGTGCTGCGCTCTCAGACAGCGCGGCTGCC  
 ATTACCGCAGAGCTCTCTGAGCGGGAGGTGGAGAAAGAGTGTGCTTGTGTCACAGAGCTGGGACTCATGTT  
 TCTTAGAGAGGGCCACAGAGGGCCACAGGGGTGGCGGGATGTGAGTCACTGATGCTGCTGAGAGGACAGGAAT  
 TGTGCGCATGAGTGTGACAGCTATGAGGAGGAGTGTCTCTTCTGGGAGGAAGAAAGTATAGCTGCTTGTGCTGAT  
 GAAAGGCCAAGGCTACAGTACAGGCGCCGACCGAGGAGTGTAAATGCCACATGAGTGTGAGGAGCTCTGGCAG  
 ATCTGTGATCCCAAGTCACTGAGCTGTACGTTTATTTATGTTTGTGGAGAGGGTGGGTGGCTTTGAATTAAGGCG  
 CTTGTAGGCTTTGGCAGGTAGAGAGGGCCCAAGGTGAAGAACAGAGACCAAGGCAAGCACTTATATTAAGT  
 GGCTCATTAGGTTGTTATTTTGTCTTATTTAAGAATTTGTTTATTTAAATTAATAATAAAATCTTTGTAATCTC  
 TAAAA

175/615

## **FIGURE 174**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL  
SPGISQVVKDHVTKPTAMAGGRVAHLIEWKWSKPSDSPAALSAFSSYSDDLSEGEQEARFAAGVAEQFAIAEAK  
LRAWSSVDGEDSTDDSYDEDFAAGMDTDMAGQLPLGPHLQDLFTGHRFSRPPVRQGSVEPESDCSQTVSPTLCSS  
LCSLEDGLLGSFARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL  
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,  
324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

175/615

**FIGURE 175**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCACCTAATTTTGTTCCTCGGCACCCCTCCTGC  
 TCAGTGCACATTGTACACTTAACCCATCTGTTTCTCTAATGCACGACAGATTCTTTTCAGACAGGACAACCTG  
 TGATATTTTCAGTTCCGTGATTGTAAATACCTCTTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT  
 TTTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTTCTTTAAAAAAAACC  
 AATACCAAGAAAGCCTACAATGTTGGCCTTAGCCAAAATTCGTGTTGATTCAACGTTGTTTATTCACTCTCCTATC  
 GGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTTTTAAAACAATGGAAAA  
 TAAACCTATTTCTTTGGAAGTGAAGCAAACTTAACTCAGATAAAGAAAATATAACCACCTCAAACTCTCAAGGC  
 GAGTCATTTCCCTCCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGA  
 GCATTTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA  
 AGTGCCTTGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT  
 GTCTTCAGAAAACITCACTTGTCTTTGGTCAATGACACCGTAAAACTCCTGATAACAGTTCATTACAGTTAG  
 CATCTCTCTTCAGAACCACTTCTCCATCTGTGACCCCTTGATAGTGGAAACCAAGTGGATGGCTTACCAAAA  
 CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAA  
 TTCAAAACCTCTTTCCAAATACGTGAGATCCCCAAAAGAAAAAGAAATACAGGAATAGTATTCGGGGCCATTTT  
 AGGTGCTATTTCTGGGTGCTCATTTGCTTACTCTTTGGGCTACTTGTGTGTGGAAAAAGGAAACCGATTCAAT  
 TTCCCATCGCGCACTTATGACGACAGAAATGAACAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT  
 GAGTTTTTGGGAATCTAGCTACTACAATCCAACCTTGAATGATTGAGCCATGCCAGAAAAGTGAAGAAAATGCAAG  
 TGATGGCATTCCTATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA  
 GCAAGTGTCTATACATCCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTTACACAAAATTACTGTCACTGGA  
 TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAAGTAGACAGAAATGTAGACAGGATGTATCATCCAAAGGTTTTT  
 TTTCTTACAATTTTTTGGCCATCTTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT  
 AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTACCATTTACAGCCCTGCCTCATAACTAAATAATAAAA  
 ATTATTCCACCAAAAAATTTTAAAACAATGAAGATGACTCTTTACTGCTCTGCTGAAGCCCTAGTACCCATAAT  
 CAAGATTGCATTTTCTTAAATGAAAATGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA  
 CATAGCCCAGAGTTTCTGTTATTTGGGAAATTTAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT  
 TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTTATGAAGCTGACAATGACTGCAATCAACGGGGCCATGGC  
 AGGAAAGCTGACCTTACCAGGAAGTAATAGCTTCTTTAAAAGCTTCTCAAGAGTTTGGGAATTTTAACTTTGTC  
 TTAATATATCTTAGGCTTCAATTAATTTGGGTGCCTTAAAACTCAATGAGATCATGGT

177/615

## **FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732  
><subunit 1 of 1, 334 aa, 1 stop  
><MW: 36294, pI: 4.98, NX(S/T): 13  
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISESEANLNSDKENITTSNLKASHSPPL  
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTITSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSENFT  
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTFLIVEPSGWLTTNSDSFTGFTPYQKTTLQPTLKFTNNSKLFPPN  
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLLCGKRKTDTSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSS  
YYNPTLNDSPPESEENARDGIPMDDIPLRTSV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domain:**

amino acids 235-262

### **N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,  
225-229, 298-302, 307-311

10055555:011502

CAGCGATCTGTATCTTCTACCTGTTCACAGTTTCGCAATTCAGTTGGAAAGAGCTCAACTGAAGCTTCTTGCGCT  
 GCAGTGAAGCAGAGATAGATATAITTCAGTAAATAAAAAACATGGCGTCCAACTGACTTTCACCTTCTTCTTA  
 CAAATTCCGATTAAGTCTGTTCTGCTGACTTGTGCGCTACAGATGGTGGGGTGGGCGCAGGTAATCAATCTTGCGGG  
 TGGCAATTCAGAGATATCTCTTAAGCAAGAAAGGATCTCATGGCTATTTCCATAAGAACCCCTCAATTTGGGGAAGAGGAA  
 AACTCTGACATAATGAAGCATCCACGAAGAGGTAAGAACTTGACAACTGTGCTTCTGTGTCTCTTACCTCAGAGG  
 CAGAGACAGCTCATTTTCAAACAGATCTTCACTTTGGAAGAGGATGACAGGACGAAATAATCCCAAGGTGTCCAGAGG  
 CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTGCATCACTCGTTCCCAACGGGAACAGAGAGAAACA  
 CCGTATGTATCAAGTCTGGGAACATCTGCATCGCTTCTGTCAGAGGCGACGCTGATATATGGCATCTACGATCATCCA  
 CCGAGTCAAGGTGAAAGAAAGTTTAACTCCGCCAAACTCTTGATATGTGGGCTATCTAGAGAGCCCTCAAGGAAGAAA  
 TTGGAGCTGCTTTATATTCCAGATGTGCAGCTGTGATACCCGAGAAATGACTTAACCTTTACAAGTGTGAGGAGCA  
 TCCGAGCATCTGTGGTGGTGGCAGGAACAGCATGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTATC  
 TCGCCCTACGAGCAGAGCAGTGTTTCAAGGTGAATGGATTCTCTTACAACATCACTGGGGATGGGGAAGCGAAGCAG  
 TGACTCTCAGACTCAGGTTGAGCTCCAAAGAAATGAATAATTTCCCGCGCCCTGCGTGAAGTGGGTAAATATACAAT  
 GGTCTTCCACATCAGAGACAAAGGCAATGAGGTGAACGCGAAGCGGATGAAGCTCTTACACCAAGGTGTACAGAGT  
 CTGGGAACAGATGGGTGAGATGGTTGTCTTATAAATAGTATCTGTGGAACAACAACCTTTATATATACAAT  
 CACAGTGGAATCTGTGGTTGGTGCACTGACGCCGGATCTTTTGGTGAATTTTGGGAAGAACTGATTTCTTTGTGCA  
 ATAAATTTTGGGCTAGAGACTCAAATAGTAGACACATTAAGAACTGTTCAGCTCATTGTGAGCTGAATTTT  
 TCCTTTGTGTATTTCTTAGCAGAGCTCCGTGGTATGTAGAGATTAACAAAGCTGTGAACAGACAGCTTCTCTAG  
 TCAATTTGATCATGAGGGTTAAATATGTATATAGATATCTGAAGCACTTATATAAAGGATGACTCAAAGAA  
 TAAATATGAACGCTATTTGAGGACTCTGGTTGAGGAGGATTTATTTAAATTTGAAGTATATATATGGGATAAAA  
 GGCCACAGAAATAAGACTGTGTAATGTTCTGAGAGAACACAGAGTTTCTCGTCCAGGTTGAGAAGGTACGAAGA  
 TACATATCTGTTATTCATTTATCTGTATCAATCATCTGTGAAGTGGTGGTGTCCAGGTGAGAAGGGTCCCAACAA  
 GAGGGGAGAAAGGCGACCAATCAGGACAGCATGAACTTGGGAATGACGAGAGTGACGAGGGGTGGAGTGTCCGC  
 TGCAAAGCGCAGAGTAGCTGAGCTGGTTGCGAGTGTGATAGCTTCCAGGSGAGAGCTGCCACGGAATGCCCTC  
 CAGTATGCCCCACAGATAACATCTTCTATTAGTTTAAAGAGTTTGTAAAGATGATTTGTACAAGTAGG  
 ATATGAATTAGCAGTTTACAAGTTTACATATTAACATTAATAAATATGTCTATCAAAATCTCTGTAGTAAAT  
 GTGAAATAAGCAAA

179/615

## **FIGURE 178**

MGFNLT FHL SYKFRLL LLL TLCLTVVGWATSN YFVGAIQEI PKAKEFMAN FHKTL ILGKGKTLTNEASTKKVELD  
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR  
QQLDYGIVVIHQAEKGKPNRAKLINVGYLEALKEENWDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR  
LRYSGYFGGVLTALSREQFFKVN GFSNNYWGWGGE DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE  
RMKLLHQVSRVVRTDGLSSCSYKLVSV EHNPLYINITVD FWFGA

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

#### **Xylose isomerase proteins.**

amino acids 191-202

2025-10-27 10:00:00

**FIGURE 179**

CGTGGGCGGGGTGCGCGAGCGGGCTGTGGGCGCGGCCGAGGAGCGACCGCGCAGTTCTCGAGCTCCAGCTGC  
 ATTCCCTCCGCGTCCGCCCCAGCTTCTCCCGCTCCGGGCCCCGCA**ATG**GCCAGGCAGTGTGGTCCGCGCTCGG  
 CCGCATCTCTGTGCTTGCTGCCTCTGCGCTGGGCCCCGGGAGGGGTGGGCCGCGAGCGCTGTATGAATCAATCT  
 CACCAACGATAGCCCTGCCACAACGGGAGCGGTGGTGACCATCTCGGCCAGCTGGTGGCCAAAGACAACGGCAG  
 CCTGGCCCTGCCCGCTGACGCCCACTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAAGAT  
 GGAGAAGGGTCTCAGCTCCACCATCCGCTGGTGGCCACGTGCCCGGGGAATTCCCGGTCTCTGTCTGGGTAC  
 TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGGTGGTCTCCCATCAAGAGTTCTCGTGGG  
 GGACCTTGTGTACCCAGAACACTTCCCTACCTGGCCAGCTCCTATCTCACTAAGACCGTCTCGAAAGTCTC  
 TCTTCCTCTCCACGACCCGAGCACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGAAGGAC  
 CCAGATGGTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGAACCTTCCCGTGAAGCTCAAAGT  
 GGTGGCGAGTGGGAAGAGTGGAGCCGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCTC  
 GCTGAAGCTGCAGGAACCTTTCGAGGCATCCAAGTGTGGGGCCACCCTAATTCAAGCTTCCAAAAGATGAC  
 CGTGACCTTGAACCTTCTGGGGAGCCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGA  
 GGAAGGGGAGTGCCACCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACTTCAGGGACCTGGGGA  
 CTACTGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACATCAGTACCAAGATCCAGGTGTGGCCCTC  
 CAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT  
 GACCTTCGGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCAGGAGCCACCTCTGGGGTCAAGTGTCTGTG  
 CCAGATGTGCTGTGGGCTTTCTGTGAGAGACTCCATCTGAGTACCTGGAATTTGTGTGTGAGAACCAGGGCT  
 ACTCCCGCCCTCTATAAGTCTGTCAAACTTACACCGTGT**GAG**CACTCCCGCTCCCAACCCATCTCAGTGTTA  
 GCTGACTGTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTGCGTGGGGCTG  
 TTGGCTGGATCATCCATCATCTGTACAGTTTCAGCCACTGCCACAAGCCCTCCCTCTCTGTACCCCTGACCC  
 CAGGCATTACCCATCTGTACAGCCCTGACCCACTGACATAAGCCCTCTCGGTTCACCCCTTGGCCCTTACC  
 TTTGAAGAGGCTCTGTGAGGACTTTGATGCTTGGGGTGTTCGTTGGTACTCTAGTGGGGCTGTGCTGCCAC  
 TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTAGTTTCTCCCCAGACAGCCCTACCT  
 GTGCCAGAGACTAGAAAGAGGCTATAAAGGTTAAAAATCCATAACTAAAGGTTGTACATAGATGGGACA  
 CTCACAGAGAAGCTGTGCATGTACACACCAACACACACACACACACACAGAAATATAAACACATG  
 CGTCACATGGGCATTTCAGATGATCAGCTCTGTATCTGGTTAAGTGGGTGCTGGGATGCCCTTGCACTAGAGC  
 TGAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCTTTGTGCTTTGTCTCTGCA  
 GTTCTTGGGCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGCCCTGGATGGGGGGCAGGACTAATAC  
 TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCATCTGTGAAGACTTTCACCTGAGGAAA  
 AGGCTTGCACCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGG  
 AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTTAACCGGTGAAACCCCGTCTCTACT  
 AAAAAAATAAAAAAGTTAGCCGGGCGTGGTGGTGGTGGCTGTAGTCCAGCTACTCGGGAGGCTGAGGACGGA  
 GAATGGTGCACCCCGGAGCGGAGCTTGCAGTGAGCCAGATGGCGCACTGCACTCAGCCCTGAGTGACAGA  
 GCAGACTCTGTCTCA



181/615

## **FIGURE 180**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLVRFHWI  
HTPLVLTKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGFVVLPITEFLVGDLVVTONTSLPWPS  
YLTKTVLKVSFLLHDPNSNFLKTALFLYSNDFGDTQMVTEDSVVYNYNYSIIIGTFTVKLVVAEWEEVEPDATRAV  
KQKTGDFSASLKLQETLRGIQVLGPTLIQTQKMTVTLNFLGSPPLTVCWRLKPECLPLEBGECHPVSVASTAYN  
LTHTFRDPQDYCFSSIRAENLIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMLTRNATQQKDMVENP  
EPPSGVRCQQMCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-24

#### **Transmembrane domain:**

amino acids 339-362

#### **N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

2025-10-20 09:55:00

**FIGURE 181**

CGGACGCGTGGGGCGGGCGCTGCGGAATCCCGTGAGGGGGCGGTGGGCCCTCGGGCCTGACAGATGGCAGTGCG  
 CACTGCGGCGGCGAGTACTGCGCCGCTCTGGGCGGGCGGCTGTGGCTGGCGGCCCGCGGTTCGTGGGGCCAGGGT  
 CCAGCGGCTGCGCAGAGGCGGGGACCCCGGCTCATGCACGGGAAGACTGTGCTGATCACCGGGCGGAACAGCGG  
 CTTGGGCCCGCCACAGGCGCGCGAGCTACTGCGCCTGCGAGCGCGGCTGATCATGGGCTGCCGGGACCGCGCGCG  
 CGCCGAGGAGGCGGGCGGTGTCAGCTCCGCGCGGAGCTCCGCGAGGCGCGGAGTGGGCTCCAGAGCCTGGGCTCAG  
 CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT  
 GCTCCAGGAAGAGCCTAGGCTGGATGTCCTTGATCAATAACGCGAGGGATCTCCAGTGCCCTTACATGAAGACTGA  
 AGATGGGTTTGAGATGAGTTCCGAGTGAACCATCTGGGGCACTTCTACTCACCAATCTTCTCCTTGGACTCCT  
 CAAAAGTTTCAGCTCCGAGCAGGATTTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA  
 CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTATTAGCCGGAGCAAACTGGCTAACATTCCTTTTACCAG  
 GGAAC TAGCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTGGTATTGTACGGACAAATCT  
 GGGGAGGCACATACACATTCCACTGTTGGTCAAAACCACTCTTCAATTTGGTGTCTATGGGCTTTTTTCAAACTCC  
 AGTAGAAGGTGCCAGACTTCCATTTATTTGGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG  
 GGATTGTAAAGAGGAAGAACTGTTGCCCAAAGCTATGGATGAATCTGTTCAAGAAAACTCTGGGATATCAGTGA  
 AGTGATGGTTGGCCTGCTAAAA**TAG**GAACAAGAGTAAAGAGCTGTTTATAAAATGCATATCAGTTATATCTG  
 TGATCAGGAATGGTGTGGATTGAGAATCTGTTACTTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA  
 GGTACATGTGGGTATTTTGGAGTTACTGAAAAAATTATTTTGGGATAAGAGAAATTCAGCAAAAGATGTTTAAAT  
 ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATTTGTAATAATAACTGGGCAAGCA  
 TGGATGACATATTAATATTTGTGAGAATTAAAGTACTCAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT  
 TTCATGGCCAAAGTGTTAACTAGTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGCCTGGTGTGTGCA  
 CACAAGTCTTACTTGAATAAAATTTACTGGTAC

183/615

## **FIGURE 182**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR  
DRARAEAAAGQLRRELQAAECGPEPGVSGVGEIVRELDLASLRVRAFQCEMLQEEPRLDVLIINAGIFQCPY  
MKTEDGFEMQFGVNHLCGHFLITNLLGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI  
LFTRELARRLEGTNVTNVNLHPGIVRTNLGRHHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG  
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

#### **N-glycosylation site.**

amino acids 212-215 and 239-242

183/615

ACAAGCATGATCTCTCTGCTGCTCTGACGCCAGGACGGCTGATTTCAGCAGGAGGCGCTACCGCGCAGCCCGAAGATTC  
ACTATGTGTGAAATATGCTTCAATACCCCTACGCCGTGCAAAAGAGGAGGCGCGCAAGACGTGTGTAGGCCGCTCT  
CTGAGCCGCGCAGCGTCAGAACTCAGATATCTGACCGCGCAGGAGGCTCGAGATTGCCACCCAGGAAAGAGGCGCTC  
TCTGGGAGAGTGATGTACTTACTCTCTTAGGCCCTTCAATCTCATCTCTGGCAGGACATTATGTGTGTGGAGCTGCATT  
TACAGATGATCTCATGCCCAAGAGCACCAATTACCGCTGGAGAGATGTCTTTTGTGATTCTGAGGATCTCGAAAT  
CCCGCTTGTGTGGAGGAGAGCTAACTTCTCTCGCTGTGACTGAGGAGGCTGACATCTGTGAGGAGATGACAACTGCA  
ATCATTGATGTGCCCTGTCCCAAGTTCTCTGATGATGACGCGCAGCAATATTCTATGCACTTTGAAAGAGGGAATG  
ACTGCTTACCTGGACTTGTGTCTGGGGAAGTCGATATCTGATGCCCTCAATACCTCTATTGTGATGTCTCCAAAA  
AATCTGGTAGAGCTCTTTGCGAAACTGCGCAGGTGGCAGATATCTGCCCTCAAATATTGTGGTCTGAGAGAGCACTTA  
GTGTGCTGCGGAGAAATTTGCGTAGTGTATGTAACCTTGGCATCTTTATTTCACCAATTTGCAATACAGAAAGTGC  
TTCCGCTCTGCTGCGCAGACACTCTTGCTGGGTTTCAACAAAGCTGCCATGTGAATAATGCTGGAAGATTAGACAC  
TTCGCCAAGCAATTTATGTGTGAGACAGATCTTCAACATGAGTAAAGGACAAAGCAATAGAGTGTCTTGTGTAATA  
AGAAGTCAGAGATTTACAATATGACTTTAACTATTAAGTGTATTGGGATATCAAGATATTTACTCATGCAATTTAC  
TCTATTGTCTTATGCTTTAAAAAAGGAAAAAAGAAAAAATCAACCACTGCAAGCTGTGTGTCAAAATTTTGTGTT  
TAATTTGGCATCTGCTGTTGTTTGAAGACTGAAATACATAGATTTTCAATTTTCTTGTGCATTTATAGGGTTTAGAT  
TCTGAAAGCAGCATGAATATACACATCAATCTGACAAATGTTGGGTTCTTTTGTTGTTTCTTGTGTTGTTGTT  
TTTTCTTCTTCTTTAAAGTAAGCTCTTTATTCATCTATGCTGGGAGCAATTTAAAAATTTGAAATATTTAAATTT  
GTTTGTGAACTTTTGTGTAATAATATCAAGCTTCAACATTTGTTGGTTCCTTTTGTTGTTTCAATTTGTACAAC  
TCTGGAATTTGAAAAATACATCTTTCGAGTTCTGTGTAGGTGTCTGTAAATTAACCTGATCTATATGTGAAACAT  
TTTCTAGAGACAGTCATTTTTAACTAATGCAAGTAACTTCTCACTACTGTCTGTGGAAGATGCACAAAAT  
TGTTGAGTGTCTGAATGCTGTGAAGAGTTTAGTGTGTATGAATTTCAACACCTATATAAATTTTACTCTATAC  
AAAAAABAAAAAABAAAAA

185/615

## **FIGURE 184**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAPNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQKEGSSGRCLMTLLGLSFLAGLIVGGACIY  
KYFMPKSTIYRGEMCFDSEDPA NSLRGGEPNPLPVTEEADIREDDNIAIIDVPVPSFSDSDPAIIHDFEKGMT  
AYLDLLLGNCYLMPLNTSI VMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCENNRKSF  
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

185/615



187/615

**FIGURE 186**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR  
SKCGMCCKT

205710.68525001

**FIGURE 187**

CTGTCAAGGAAGACCATTCTGAAGGCTGCAATTGTCTTCTAGGGAGGCAGGTGCTGGCCTGGCTGGATCTTCCAC  
**CAT**GTCTCTGTTGCTGCCCTTTTGTAGAGCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTCCACCCT  
 CCTTCTCGCTTTTATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCT  
 GTTAAAAATCTTTGCGTGGGCTACCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACACCACGCTTTACAAGCC  
 CTACACCAACGGAAATCATTTGCAAAAGGATCCCACTTCACCTAGAGAAGAGATCAAAAGAGATTCTGCTCAAGTGGTAG  
 TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTCCGGAAGGAATGGAGAC  
 CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAGAAGCTGGAGTCTTGGAACTGCTGAGCAGAAACCAA  
 TTATAACTTCCAGTACATCAGCCTTCGGCTCAGGCTCTGTGGGGTTAGGAGTGTCTGATTCTGGTACTGCTTTCT  
 GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGGATTAGCCTTCTGGTGGTGGGCACTGCTGGTGGGATACTT  
 GCCAAATGGGAGGTTTAAAGGAATTCATGAGTAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGAGCGCT  
 GACAGCCATCATCACTACCATGACAGGGAACACAGCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC  
 ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCAAGGGGACTCATGGG  
 TGTGATTCAGAGAGCCATGTTGAAGGCCTGCCACACGCTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCT  
 GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG  
 CATCAATAATACATCGGTGATGATGTTCAAAAGGGAAGTTTGAATTTGGAGCCAAGTTTACCTGTTGCTAT  
 CAAGTATGACCTTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAATACCGGATGGTGACGTACCTGCTGCGAAT  
 GATGACCACTGGGCCATTTGTCTGACGCGTGTGTGTTACCTGCCCTCCATGACTAGAGAGGCAGATGAAGATGCTGT  
 CCAGTTTGCGAATAGGGTGAATCTGCCATTGCCAGGCAGGAGGACTTGTGGAAGCTGCTGTGGGATGGGGGCT  
 GAAGAGGGAGAAGGTGAAGGACAGTTCAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA  
 CAAGGACAGGAGCGCTCT**CGA**GCCTGCTCCAGCTGGCTGGGGCCACCGTGGGGGTGCCAACGGGCTCAGAGC  
 TGGAGTTGCCGCGCGCGCCCACTGTGTGTCTTTCAGACTCCAGGGCTCCCGGGCTGCTCTGGATCCGAG  
 GACTCCGGCTTTCGCGAGCCGAGCGGGATCCCTGTGCACCCGCGCAGCTACCTTGGTGGTCTAAACGGAT  
 GCTGTGGGTGTTGCGACCCAGGACAGATGCTTGTCTTTTACAATAAGTCTGTTGGAGGAATGCCATTAAAG  
 TGAATCCCAACCTTTGCACCTGTGCGGGCTGAGTGGTTGGGGAGATGGGCCATGGTCTTGTGCTAGAGATGG  
 CGGTCAAGAGTCTGTTATGCAAGCCGCTGTGCCAGGATGTGCTGGGGGCGGCCAACCCGCTTCCAGGAAGGCC  
 ACAGCTGAGGCACTGTGGCTGGCTTCCGCTCAACATCGCCCCCAGCTTGGAGCTCTGCAGACATGATAGGAAG  
 GAACTGTGATCTGACAGGGCTTTTCACAAAATGAAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTTAA  
 GGGAGGGGAAGAGGCCAGTGGCCGCTGACTGGGCCATGGGAGAACTGTGTTGCTACTCCAGCTTAACCTG  
 AACTCCCCATGTGATGCGCGCTTGTGTAATGTGTCTCGGTTTCCCATCTGTATAATGAGTCGGGGGAATG  
 GTGGTGATTCTCACTTCCAGGGCTGTTGTGGGATTAAAGTCTGCTGGGTGAGTGAAGGACACATCACGTTTCA  
 GTTTTCAAGTACAGGCCCAAAAACGGGGCACGGAGGCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG  
 TCTTGTGAGTAAATAAACTGGCTGGTGAATGA



189/615

**FIGURE 188**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSPFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP  
YTNGIIAKDPTSLIEEEIKERRSGSSKALDNTPEPELSDIFYFCRKGMETIMDDEVTKRFSABELESWNLLSRTN  
YNFQYISLRLTVLWGLVLIKYCFLLPLRIALAFTHGSLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRAL  
TAIITVHDRENRPNGGICVANHTSPIDVILASDGYAMVQGVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL  
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFELGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM  
MTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGGLVDLLWDGGLKREKVKDTFKEEQQKLYSKMIVGNH  
KDRSRS

2025.04.15 10:52:56

**FIGURE 189**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGA.CCCCTGGCCCTCAGTCTCCTCCAGG  
 GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCAGGCTGTTCCAC  
 CATCCTGCCCTGGGCTGGCTCCAGACACCTTTGACGATACCTATGTGGTTTGTGCAGAGGAGATGGAGSAGAA  
 GG.CAGCCCCCTGCTAAAGGAGGAAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCC.CAGGAGAC  
 CTGGGAGGACAAGCGT.CGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAAATAGCCATTATGGTCTA  
 CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGAGCTCTA  
 CATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG  
 CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAAGAGGCTGGGGGA  
 CTCTGTCCGCTTGGGCCAGTTTGCCCTCAGCTCCCTG.GATAAGGCAGTGGGCCACAGATTTGGGAGAAAGAGCG  
 GGGCTGTGTCTGCGCCAGGGGTGCAGCTAGGGT.CACAATCTGAGGGGGCTCCTCTCTGCCCCCTGGAAGAC  
 TCTGCTCTTGGCCCCCTGGAGAGTTCAGCTCTCAGGGGTGGGCCCTGAAGTCCAACATCTGCCACTTAGGAGC  
 CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAA.CATGGTTCCGAC  
 CCAGCCCTAGCAGCCTTCTCCCCAAC.CAGGATGTTGGCTTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTA  
 TGTGATGGGGACTTCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA  
 GACATGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

2024.03.25  
 10:55:33

1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Discussion**  
 6. **Conclusion**  
 7. **References**  
 8. **Appendix**  
 9. **Index**  
 10. **Table of Contents**  
 11. **Abstract**  
 12. **Keywords**  
 13. **Subject Headings**  
 14. **Summary**  
 15. **Notes**  
 16. **References**  
 17. **Appendix**  
 18. **Index**  
 19. **Table of Contents**  
 20. **Abstract**  
 21. **Keywords**  
 22. **Subject Headings**  
 23. **Summary**  
 24. **Notes**  
 25. **References**  
 26. **Appendix**  
 27. **Index**  
 28. **Table of Contents**  
 29. **Abstract**  
 30. **Keywords**  
 31. **Subject Headings**  
 32. **Summary**  
 33. **Notes**  
 34. **References**  
 35. **Appendix**  
 36. **Index**  
 37. **Table of Contents**  
 38. **Abstract**  
 39. **Keywords**  
 40. **Subject Headings**  
 41. **Summary**  
 42. **Notes**  
 43. **References**  
 44. **Appendix**  
 45. **Index**  
 46. **Table of Contents**  
 47. **Abstract**  
 48. **Keywords**  
 49. **Subject Headings**  
 50. **Summary**  
 51. **Notes**  
 52. **References**  
 53. **Appendix**  
 54. **Index**  
 55. **Table of Contents**  
 56. **Abstract**  
 57. **Keywords**  
 58. **Subject Headings**  
 59. **Summary**  
 60. **Notes**  
 61. **References**  
 62. **Appendix**  
 63. **Index**  
 64. **Table of Contents**  
 65. **Abstract**  
 66. **Keywords**  
 67. **Subject Headings**  
 68. **Summary**  
 69. **Notes**  
 70. **References**  
 71. **Appendix**  
 72. **Index**  
 73. **Table of Contents**  
 74. **Abstract**  
 75. **Keywords**  
 76. **Subject Headings**  
 77. **Summary**  
 78. **Notes**  
 79. **References**  
 80. **Appendix**  
 81. **Index**  
 82. **Table of Contents**  
 83. **Abstract**  
 84. **Keywords**  
 85. **Subject Headings**  
 86. **Summary**  
 87. **Notes**  
 88. **References**  
 89. **Appendix**  
 90. **Index**  
 91. **Table of Contents**  
 92. **Abstract**  
 93. **Keywords**  
 94. **Subject Headings**  
 95. **Summary**  
 96. **Notes**  
 97. **References**  
 98. **Appendix**  
 99. **Index**  
 100. **Table of Contents**  
 101. **Abstract**  
 102. **Keywords**  
 103. **Subject Headings**  
 104. **Summary**  
 105. **Notes**  
 106. **References**  
 107. **Appendix**  
 108. **Index**  
 109. **Table of Contents**  
 110. **Abstract**  
 111. **Keywords**  
 112. **Subject Headings**  
 113. **Summary**  
 114. **Notes**  
 115. **References**  
 116. **Appendix**  
 117. **Index**  
 118. **Table of Contents**  
 119. **Abstract**  
 120. **Keywords**  
 121. **Subject Headings**  
 122. **Summary**  
 123. **Notes**  
 124. **References**  
 125. **Appendix**  
 126. **Index**  
 127. **Table of Contents**  
 128. **Abstract**  
 129. **Keywords**  
 130. **Subject Headings**  
 131. **Summary**  
 132. **Notes**  
 133. **References**  
 134. **Appendix**  
 135. **Index**  
 136. **Table of Contents**  
 137. **Abstract**  
 138. **Keywords**  
 139. **Subject Headings**  
 140. **Summary**  
 141. **Notes**  
 142. **References**  
 143. **Appendix**  
 144. **Index**  
 145. **Table of Contents**  
 146. **Abstract**  
 147. **Keywords**  
 148. **Subject Headings**  
 149. **Summary**  
 150. **Notes**  
 151. **References**  
 152. **Appendix**  
 153. **Index**  
 154. **Table of Contents**  
 155. **Abstract**  
 156. **Keywords**  
 157. **Subject Headings**  
 158. **Summary**  
 159. **Notes**  
 160. **References**  
 161. **Appendix**  
 162. **Index**  
 163. **Table of Contents**  
 164. **Abstract**  
 165. **Keywords**  
 166. **Subject Headings**  
 167. **Summary**  
 168. **Notes**  
 169. **References**  
 170. **Appendix**  
 171. **Index**  
 172. **Table of Contents**  
 173. **Abstract**  
 174. **Keywords**  
 175. **Subject Headings**  
 176. **Summary**  
 177. **Notes**  
 178. **References**  
 179. **Appendix**  
 180. **Index**  
 181. **Table of Contents**  
 182. **Abstract**  
 183. **Keywords**  
 184. **Subject Headings**  
 185. **Summary**  
 186. **Notes**  
 187. **References**  
 188. **Appendix**  
 189. **Index**  
 190. **Table of Contents**  
 191. **Abstract**  
 192. **Keywords**  
 193. **Subject Headings**  
 194. **Summary**  
 195. **Notes**  
 196. **References**  
 197. **Appendix**  
 198. **Index**  
 199. **Table of Contents**  
 200. **Abstract**  
 201. **Keywords**  
 202. **Subject Headings**  
 203. **Summary**  
 204. **Notes**  
 205. **References**  
 206. **Appendix**  
 207. **Index**  
 208. **Table of Contents**  
 209. **Abstract**  
 210. **Keywords**  
 211. **Subject Headings**  
 212. **Summary**  
 213. **Notes**  
 214. **References**  
 215. **Appendix**  
 216. **Index**  
 217. **Table of Contents**  
 218. **Abstract**  
 219. **Keywords**  
 220. **Subject Headings**  
 221. **Summary**  
 222. **Notes**  
 223. **References**  
 224. **Appendix**  
 225. **Index**  
 226. **Table of Contents**  
 227. **Abstract**  
 228. **Keywords**  
 229. **Subject Headings**  
 230. **Summary**  
 231. **Notes**  
 232. **References**  
 233. **Appendix**  
 234. **Index**  
 235. **Table of Contents**  
 236. **Abstract**  
 237. **Keywords**  
 238. **Subject Headings**  
 239. **Summary**  
 240. **Notes**  
 241. **References**  
 242. **Appendix**  
 243. **Index**  
 244. **Table of Contents**  
 245. **Abstract**  
 246. **Keywords**  
 247. **Subject Headings**  
 248. **Summary**  
 249. **Notes**  
 250. **References**  
 251. **Appendix**  
 252. **Index**  
 253. **Table of Contents**  
 254. **Abstract**

FIGURE 190

MALAALMIALGSLGHTWQAQVPTILPLGLAPDTFDDTYVVGCAEEMEEKAAPLLKEEMAHHALLRESWEAAQET  
 WEDKRRLGLTPPGPKAQNGIAIMVYTNSNTLYWELNQAQVTRGGGSRELYMRHFFPKALHFYILRALQLLRGSGG  
 CSRGPGEVFRFGVSLRLEFPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCSAPGVQLGSGSQSGASSLLPPWKT  
 LLLAPGFEQVLGSGVGP

**FIGURE 191**

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACAATGCCTCACCCCTCATCTATAT  
 CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCCTGAAAGAGCTGGTCGGTTCCCGTTGGTGGGCGCGTGAC  
 TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTTCTGGACCTTCAACACAACCCCTCTGTCAACCAT  
 ACAGCCAGAAAGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGGCTA  
 CTCCTGAAGCTCAGCAAACTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA  
 GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA  
 GAGCAATAAGAAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTATAC  
 CTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTCCCAATAATGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA  
 AAGTGATATGACCTTCATCTGCGTIGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA  
 GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTGTGGTGGCCCTCCTGCT  
 CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGGTACATTGAAGAGAAGAA  
 GAGAGTGGACATTGTTCGGGAACTCCTAACATATGCCCCATTCTGGAGAGAAACACAGAGTACGACACAATCCC  
 TCACACTAATAGAACAACTCCTAAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGAT  
 GGAAAAATCCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTGCTTATGAGAATGTTATCTAGACAGC  
 AGTGCACTCCCCTAAGTCTCTGCTCA

193/615

**FIGURE 192**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVMTFNNTPLVTIQPEGGTIIIVTQN  
RNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLKPKVMTMGLQSNKNGTCVTNLT  
CCMEHGEEDEVITYWKALQQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSS  
MVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPA  
NTVYSTVEIPKKMENPHSLLTMPDTPPLFAYENVI

193/615

**FIGURE 193**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGCACCCAGCAGGACTCTCTCTTCCAGCCAGG  
 TGCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTCTGACGCCAAGGAACTGGTCTTGGGGGACCCATG  
 GTTTCGGCGGCAGCCCCAGCCTCTCTCATCTTCTGTGTCTGCTGCTGGGGTCTGTGCTGCTACCGACGCCCGC  
 TCTGTGCCCCGTGAAGGCCACGTCTCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCCCTCTCC  
 CCGAGCCTCCCGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCAACCCCTGGGGGGC  
 CCATCACCCCCCACTTCTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGATGCTGATTGCTGTGGTG  
 GGCTCCCTGGCCCTTCTGCTGATGTTCTCATCTGTGTGCCCGGTGATCACCGGCAGAAAGCAGAGGCTCGGCC  
 TATTACCCATCGTCTTCCCCAAGAAGAAGTACGTGGACCCAGAGTGACCGGGCCGGGGGCCCGCCGGCCCTTCACT  
 GAGGTCCCCGACAGAGCCCCGACAGCAGGCCCCAGGAAAGCCCTGGATTCTCTCCCGCAGCTCCAGGCCGACATC  
 TTGGCCGCCACCCAGAACTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGSAACGAGCCAGGATGGTGGAG  
 GGCAGGGGCGCAGAGGAAAGGAGAAAGGGCAGCCAGGAGGGGGACAGGAAGTCCAGGGACATGGGGTCCAGTGT  
 GAGACACAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGAAGGGGCTGTGGTGGCCGGTGAGGGCCAAAGGG  
 GAGCTGGAAGGTCTCTCTTGTAGCCCAAGGAGCCAGGACCCAGTGGGTCCCCCGAAAGCCCTGTGCTTGC  
 AGCAGTGTCCACCCAGTGTCTAAAGTCTCTCCGGCTGCGAGCCCTGACTGTGGGGCCCCAAGTGGTCACTC  
 CCCCCTGTATGAAAGGCCCTCAGCCCTGACTGCTTCTTGACACTCCCTCCTTGGCCCTCCCTGTGGTGGCAATCC  
 CAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGAGGAATCTTACCAAGTGCCATCA  
 TCCTTCACTCAGCAGCCCCAAGGGCTACATCTACAGCACAGTCCCCTGACAAAGTAGGGGAGGGCAGTGT  
 CCCTGTGACAGCCAGGATAAAACATCCCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAC  
 TACTTTTAAACAGCTACAGGGTAAATCCTGACGACCCACTCTGGAATACTGCTCTTAATTTTCTGGAAG  
 GTGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCTCTCAAGCGCTCTC  
 CAAGCACCCCCGGCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGGGATCAGGTGMAATGAATGGAATCTCT  
 TCTGTCTGGCCCTCAAAGCAGCTAGAAAGCTGAGGGGCTGTGTTTGAAGGGACCTCCACCTCGGGGAAGTCCGA  
 GGGGCTGGGGAGGGTTCTGACGCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTGTGCTCACACATGT  
 CTGGCAGCTGTGTCACATAATTCTGTCAGTCTCGACAGCGAGCCTGGGCTCCGCTCTGCTTATAGGAGGCTCT  
 GGCAGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGACAGCTCTCCAGGTGCTGAGATA  
 TAATGCACAGCACAAATAACCTTTATTCGGGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAGA

195/615

## **FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEABGSSASSPSLPPPWTPALSPPTSMGPQPTTLG
GPSPTTNFLDGI VDFFRQVVMILAVVGSLLAFLLMFIVCAAVITRQKQKASAYYPSSFPPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRP EALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGA VVAGEGQGELEGSLLLAQEAQGPGVGPPEPSPACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,  
242-248

195/615

196/615

**FIGURE 195**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA  
CTGACCCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACCTTTAATGTAGAAAAGATTAAATGGG  
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG  
GAGCHAAATCCATGTCTTGGAGAAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA  
TCTATGGTTGCTGACAAAAAGAGAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACTATA  
CCTAAGACAGACTATGATAACCTTTCTTATGGCTCACCTCATTAAAGAAAAGGATGGGGAAACCTTCCAGCTGATG  
GGGCTCTATGGCCGAGAACAGATTGAGTTCAAGCATCAAGGAAAGGTTTGACACAATATGTGAGGAGCATGGA  
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCCTCCAGGCCCGAGAATGAAGAATGGCCTGA  
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCATATCCATAAGCATCCCCAGTA  
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACCTAGGAT  
ACCTCATCAAGAAATCAAGACTTCTTTAAATTCTCTTTGATACACCCTTGACAATTTTTCATGAATTTATTCCT  
CTTCCTGTTCAATAAATGATTACCTTGCACTTAA

1005336.01502



197/615

**FIGURE 196**

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQIHVLENSLVLKVH  
TVRDEECSELSMVADKTEKAGEYSVTYDGENTFTIPKTDYDNFLMAHLINEKDGETPQLMGLYGREPDLSSDIKE  
RFAQLCEEHGILRENIIDLSNANRCLQARE

10052586.01507

198/615

## **FIGURE 197**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTCGAAGGATGGACATCCTGCAATGGATTGAGCCTG  
CTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTGAGCTTAGTTGAGGAAGACCAATTT  
TCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTCCAGGAATATAGGAGCAGGTCTGATGGCCATTCCAGCA  
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTC  
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAAGTCCCTCTCATG  
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTATCCAGAATCC  
TTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAAACCCAGTAACGACACC  
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCA  
GTATTTTATAGGTCTATTGCTTGTGGAATCTGGAGGTCTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT  
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAAGTCAAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTATCAGTA  
GTTTGAAAAA

198/615

199/615

**FIGURE 198**

MTCCEGWTS CNGPSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR  
ACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGFLMCNFSNSNANCEFSLKNISDIHESFNLQWFFNDS  
CAPFTGPNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR  
SQIV

2025-04-15 10:55:36

200/615

**FIGURE 199**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG  
AGGAACCTGCAAGTACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC  
CGCCCCAGTGCTCTCCCCCTGCAGCCCTGCCCTCGAAGTGTGACATGGAGAGAGTGAACCTGGCCCTTCTCCT  
ACTGGCAGGCTGACTGCCCTTGAAGCCAATGACCCATTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA  
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA  
ATGCAAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC  
TGCCACTACTTGTGAGACACAGGACTGGCTCCAGGGATGGCTGAAGCCTAACACTGGCCCCCAGCACCTCTC  
CCCTGGGAGGCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTAGGCCCTTCTGATCAGGAGG  
TTCTTTTATGAATTAAACTCGCCCCACCACCCCCTCA

2025.10.09 09:50:42



[illegible]

203/615

## **FIGURE 202**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKPQGPLACLILLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALQGGT
REAVCTGVRQVPFGFCAADALCNRVGEAAHALGNTGHETCRQAEDVIRHCADAVRGSWQGVPGHSCAWETSGGHGI
FGSQGGGLGGQGGNPGGLGTFWVHVGYPGNSAGSFGMNPQGA PWGQGNGGPPNFGTINTQGA VAPQPGYGSVRASNQ
NEGCTNPFPSGGSGGGSSNCGGGSGSQSGSSGSGSGNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSGGS
RGDSGSESSWGSSTCGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGRFGQGVSSNMREISKEGNRLLGGS
GDNYRGQGGSSWGGGGDAVGGVNTVNSETSFGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIIP
```

### **Signal peptide:**

amino acids 1-21

### **N-glycosylation site.**

amino acids 265-269

### **Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### **Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### **N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,  
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,  
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,  
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,  
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,  
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

### **Cell attachment sequence.**

amino acids 301-304

203/615





205/615

## **FIGURE 204**

MSLLSLPWLGLRPFVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPQPPKRNWFWGHLGLITPTTEGLK  
DSTQMSATYSQGFTVWLGPITIPFIVLCHPDTIRSIITNASAAIAPKDNLFIRFLKPWLGEIGILLSGGDKWSRHRM  
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATI  
LELSALVEKRSQHILQHMDFLYLSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDDFFKDKAKSKTLD FID  
VLLLSKDEEDGKALSDEDI RAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEWDDL  
AQLPFLTMCVKESLRLHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPPFRFDPENS  
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVBEPLNVGLQ

205/615

**FIGURE 205**

TCCCTTGACAGGTTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT  
 TTTGCCACAGCAGTTCTCTGACGTTCTCTGAGGTTGAAACCCACATCTCTGCCCCAGAGGCCACTCGACGAGTCG  
 CGACACCTACCCCTCAGCAGAGCGCCGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCTGTATC  
 CTCTTTGGCCCTCATCACCATTCTCATCTCTACAGCTCCACAGTGCCAAATGAGGTCTTCCATTACGGCTCCCTG  
 CGGGGCGGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCATTTCTCGGCAAC  
 AAGACACTGCCCTCTCGGTGCCACCACTGTGTGATTGTACGAGCTCCAGCCACTGCTGGGCACCAAGCTGGGC  
 CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGACCCACCACTGGCTACTCAGCTGATGTGGGC  
 AACAAGACCACTTACCGCGTCTGTGGCCATTCCAGTGTGTTCCGCGTGTGAGGAGGCCCCAGGAGTTTGTCAAC  
 CGGACCCCTGAACCGTGTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCTCGTGCCT  
 GTGATCCAGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCCGCATGCGGCAATTT  
 GACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAAGTCTCATTTCTGGTTGAGCACAGGCTGGTTTACC  
 ATGGTGATCGCGGTGGAAGTTGTGTGACACGTCATGTCTATGGCATGGTCCCCCCTCACTGTCAGCCAGCGG  
 CCCCCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGCCGGAAGAATGTGTCACTACATCCAGAAT  
 GAGCACAGTCGCAAGGGCAACCAACCACCGCTTCATCACCAGAGAAAGGCTTCTCATCTGTGGGCCAGCTGTAT  
 AGCCTCCGCCAGCGCTAGGCCAGGGACCACTTCTGGCCAAATCAAGGCTTGTGGAGTGTCTCCAGCCAAATC  
 AGGGCCTTGAGGAGGATGTATCTCCAGCAATCAGGGCTCGGGGAATCTGTGGCGAATCAGGAGTTTGGGAGT  
 CTATGTGGTTAATCAGGGGTGTCTTCTTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT  
 TCTGAGTCAATCTGAGGCTAAGGACATGTCTTCTCCATGAGGCTTGGTTGAGAGCCCGAGGAATGGACCCCC  
 AATCACTCCCCACTCTGTGGGATAATGGGGTCTGTGCCAAGGAGCTGGGAATCTGGTTTCCCCCTCAATTT  
 CCAGCACAGAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAAATTTGTGGGGTGTGG  
 AGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGAGGCTGGGCATCCAGTCTTGGCTCTGCCCTGAGACCTTG  
 GACAAACCTTCCCCCTCTCTGGGCAACCTCTGCCCCACACAGTTCAGTGGCGAGTCTGAGACCTTTCCAC  
 CTCCCCACAAAGTGCCCTCGGGTCTGTCTCCCCGTCTGGAACCTCCAGGCCACTATCCCTGTGCTGGAAGGCTCA  
 GCTCTTTGGGGGTCTGGGGTGAACCTCCCCACCTCTGGAAACCTTTAGGGTATTTTGGCGAAACTCCTTCAGG  
 GTTGGGGCACTCTGAAGGAAACGGGACAAACCTTAAGCTTTTTCTTAGCCCTCAGCCAGCTGCCATTAGCTT  
 GGTCTCTTAAAGGGCCAGGCCCTCTTTTCTGCCCTTAGCAGGAGGTTTCCAACTGTGAGAGCGCTTTGGGG  
 CTGCCCCCTTGTCTGAGTCACTGGGGCTTCCAGGGTCTCCCTCGACCTCTGTCTGCTCTGGGATGGCTGTCTG  
 GGAGCTGTATCACTCTGGTTCTGTCCCCCTGGCTCTGTATCAGGCACTTTATTAAGCTGGGCCCTCAGTGGGGTGT  
 GTTTGTCTCTGTCTTCTGGAGCTCGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGACAGCATG  
 GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGGGTGGGGCGGTGACTGCCACAGACTTGGTTTTGTA  
 ATGATTTGTACAGGAATAACACACCTTACGCTCCGGAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC

# **FIGURE 206**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVPHYGSLRGRSRPVLNKKWSITDGYVPILGNKTLPSRCHQCV  
IVSSSSHLGLTKLGPETIERAECTIRMNDAPTGTYSADVGNKTTYRVVAHSSVFRVLRPPQEFVNRTPTVFIIFWG  
PPSKMKQPGQSLVRVIQRAGLVFPNMEAYAVSPGMRMQFDDLFRGETGKDREKSHSWLSTGWFTMVIIVELCDHV  
HVGVMVPPNYCSQRPRLQRMPIHYIEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

207/615

**FIGURE 207**

GTAGCGCGCTCTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCAC  
CGCCATCGCGAGGCATCAAAGCTTTGATAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTGTGATGCTTGG  
ATGTGCTCTTCCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTCATCTCTTTCACCTTTTCCATTCATA  
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTGAAGAACTTGCATCTTTCTTCATC  
AACGGGCGATTGTCGTGTGAGCTTTTGGACTCCCTATTGTATTTGCGAGAGCACATCTGATTGAGTGGGGAGCTTG  
TGCACTTGTCTCACAGGAAACACAGTCATCTTTGCACTATACTAGGCTTTTCTTGTCTTTTGGAAAGCAATGA  
CGACTTCAGCTGCGCAGCAGTGGTGTAAAGAAATTAAGTAACTTGTGAACTATTGTCAAATGGACTTCTGTCAATTGTTGGCC  
ATTACGCGCACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTAGGTGCTCC  
CTTCTCACCTTTTATGTAAGCATACTATTTTACAGAGACTGCTGGAAGGATTAAGAGGATTTTCTCTTTGGAA  
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT  
TTCTGTAGGTGATTTTGTGGAATCAATATGCAATGTTAAACACTTTTAAATGTAATCATTTGCATTGGT  
TAGGAATTCAGAAATCCCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTATTTAGCCTCCATTA  
TTACAAAAAATTATAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCGAGACATACAGAC  
GGTTGGCATACGTTATAGACTGTATACCTAGTGCAAAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTAA  
TGCCCATGCCCTCCGTTAAGGGTGTGTGTTTACTGGTAGACAGATGTTTGTGGATTGAAAAATTTATTTATG  
AATTGCTACAGAGGAGTGTCTTTCTCTCAATGTGTAAGAATTTATGTTAAACTTTAAGGTAAAGGGGTGAAAA  
ACATTTTGTAGATAAGGTCTTTTATTTATGTTTATTTATGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG  
AAATCCAGTTTGTGAATCCTGTTTCTATTTATAAGTAAATTTGTGATCTCCTATCAACCTTTCATGTTTATACC  
CTGTTAAATGGACATACATGAACCACTACTGATGAGGGACAGTTGTATGTTTGCATCATATATGCGCAAGAAAC  
CTTCTCTGCTTCTCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAATAACTTTTCAAATATAGTTT  
AATAACACTTGAAGTGTTTACTTACCTGAAAAATAATGCTATGCCGTACATTGAGAGTGGCCCCCTCCCTGCA  
AGGCTTGCCATGATTAAACAAGTAACTGTGTTAGTCTTACAGATAAATCATGATTAAAGTGTAAAGATTTAGACC  
ATGGCTTAATAGTAGTCTTATTTCTCAAGGTTATATCATATGTAATTTAAAGTATTTTAAAGCAAGTTTCTGCT  
ATACCTCTGAACGTGTTTGGATTTTGGTTTACATCTAATAAATTTATCAGGACTTTTTCAGGAGTGGGTATAAAA  
GAGGATGATCAAAATTTATAGTGGTCTGTTACATCTAATAAATTTATCAGGACTTTTTCAGGAGTGGGTATAAAA  
CATTCAAGTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATGTTTATTCAGTATACTTACATAAAAAAT  
ATTTCCGCCATCAGCCAAACTCAGTAATCATGACAGCTGCTGTTGTTTATGAAGTTTATTTTCAAGAAATG  
GGAATAAATTTGGGATTTGTTTACGCTTTTACTTAAAGTGCCTAAAGCCACAGGTTTATTTGCTCTAATTAAGC  
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGCGCTGTGGCTGGAGCCTTCCCACTGGAGGC  
TGAAGTGGCTTGTGATTTATAATGTTTCAAGTTTCAAGAGGAAGCTGCAGGTACACATGAGTTAGAGAGCTGCT  
GAGACAGTTGGGAACCTCTTGTGCTTGTGATCTACTGGACTTTTTCAGGAGGAGTGCATTTCTGCTGCTTC  
CCTATTTTCTGTTTGTGATGTCAGTGCAGTGCATCTGCTGTTTATCCACTTGGCCACAGACTTTTCTTAACA  
GCTGCGTATTTTCTATATACATAAATGCTATGGCAGCATGTTGCTTTGACCTTGTATATCTAGCTTGCATAGT  
GCTGTCCTGATTTCTAGGCTAGTTTCTAGATATGAATTTCCATAGAAATATGCAGTGATACACATTAACCAT  
TCTTCTATGGAAGAAAACTTTTGTGATGAAACAATAAAGATTTTAAATATCTATTTTAAAAA

209/615

**FIGURE 208**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIPLTT  
GIVVSAFGLPIVFAHAHLIEWGACALVLTGNTVIFATILGFPLVFGSNDDFSQQW

2025.10.08 09:55:00



211/615

## **FIGURE 210**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602

<subunit 1 of 1, 223 aa, 1 stop

<MW: 24581, pI: 9.28, NX(S/T): 0

MKFVPCLLLVTLSCGLTLQAPRQKQGSTGEEFHFQTGGRDSCCTMRPSSLGQGAGEVWLRL  
VDCRNTDQTYWCEYRGQPSMCQAFADPKFYWNQALQELRRLHHACQGAFLRPSVCREA  
GEQAHMQQVTSLLKGSPEFNQQPEAGTPSLRPKATVKLLEATQLGKDSMEELGKAKPTTR  
PTAKPTQPGPRPGGNEEAKKKAWEHCWKPFQALCAFLISFFRG

**Important features:**

**Signal peptide:**

Amino acids: 1-19

**N-myristoylation sites:**

Amino acids: 38-44;51-57;194-200

**DNA photolyases class 1 proteins:**

Amino acids: 58-69

**Tyrosine kinase phosphorylation site:**

Amino acids: 64-71

**N-myristoylation sites:**

Amino acids: 38-44;51-57;194-200

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids: 4-15

2025 RELEASE UNDER E.O. 14176

212/615

## **FIGURE 211**

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG  
GTCTCCAAACTCTGGGTCCCCAACACGGAATTTCAGCGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC  
GGCGGGCGCCGTGAGTTCGCGCGGACAAGATGGTGTTCAGTCTGGTGC AAGAAGGTACGCGCTCTCAGACATG  
CTCTGCGCGCTGGATGGGAACTCGTCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTG  
GACTGTGGCGCGGGCGAACTGCGCGTCTTCCGCGACTCTGACCGCTTCTCTGGCATGACCGCACCTGTGGCGCT  
CTGGGGACGAGGCACTGGCCCTCTTCTTGGTGGACGCCGAGCGCGTGGCCCTGCGCGCACGACGACGTCTTCTTTC  
CGCTAGTGCCCTCCTTCCGCGTGGGGCTCGGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG  
GCCGACGTTTACGCGCGACGAGGACCTGGCTGTTTCTTGGCGTCCCGCGCGGGCCCGCTACGCTTCCACGGGC  
CGGCGCGCTGA GCGTGGGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC  
CGTGGATCTGCGCGGCCCTGCTCCAGCCCT

10052536.011502



213/615

## **FIGURE 212**

</usr/seqdb2/sst/DNA/Dnasegs.min/ss.DNA59603

<subunit 1 of 1, 197 aa, 1 stop

<MW: 20832, pI: 8.74, NX(S/T): 2

MGVLGRVLLKQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV  
QEGHAVSDMLLPDGLVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTICGAL  
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRITWL  
FSWRPARAAAYASTGRAR

### **Important features:**

#### **Signal peptide:**

Amino acids 1-19

#### **N-glycosylation site:**

Amino acids 35-39

#### **Glycosaminoglycan attachment site:**

Amino acids 81-85

#### **N-myristoylation sites:**

Amino acids 82-88;118-124;153-159

#### **C-type lectin domain proteins:**

Amino acids 108-118

213/615

**FIGURE 213**

ATGCGATCAATTGGGAGTACCATCTTCCTC**AT**GGGACCAGTGAAACAGCTGAAGCGAATGTTTGAGCCTACTCGT  
 TTGATTGCAACTATCATGTGCTGTTGTGTTTGCACTTACCTGTGTTCTGCCTTTTGGTGGCATAACAAGGGA  
 CTTGCACTTAICTTCTGCATTTTGCAGTCTTTGGCATTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGG  
 GATGCTGTGAAGAAGTGTTTGGCGTGTCTTTGCAT**TA**ATTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTA  
 TGGACAGAAGCTGGTGGACAGTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGC  
 AGCAATGTGTGCTGTGATTGGAACATTTGAGGGTTACTTTTGGAAAGCAACAATACATTCGAAACCTGAATGT  
 CAGTAGCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTCTCTGG  
 ATGTTGTCCCCTGAATCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

215/615

**FIGURE 214**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIIQSLALTWYSLSFIPFARDAVKKCFVCLA

10510-8828001

216/615

## FIGURE 215

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCAGGACAGGCCACCC  
TGCGGGGCGGGAGGCAAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGCGAGAGAGGCCAAGCCCCCTTGCCCTGGG  
TCAACAGCCAAAGGAGGCGAGGCCAGAACTCACACCAGATCCAGAGGCCAACAGGGACATGGCCACCTGGGACG  
AAAGGCACTCACCCGAGGGCCAAGGTGGCTCCGCTGAGAGGATGAGCAAGTTCTTAAAGCACTTCACGGTCG  
TGGGAGACGACTACCATGCTTGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGGAGC  
AGCCACCCACACACAGTCTCAGGCGAGGAAGGAGAGCTGCAGCCCCCTGACGTTGCCCTTGCCCTTGCCCTCG  
CAGCCAGGGCCCCCTTGACTTCAGGGGACATGTTGAGGAACTGTTTACGCTCCACAGGTTTCAGGTCATCATCA  
TCTGCTTGGTGGTCTCGGATGCCCTCCTGGTCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCCGACA  
AGAATAACTATGCTGCCATGGTATTCACACTACATGAGCATCACCATCTTGGTCTTTTATGATGGAGATCATCT  
TTAAATTAATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCGCTGCTGGTGGTGGTCT  
CATTCATCCTGGACATGTGCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCTGCTGATTTCTGCTCCGGC  
TGTGGCGGGTGGCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAGAACGGCAACTCTTAAGGT  
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTACGCTGCTCTGAGAAAGCCCCCTGGACT  
GATGAGTTTGTCTGATCAACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAAATCCGACTTCTA  
CTCTCACACAGCCACCGTGAAAGTCTGGAGTAAATGTGCTGTGTACAGAGAGAGAGAAGGAAGCAGGCTGGC  
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA  
CAGAGCATCTGCCGTGTTTCAATCACAGAGAACAAAACCAAATCTATAAAGATATTTCTGAAAATATGACAGAA  
TTTGACAAATAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

[illegible]

**FIGURE 216**

MATWDEKAVTTRRAKVAPAKRMSKFLRHFTTVGGDYHAWNINYYKKWENEEEEEEEEQPPPTVSGEEGRAAPDVA  
 PAPGPAPRAPLDFRGMRLKFLSSHFRQV I I C L V V L D A L L V L A E L I L D L K I I Q P D K N N Y A A M V F H Y M S I T I L V F F  
 M M E I I F K L F V R L S S F T T S L R S W M P V V V V S F I L D I V L L F Q E H Q A L G L L I L L R L W R V A R I I N G I I I S V K T R S E  
 R Q L L R L K O M N V L A A K I O H L E F S C S E P L D

**FIGURE 217**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCAGCC**AT**GGCTTCCCTGGGG  
 CAGATCCTCTTCGGAGCATAAATAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT  
 ATTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGAGGATGGAATCCTGAGC  
 TGCACCTTTGAAACCTGACATCAAACCTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTAGGCTTGCTC  
 CATGAGTTCAAAGAAGSCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGGCCGACAGCAGTGTGTTGCT  
 GATCAAGTGATAGTTGGCAATGCCTCTTTGCGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT  
 TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG  
 AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGCTCCCGATGGTTCCCCAGCCCACAGTGGTC  
 TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAAT  
 GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC  
 ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAAC  
 TCAAAGGCTTCTCTGTGTGCTCTCTTCTTCTTTGCCATCAGCTGGGCACTTCTGCCCTCAGCCCTTACCTGATG  
 CTAAAT**TAA**TGTGCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAAATCATATCTAGAAGTCTGGAGTGAGCAACAAG  
 AGCAAGAAACAAAAAGAACCCAAAGCAGAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA  
 GAAAGTTGGGAAAAATAATTCATGTGAAGTACAGACAAAGTGTGTTAAGAGTGATAAGTAAATGCACTGGAGACAAGT  
 GCATCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG  
 TCTCTGAATTTTGTATATATGTGCTGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCA  
 CATCTATATTTCCACAAATTAAGCTGTAGTATGTACCCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG  
 GGGCGGTGCTCATTTTAGTAAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCCTTGGCTTCTCTC  
 CCAACTGACAAATGCCAAGTTGAGAAAAATGATCATAATTTAGCATAAACAGAGCAGTCGGGGACACCGATTT  
 TATAATAAACTGAGCACCTTCTTTTAAACAAAAA  
 AAAAAA

219/615

**FIGURE 218**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEEDIKLSDIVIQWLKEG  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF  
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC  
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

2025.05.25 15:00

**FIGURE 219**

GAATTGTGTAAGACAGCGGCGTTGCCATGGCGGCGTCTCTGGGGCAGGTGTGGCTCTGGTGCTGGTGGCGGCT  
 CTGTGGGGTGGCAGCAGCCGCTGCTAAGCGGGCCCTCGCCGGCCCTGCAGCGGGTTCAATGAGCCGACCTGGGCC  
 CAGCAGTTGCTACAGGAGATGAAGACCCCTCTCTTGAATACTGAGTACCTGATGCCCTTTCTCTCAACCAGTGT  
 GGATCCCTTCTCTATTACCTCACCTTGGCATCGACAGATCTGACCTTGGCTGTGCCCATCTGTAACCTCTCTGGCT  
 ATCATCTTCACTGATTTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAAACGTAAGTTAGACTACTGCGAG  
 TGGGGGACGCAGCTCTGTGGATCTCGACATACTGTGTAGTTCTTCCAGAACCCATCTCCCCAGAGTGGGTG  
 AGGACACGGCCCTTTCCCATCTGCCCTTCTCTCTGCAGCTGTTTGTCTCTTGTGGCCATCAGAGTTCCCTTC  
 CCCTGGACAGTCTGGAGAAAGACAGAGGCTGGGGTTTGGGATTGAAGACCAGACCCCATCTGAGCCCTTCTCTCA  
 GCCCTGTACCAGCTCTACTGGCATGGCTGAGCTCAGACCTCCTGATTTCTGCTCTATTATCCAGGAGCAGTTG  
 CTGGCATGGTGTCTACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGCCAACAGT  
 CTACCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCTGGGCCATGAAGTGTGGCA  
 GTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCCTTAGCTTCTCTCTCTTATGGGGATAACAGCTACCTCA  
 TGGATCACAATAAGAGAACAGAGTGAAAGAGTTTTGTAACTTCAAGTGCTGTTAGCTGCGGGGATTTAGCAC  
 AGGAGACTCTACGCTCACCTCAGCAACCTTTCTGCCCGAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCGAG  
 CCCAGCCACCTATTACTGTGGCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACTCCAGCTGCA  
 TGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAACGGGAGGCCCTCTGGGACTCAGTCAGAGCGCTTTGG  
 CTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCTGAGTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCT  
 TGCCTGCCCCACCCATGAGGTAGGCAGAAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCC  
 CAGCCCCACCTGACTCCAGCACACTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

10052586-01502



221/615

**FIGURE 220**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTRYLMPFLNQCGLLYLTL  
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCEGTQLCGSRHTCVSSFPFPISEFWVRTRPPFILP  
FPLQLFCFLVAIRVPPFWTVWRKTEAGVWD

1052386.01502

**FIGURE 221**

CTTCTGTAGGACAGTCAACAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA  
ATTATAGCAGGACCCCTGCCAGGCTGTGCAAAAGATTCCGCAATAAACTTTGCCAGTGGGAAGTACCTAGTGAAA  
CGGCCTAAGATGCCACTTCTCTCATGTCCCAGGCTTGAGGCCCTGTGCTCCCATCCTTGGAAGAAAGTCAAGCTC  
CAGCACCAATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGTGTGCAGCTGTAGAACTCTCTGAGCTGCGT  
GCAGTGTAAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACAGCTG  
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACAGTCAGATTATACCAGAAATATGTTCTGCTCAGCGGAGAA  
CTGCAGTGAGGAGACACATTAAGCCTTCACTGTCCAGCTGTCTGTGGAAGAACACTTTCATTTTGTAAAGCA  
GTGCTGCCAAGGAAGGAATGCAGCAACACAGCGATGCCCTGGACCCCTCCCTTGAAAGAACGTGTCCAGCAACGC  
AGAGTGCCCTGCTTGTATGAATCTAATGGAACCTTCCTGTCTGGGAAGCCCTGGAATGTCTATGAAGAAAGCA  
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACT  
CAGTAACGCCACCTGTCTAGTTCTCTGTCTGGTGAAGAACAGACTCTTGAGGAGTCACTCTTCGAAAGTTTGAAGT  
TGCAAAATGAAACAGCTTAAACCCCAAGTCTGCAACCAACCACTTCCCAACAGTGGGCTCCAAAGCTTCCCTCTA  
CCTCTTGGCCCTTGCCAGCCTCCTTCTTCGGGGAAGTCTGCCCTGAAGGTCTTGGGGCTGCACTTTGCCAGCACC  
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAA  
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCAGAGCTGCCTTGTCTTCTATTATTAAGCACTG  
TTCATTCACTGCCAAAAA

223/615

**FIGURE 222**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLETFPVRLYQNMFCSAENC  
EETHITAFTHVSAEEHFFHVSQCCQKCSNTSDALDPPLKNVSSNAECPACYESNGTSCRGKPKCYEEECV  
FLVAELKNDIESKSLVLKGCNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTHNVGSKASYLL  
ALASLLLRGLLP

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 223**

GGCCTCGGTTCAAACGACCCGGTGGGCTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGGCTTGCTCTAC  
 TGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCGCGCGCTGCTGTGGGTCTGTGCTGCTG  
 AATCTGGGTCCCCGGCGCGGGGGCCCAAGGCTTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACG  
 TTTGGGGGCCCATGACCCGCACTACCGGAGCACCGCCGGAAGTCTTCCCCGGAAGACAAGGATAATCCTA  
 GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACAGCGGCTGCCGAGCTCTTGGCCGCCACG  
 GTGTCCACCGGCTTTAGCCGGTCTGTCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTGTGATTAAT  
 GCCGGAAGGATAGCACCGAGAGAGCTTCCAGTGCAGCTCCCAATACAGCGGGGAGTTCAGACAGAGGTTT  
 ATAGCCAATAGTCAGGAGCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCCGGAGGTCTCTGAGGAC  
 CTGCCAGGCTCGCAGGCCACCTGAGCCAGTGGTCCACACTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCA  
 CCCACAGCCATGCCATCTCCTGAGGATCTGCCGCTGGTGTGATGCCCTGGGGCCGTGGCACTGCCACTGCAAG  
 TCGGGCCATGAGCCGAGCGGCTCTGGGAAGCTGCAAGGCTTTCCGGGCGCTTCGAGTTGGGGCGCTGAGC  
 CAGCTCCGACGAGACAAAGCCTTGCACTTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG  
 GACACAAGTCTCTGTACTGACACCAACTGTGCTCTCAGAGCACCAACAGTACAGGACCAACCACTACCCCTTC  
 CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCGAGCCCTGCCAGCCCTGGCTTTTGGAAACGG  
 GTCAGGATTGGCCTGGAGGATATTGGAAATAGCCTCTCTCAGTGTTCACAGAGATGCAACCAATAGACAGAAAC  
 CAGAGGTAAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCTTTCAATCCTAGCAC  
 CCACTAGATATTTTAGTACAGAAAAACAAACTGGAACACAA

1052556.01502

225/615

**FIGURE 224**

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD  
RIAGPAAAEALLATVSTGFSSAINEEDGSSEEGVVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL  
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRNPSPTAMPSPEDLRVLMPWGPWHCHCKSGTMSRSRSGK  
LHGLSGRLRVGALSQRLTEHKPCYQQCCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTTPTIHLRSSPSL  
PPASPCPALAFWKVRVIGLEDIWNLSVFTMQPIDRNQR

105536-0450

**FIGURE 225**

CCCGGGTGAGCCACGCGTCCGGGGAGAAAGGATGCGCCGGCTGGCGGCGCGGTGTGGTCTGCTAGCTGGGGCAG  
 CGCGCTTGGCGAGCGCTCCGAGGGCAGCCTGTAGCGCGGTGTACCGCGACTGCGTACTGCATGCGAAGAGCAGA  
 ATGCTCTTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAACTTCAATGAGTGTACGAGGCTGGACCTGTG  
 GGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGTTGGGCTTACCTCCAGAGAAAGTCACAAAGTGCCTCACT  
 TCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCGGTGGCTCTGTTCTCAATG  
 GCCTGGCGAGCGCTGTGATGCTCTGCGGCTACCGCACTTCTGTGCCAGCGCTCTCTCCCCATGTACACACCTGTG  
 TGGCTTTCGCTGGGTGTCCCTCAATGCATGGTCTGGTCCACAGTCTTCCACACCCAGGGACACTGACCTCACAG  
 AGAAAAATGGACTACTTCTGTGCCTCACTGTATCCTACACTCAATCTACCTGTGCTGGGTGAGGACCGTGGGGC  
 TGCAGCACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCTGCTGCTCATGCTGACCGTGACAGCTCTCTCTACCTGA  
 GCCTCATCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGGCTATGGGCTGGTCAACGTGGTGTGGTGGC  
 TGGCTTGGTGCCTGTGGAAACGAGCGGCGGCTGCTCAGTGCAGCAAGTGCCTGGTGGTGGTGGTCTTGTGCTGCAAG  
 GGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCATCTGGGCACATCA  
 GCACCATCCCTGTCCACGCTCTCTTTTTCAGCTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG  
 ACAAGTTCAGCTGGACTGAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCTCTGCTGGCCCTC  
 CCTTCTCCCTCAACCTTGGAGATGATTTTCTCTTTCAACTTCTGAACTTGGACATGAAGGATGTGGGCCGAC  
 AATCATGTGGCCAGCCCAACCCCTGTTGGCCCTCACAGCCTTGGAGTCTGTTCTAGGGAAGGCTCCAGCATC  
 TGGGACTCGAGAGTGGCGAGCCCTCTACCTCCTGGAGCTGAACTGGGTGGAACTGAGTGTGTTCTTAGCTCTA  
 CCGGGAGGACAGCTGCCTGTTTCTCTCCCAACAGCCTCTCCCCACATCCCCAGCTGCGTGGCTGGGTCTGAAG  
 CCCTCTGTCTACCTGGGAGACCAGGGACCAAGGCTTAGGGATACAGGGGGTCCCTTCTGTTCACACCCCCCA  
 CCCTCTCCAGGACACCCTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAGGTTCA CGGCGATTTCTCCCC  
 ATGGGATCTTGGGAGCCAAAGCTGCTGGGATTTGGGAAGGAGTTTCAACCTGACCGTTGCCCTAGCCAGGTTCCCA  
 GAGGGCTCAGCATACTCCCTTTAGGGCCAGGGCTCCAGCAAGCCCAAGGATCCTGTGCTGCTGTCTGG  
 TTGAGAGCTGCCACCGTGTCTGGGAGTGTGGGCGAGGCTGAGTGCATAGGTGACAGGGCGGTGAGCATGGGCC  
 TGGGTGTGTGAGCTCAGGCCCTAGGTGCGCAGTGTGGAGACGGGTGTTGTGGGGGAAGAGTGTGGCTCAAAG  
 TGTGTGTGTGCAAGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGCTGTGTGCGCGCTGCTGGTGGGCATGTGAAG  
 TGAAGTGTGCAAGGCTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGGAATCTGTACACCATCAATAAT  
 CACTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCTCT  
 GTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCTCTCTGCAAACTCACAGGGTCCCAACAAACAGTGGCC  
 TCCAGAACGACCCCTCGGAGGCGAGGGAAGAAATGGGGATGGCTGGGGCTCTCTCCATCCCTCTTTCTCTCT  
 TGCCTTCGATGGCTGGCTCTCCCTCCAAAACCTCCATTCCTCTGCTGCCAGCCCTTTGCCATAGCCTGATTT  
 TGGGAGGAGGAAGGGCGCATTTGAGGAGGAAGGGAGAAAGCTTATGGCTGGTCTGCTTTCTTCTCTCCCTCCAG  
 CCCAAGGCGAGTCTCGTGGTTGAAGCAGACTGGATTTTGTCTGCGCCCTGACCCCTTGCCTCTTTTGGGGA  
 GGGGAGTCTCTAGGACTCCAACTCAGGACTCGGTGGCTGCGTAGCTCTTTTGATGACTGAAACTTTT  
 AAGGTGGGAGGTGGCAAGGATGTGCTTAATAAATCAATTCGAAGCTCAAAAAAAAAAAAAAAAAA

227/615

## **FIGURE 226**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV  
TVGLYLQEGHKVPQPHGKWPFSSRPLFFQEPASAVASFLNGLASLVMLCRYRTFFVPASSPMYHTCVAPAWVSLNAN  
FWSTVEHTRDTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNL  
VANVAIGLVNVVWNLAWCLWNQRRLPVVRKCVVVVLLQLGLSLELLLDFFPLFWVLDAHAIWHISTIPVHVLFFS  
FLEDDSLYLLKESEDKFKLD

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

227/615-227/615





229/615

**FIGURE 228**

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTD RSDARLQYGLLIFG  
AAVSVLLQEVFRPAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLSFGIISGVFVINILADALGPGVVG I H  
GDSPIYYFLTSAFLTAATLLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNFWYEASLLPIYAVTVSMG  
LWAFITAGGSLRSIQRSLLCKD

1052536.01502

**FIGURE 229**

CGGGAGGCTGGGTCGTATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCTCCAGGGCTCCCGCG  
 GCGGACCCCGCGCAACATGACAGCCACGGGCGCGAGGGTTCCGCGCGCTCAGCGGCGGTATCTGCGGCGTC  
 TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCGAGCCGTAACCCGCGCGAGACACGCCGGGCGCCCCAGAG  
 CCCTCTCCACGCTGGGCTCCCCAGCCTCTTACACACGCCGGGTGTCGCCAGCGCCCTCACTACCCAGGCTCA  
 CTACGCCAGGCACCCCCAAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG  
 ACGGCCCAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACTGCGAAATT  
 TCAGCCATGGTCAGACCACCTTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT  
 CATGCCAGTCCCAGGACAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCAATCACCGCATGTGTGCCCT  
 CCTACTCTGAACTCGAGCTTGTGACCTCAGCTGAAGGCTGGAACAGCTCTCAAAGCTGGCCTGCCTCATTTGGCG  
 TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA  
 CACTTACCTTCACTGCACTACACCATGGGCGAGAGTTCACCAAGTTTACAGACCCACATGTACACCAACGTGA  
 GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCTCTATG  
 CATCGGACACCTTGATAAGAAAGGGTCTCGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG  
 CTGTGTGTGACAATTTGTTGAATGTTCCTCGATGATATCCTGAGCTTCTGAAGAACGGTGCCATCGTGATGGTGA  
 CACTGTCCATGGGGGTGCTGCACTGCAACCTGTCTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA  
 GGGCAGTCAATTGGATCTGAGTTTATCGGGATTGGTGGAATTATGACGGGACTGGCCGGTTCCTCAGGGGTGG  
 AGGATGTGTCCACATACCAGTCTGATAGAGGAGTTGCTGAGTGTCTGAGTGGAGGCGAGGAAAGAGCTTCAAGGTG  
 TCCTTCGTGGAACCTGCTGCGGGTCTTACAGCAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCG  
 TGGAGGCTGAGTTTCCATATGGGCACTGAGCACATCTGCCACTCCCACTCGTGCCCTCAGAATGGACACCCAGG  
 CTACTCATCTGGAGGTGACCAAGCGACCAACCAATCGGGTCCCTGGAGGTCCTCAAATGCTCCCACTACCTTG  
 TTCCAGGCCTTGTGGTGTGTCACCATCCCAACCTTCAACCAGTGGCTCTGCTGACACAGTCGCTCCCGCAGA  
 GGTCACTGTGGCAAAGCTCAAAAGCCCCCTCTCTAGTTTCAATTCACAGCATATGCTGAGAAATAACATGTTA  
 CACATGAAAA

205746.9825001

**FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTPGLTTPGTP
KTLDLRGRAQALMRSPFLVDGHNDLPQVLRQRYKQVLQDVNLRNPSHGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLLIHRMCASYSELELVTSAEGLNSSQKLACLGIXGGHSLDSSLSVLSRFYVLCVRYLTLTFTC
STPWAEBSSTKFRHMYTNVSGLTSPGEEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVDDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIFIGGNYDGTGRFPQGLEVDSTY
PVLIEELLRSRWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFFYQGLSTSCHSHLVPQNGHQATHLEV
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,  
357-362, 394-399, 427-432 and 472-477.**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 231**

GCTCTGGCCGGCCCCGGCGATTGGTCAACGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG  
 CCACCTCCCCACACCCCTTTGCGAACGCTCCCTAGTGGAGAAAGGAGTAGCTATTAGCCAATTCCGACAGGGCCC  
 GCTTTTGAAGCTTGATTTCCTTTGAAGATGAAGA CTAGCGAAGCTCTGCCTCTTTCCCACTGGGCGAGGG  
 AACTCGGGCGGATTGGCTGGGAACGTATCCACCCCAATGTCAACCGATTCTTCCTATGCAAGGAATGAGCAGAC  
 CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAAATGGTTGGCCCCCAGGAAGCCACGACA ACTGGAGGCAAGAGG  
 GTTGCTCAACGCCCCCGCTCAATTGGAAAAACCAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGCGGAT  
 GATTGTCTCGCTCGCACCCCACTGCAGCTGCGCACAGTCGCATTCTTTTCCCCGCCCTGAGACCTCGCAGACCA  
 TCTGTCA**Atg**CGCGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGACGCGGCGACGCGAGGGCTCCCG  
 GCCGCCCGCGCTCGCTGGGAATCTAGCTTCTCCAGGACTGTGTCGCCCGCTCGCTGTGGCGGGAAGCGGCC  
 CCAGAACCGACCAACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACTTGATGAGAAGAACCCAGACTCC  
 CATGGTTATGACAAGGACCCCGTTTGGACGCTCGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATC  
 CTGGTCCTTGGCAGCACCTTTGTGSCCTATCTGCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAG  
 AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACTGCTTCGACCCCAAGATCCAG  
 CTGCCAGAGGATGAG**Tga**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCAACCCCTGCGCTGCCATT  
 TGACCTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

205110.9855001  
 1005556.01502

233/615

**FIGURE 232**

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPEDENLYEKNPDSHG  
YKDPVLDVWNMR LVFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPTMESNCFDPSKIQLPEDE

1002536.011502

**FIGURE 233**

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGCTCTGCTCTGCTCTGCGGGCCCGGGCGCTGGTGCCTTGCAAGACCCCA  
 CGCGACAGCCTGCGGGAGGAACCTGTTCATCACCCCGCTGCCCTTCCGGGACGTAGCCGCCACATTCCAGTTCGCC  
 ACGGCTGGGATTCGAGCTTCAGCGGGAAGGAGTGTCCATTACAGGCTCTTTCCAAAGCCCTGGGGCAGCTG  
 ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCAITTCACACAAGGCTTTTGGAGGACCCGATACCTGGGGGCCA  
 CCCTTCTGTCAGGCCCCATCAGGTGACAGAGCTGTGGGTCTGGTTCCAGAGACACTGTCACTGATGTGGATAAATCT  
 TGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCTCTCTCAACTCATGACTCCACCAACACAGTC  
 ACTCCCACTGCGCTCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTCTGCGCTATGCTGTGCTG  
 CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGGAAGAAGCTCTTGCCCTGTAGTTCCAAAGGCAGGCCTC  
 TCTGTGCTGCTGAAGGCAGATGCTGTGTTCCACACCAAGCTACCACTCCCAAGGCAGTGATATCCGCGCTGTTTGC  
 AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTGAGTTGATTGATGCCCTCATCACG  
 GGGCAGGGAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCGAAACCTCACGGAGCCCTGCCCTTGGCTTCA  
 GAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACAAAGAGACATTAGAGGTGCACCCACCCCGACC  
 ACTACATATCAGGACGTCATCCTAGGCACCTCGGAAGACCTATGCCATCTATGACTTGTGACACCGCCATGATC  
 AACAACTCTCGAAACCTCAACATCCAGCTCAAGTGGAGAGACCCCCAGAGAAATGAGGCCCCCCCAGTGCCCTTC  
 CTGCTGCCCGAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC  
 CCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCAC  
 ATCACTCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC  
 CTCTGGAGATGCTGATTACAGCTCCCGGCCAACTCAGTCAACAAGTTTCCATCCAGTTGAGCGGGCGCTGCTG  
 AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATGTGCTCCTGAGCGCCCTGTGCGCC  
 AGCATGGTAGCAGCCAAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC  
 TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC  
 AACGTGATCTGCTCAGTGCACTGTGGTGGCCGTGTGCTACGGCTCCTTCAAACTCTCTCACCAGAACCTTC  
 CACATCGAGGAGCCCGCACAGGTGGCTGGCCAAGCGGCTGGCCAACCTTATCCGCGCGCCGAGGTGTCCCC  
 CCACT**CGA**TTCTTGCCCTTTCCAGCAGCTGCAGCTGCCCTTTCTCTGCGGAGGGGAGCCCAAGGGCTGTTTC  
 TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCTGGACCAAGTCAGGGCCTACAGTGTGTTGT  
 CCAGTACAGGAGCCAGAGCCAAATGTGGCAATTGAATTTGAATTAACCTAGAAATTCATTTCTCACCTGTAGT  
 GGCACCTCTATATGTAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGTATTGGACAGCACAGAAAAGAT  
 TTCCATCACCAAGAAAGTCCGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGT  
 GTAGTGGATGGAGTTTACTGTTGTGGAAATAAACCGGCTGTTCCGTGGAAAAAATAA

235/615

**FIGURE 234**

MPLALLVLLLLPGGGWCLAEPFRDLSREELVITPLPSGDVAATFQFRTRWDSSELQREGVSHYRLFPAKALGOLISK  
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWKELSNVLSGIFCASLNFIDSTNTVTPT  
ASFKPLGLANDTDHYFLRYAVLPREVUCTENLTWKKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA  
RCTSISWELRQTLGVVFDAFITGQKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTY  
QDVILGTRKTYAIYDLLDTAMINNSRNLIQLKWKRPFENEAPFVFFLHAQRYVSGYGLQKGELSTLLYNTHPYR  
AFPVLLLDTPWYLRRLYVHTLITTSKGKKNKPSYIHYQPAQDRLQPHLEMLIQLPANSVTKVS IQFERALLKWT  
EYTPDENHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLNLPTPDFSMPYNVI  
CLTCTVVAVCYGSFYNLLTRTFHIEEPTGGLAKRLANLIRRARGVFL

205110-9852501





**FIGURE 236**

MASYPYRQCCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPFGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG  
 TPGGPYGGAAPGGPYGQPPSSYGAQQFGLYGQGGAPPNVDPEAYSWFQSVDSHSGYISMKELKQALVNCNWSS  
 FNDETCLMMINMPDKTKSGRIDVYGFSAWKFQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL  
 VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAPFREKDTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

**FIGURE 237**

CAGG**ATG**CAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCTGCTCCTGGTCTGTCTTCATCTCCCAGGCCCT  
 CTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCAAAACTTCGGGACCAACTTGCCCTCAGCTCGGACA  
 ACCTTCTCTCACTGGCCCTCTAACTCTGAACATCCGCAGCCCGCTCTGGACCCCTAGGTCTAATGACTTGGCAAG  
 GGTTCTCTGAAGCTCAGCGTGCCCTCAGATGCGCTTCCACCTGCAGGAGGTCTGCAGTGCAGAGGTGGCC  
 TCCATCGTGGGGGCTGCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGA  
 GGACCGCTGGGGGAGCGCTGCCTGAAGAACTCTCTTAACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCACTGG  
 CCCTTGGCTGGGGAGTCTCTCCCGATGCCACAGGCCCTCTCACCTGAGGCTTCACTCCTCCACAGGACTCGGA  
 GTCACAGCACTGCCCGTTCTAATTCACTGGGAGCCGGGGAAAAATCCTTCCCAAGCCCTCCCTGGTCTCT  
 CATCCACAGGGTTCTGCTGTATCACCCCTGGGGTACCCCTGAATCCCAGTGTGTCTGGGGAGGTGGAGGCCCTGG  
 GACTGGTTGGGGAACGAGGCCATGCCACACCCCTGAGGGAATCTGGGGTATCAATAATCAACCCCGAGTACCAG  
 CTGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAA  
 TATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCTCTGG  
 AGTTCTCCGCCCTCCTGGCTCTTCTTGGAACTCCAGCTGGCTTCCCTAATCTCCAAGCCCTAGGTTGCAGTG  
 GGGCT**AG**AGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCTTGCTGTGTGGGCTCA  
 ATCCAGGCCCTGTAAACATGTTTCCAGCAGTATCCCACTTTTCAGTGCCTCCCTGCTCATCTCCAATAAATA  
 AAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

239/615

## **FIGURE 238**

MQGRVAGSCAPLGLLLVCLHLPLGFARSIGVVEEKVSNFGTNLPQLGQPSSTGFPSNSEHPQFALDPRSNDLARV  
PLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEADRLGEALPEELSYLSSAAALAPGSGP  
LPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRPPWSLIHRVLPDHPWGTLNPSVSWGSGPGT  
GWGTRPMHPHEGIWGINNQPPGTSWGNINRYPGGSWGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFGV  
LRPPGSSWNI PAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-  
274, 270-275, 280-285, 281-286, 305-310

FIGURE 238

**FIGURE 239**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCCG  
 CTGCTACCGCTCTGCTGACCGCGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCC  
 AGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCTT  
 GGGTGGTGTATCCCTTTGGGGCTGCTGTTCCCTGGTCTGCGGATCCCAGGCTACCTCTGTGCCAACGTCACTCT  
 CTTAGAGGAGTGTCTCAGCAAAATACCAAGCAACAGAGTCTCACTCCCGGGTCCGAGAGCCATCCCGAGGAGGA  
 CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT  
 GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGTGGGGCTTGGGCCACAGCCTGCTCTGTTCCCGAG  
 CCAGCTCTGTTCCCGAGCAGTGGCTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG  
 TTCTGTTTGTGTTTGTGTTTGGAGCAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCA  
 TGCCCTGAAACCT**TAG**ACTCCCGGGGTTAAGCGATCCTGTTCAGCCTCCCAAGTAGCTGGAACCTACAGGCATGC  
 ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGCTTGTCACTGCTGCCAGGCTGGTCTTGAA  
 CTCTAGGCTCAAGCAATCCTCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCAACCTGTCTGG  
 CTCTGGCTCTGTTCTTAACAATCTCTGCCAAACAAACACAGTGGGTTCCTCTGTGAGAGCCTGCCCTCGTTGCCCTC  
 ATGTCACTCTTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCC  
 AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACAGCTAGCTGCACCAACCTGACTTCTCCTTAGCCCG  
 TGTGAGCCTCACTTCCACTTGGAGAGTCTTCTCTCGCTGGTTGCCATGACTGTGAGATAAGTCAGGCTGTGA  
 AGGGCCGGCAGAGCTGACCTGCCTCCCAACCCCTAGGCTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGA  
 AGACAGCCAAGGTCAACCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC  
 CCCAAGCTCCAGTGTGAAACTTCTCTCTGGCTGGTTTCCAGCACTACAGAGGAATGGACACAGTCTTCCAG  
 GGTCTCTCTCGTGCACCAACCGGGAGCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTTTTAAACAAACCC  
 CACGTCCAGCCTGGGTAACTGGTAAAGCCCGCTCTACAAAAAATCAGGTAGCCGGGCATGGTGGTGGC  
 CACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATGCG  
 TTGAGCCTGGGAAGTCGAGGCTGCAGTGAAGTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGAC  
 CCTGTCTCAAAA

241/615

**FIGURE 240**

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS  
NMEYMVVSAGSGRRGWHRGWLGHQPALFPSQLCSPASACDGWLRVSSGRGGSRLCSVLFCFETGSHSATDAGVQ  
WHNRHALKP

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 27-31, 41-45

**N-myristoylation site.**

amino acids 126-132, 140-146

**Amidation site.**

amino acids 85-89

2025-10-29 09:23:00

242/615

**FIGURE 241**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GGGTCTGGGCTGCCC  
CTTGTCTCTCTTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG  
GAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT  
CTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCA  
TTGAAGCCTGTGTCTCTTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCCCTGTCTTTCCAG  
CAGGCCCCACCCCTCCTGAGTGGCAATAAATAAAATTCCGGTATGCTG

1052586.01503

243/615

**FIGURE 242**

MGSGLPLVLLLTLLGSSHGTGPGMTLQQLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTLHHARSQHHVVCNT

205110.9352501

244/615

**FIGURE 243**

GGCAAGTGAACCACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAAACTCCTGAAAAATATCCAGAT  
AACTGTCA**TGA**AGCTGGTAACATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCCTTCCT  
CATCAACAAAGTGCCCTTCCCTGTGACAAAGTTGGCACCTTTACCTCTGGACAACATTCCTCCCTTTATGGATCC  
ATTAAAGCTTCTCTGAAAACCTGSGGCATTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAATGA  
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTG**TGA**CATCAAGATAA  
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT  
CAAAATGCCCTAAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

105556.01502



245/615

## **FIGURE 244**

</usr/seqdb2/sst/DNA/Dnasegs.min/ss.DNA59855

<subunit 1 of 1, 93 aa, 1 stop

<MW: 10161, pI: 7.39, NX(S/T): 0

MKLVTIFLLVTISLCSYSATAFLINKVPLFVDKLAFLPLDNLPLFMDPLKLLKLTGISV  
EHLVEGLRKVCVELGPEASEAVKKLLEALSHLV

**Important features:**

**Signal peptide:**

Amino acids 1-18

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93

**FIGURE 245**

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT  
 GCAATGTGAGGTGTCCGGCTTTTGCTGCGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT  
 CCGGTGTTTGCTGGTGCCCCAGCTGAAGCCACAGAGTTCTGAAGATATCCGGTGCAAAATGCATCTGTCCACC  
 TTATAGAAACATCAGTGGGCACATTTACAACCAGAAATGTATCCAGAGGACTGCAACTGCCTGCACGTGGTGGGA  
 GCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGGAGTGCAGGTACGAGGAGCGCAGCAC  
 CACCACCATCAAGSTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCCTTCTTGAT  
 GCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCAACATGAGGAGGAAATGAGGATGC  
 TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCGAGCAAAACACAGTCTGGAGCGTGTGGAAGGTGC  
 CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT  
 GGGCTGGTGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAGCAGGGGGCTACTT  
 CTCCTTCCTCCGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCCTCTTCTCCCTAACTTAGAAATG  
 TTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTGTCTTCTTGGGTCTTTGGGGTT  
 GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCCATCTGTCTC  
 TCCTGGCTCCACTCTTGCCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAAGATAAAGCTGGGTC  
 TTCAGAACTCAGTGTCTGGGAGGAAGCATGGCCAGCATTGAGCATGTGTCTTCTTCTGAGTGGTCTTATC  
 ACCACCTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC  
 TGGGCCCCCTGAGCCACTGGGTCTTCAGGTGCACTGGAAGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCA  
 CTGGGGCATGGAGTGCCCATGCATCTCTGCTGCCGGTCCCTCAGCTGCACTTGAGGGGTCTGGGCAGTCCCTC  
 CTCTCCCACTGTCCACAGTCACTGAGCCAGACGGTGGTGGAAATGAGACATCGAGGCTGAGCGTGGATCTGA  
 ACACACAGCCCCCTGTACTTGGTTGCCCTTGTCCCTGAACTTCGTTGTACCACTGATGAGGAGAGAAAATTTG  
 TCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTGTTTATTCTCTCA

247/615

## **FIGURE 246**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCCLLVPPAPANKSSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMVPVPGHDVEAYCLL
CECRYEERSTTTIKVIVIIYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTTFDRHKMLS
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

2025.05.20 14:55:00

AATTGTATCTTGGAATGTAAAAACAAACGAAATAAAATAGAGGAAAAAATCTTCTGAGTTTCAAAAAACAACAGACATAGTACTCTAGAGAACTTTTAAAAACAAATAACTGTGTAGGATTTGAGTTTGCATTATGGATTAATTAATTTCTCTCTGATCTGTGGGTTTCTCTCACTGTGTCTTAAATATTAATTTGAGTTTCTGATTTGATTAATTAATTTCTCTGTTAAATGAATGCTTGTAGGATCTGTGCTCTTCAGCATATGTACAAATATCTCTGGAGTCTCTCAATGAGCAGAGTTCCCTCTCCCTCGAGTTCTTAAATTAATTAAGAGATGTCTGCTGTGGAAAAAGGCGATGATTAATTAATCTGTATGATTTCTCAACATCTTGTATGGGAAGAGTCTTGAAGACCAATGGAAATACTTTTTTTTCTTCTGGCCATCAATCAAGTGGTGTACCTTTTCACTAGTAGAGTGTGTGTCACTGTAGTAATAAGAAACCTGTGTTTATTTCTCAATGTATTTGTAGAAACACAGCCATCATTTTATTTATGTGTGTTTCTTGGCTGTATCATAAATTTATATATTTGGCGTACAAATTACTTCACTTCAATAATAAACAATAGTAGAGTTGTTTACTAGATATTTCTCTGATGTCACTTTCTCAGCCTGTGTAGAGATCACTTTGTGTATAGTCCCTTGGAAATTTACAGTACTGTCTCTCATATCTTCAAGTACTTGTATCAATAAACCAATTTGTTTGTAATTTGATATTAATAAACACAGATAAAGGTTCAATCTCACTCAAC

249/615

**FIGURE 248**

MIGYYLILFLMWGSSTVFCVLLIPTIAEASFVENECLVDLCLLRICYKLSGVFNQCRVPLPSDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

249/615

**FIGURE 249**

AGCGSGTCTCGCTTGGGTTCCGCTAAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACCAATCTGCAAGCCCCGCGACCCCAAGTGAGGGGGCCCCGTGTTGGGTCTCTCC  
 TCCTTTGCAATTCACCCCTCCGGGCTTTGGCTCTTCTGGGGACCCCTCGCCGGGAGATGGCGCGGTGTGATG  
 CGGAGCAAGGATTCGCTCTGCTGGCTGCTCCTACTGGCCGGGTGCTGATGGTGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAGGCCCCAATCGATCTCGG  
 GGCATGTACCAAGGACTGGCATTCGCGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCCTACCCCTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCCTGCATGGTGTGTCGGAGA  
 AAAAAAGAAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
 ACTGAAGAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
 TCAAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTACATATAAAGGGCATGAAGGA  
 GACCCCTGCTCATACGATCATCAGACTGCATTGAAGGGTTTGTGTGCTCGTCAITTTCTGGACCAAAATCTGCAAA  
 CCAGTGTCCATCAGGGGGAAGTCTGTACCAAAACACGCAAGAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
 TGCAGCTGTGCGAAGGGGCTGTCTGTGCAAGATATGGAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTAAATGCATTATAG  
 CATGGTGGAAAATTAAGGTTTCAGATGCAGAGAATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAAGGGAGAAAGAAAACATGAATGAATAGATTAGAATTGGGTGACAAAATGCAAGTGCAGCCAGCTGTTTCCATTATG  
 CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAAACCAAGCACACATGGAAATTC  
 ACTGTAGTAGTGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTCTTCAGATTGCTGATTTG  
 TTATACAAATAACCTACATCGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACCTCTAGATTAACCTTGTTA  
 TACAATAGGTTCTAAAAATTAATTTGTCTAAACAGAAATGAAACATGAGCAATTGTAAATTTACAACAGAAAAT  
 TACCTTTTGATTTGTAAACACTACTCTCTGCTGTCTCAATCAAGAGTCTTGGTAGATAAGAAAATAATTCAGTCAAAAT  
 TTTCAAAATATTGCAAAATTTAGGCCAGTTGTTTAGGAAGCGCTTTAGGAAGACAAATAAATAACCAACCAACAG  
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAAATTAATAAGACCTGCATACAGACAAAACAGTTTCC  
 TTCAGATTTCACGAATGCAGATATATCTCTCTTTATCCTATGTGATTCTGTCTCTGAATGCATTATATTTTCCA  
 AACTATACCCAATAATTTGTGACTAGTAAAAATCTTACACAGAGCAGAATTTTACAGATGGCCAAAAAATTTAA  
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTTATTTCTTAAAGATTGGCCATAACCTATATTTT  
 GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTTGGGAAAATCTTTTCGTTTGTTCAGGTTTGGGCAACATAGATCATATGCTG  
 AGGCACAAGTTGGCTGTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGTCTAT  
 CATATAATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCTTCAAAATATTTATTTTATAG  
 TGTCTGAGATCCTCAAAATATCTCAATTCAGGAGGTTTCAAAAATGTACTCTGGAAGTAGACAGAGTAGTGAGG  
 TTTCAATGGCCCTCTATAAGCTTCTGACTAGCCAAATGGCATCATCCAATTTTCTTCCCAACCTCTGCGAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTGGTTTTCTGCGAGCCATTGCGGTTAAAAAATAAAGTAGGATAACTTTGTA  
 AACTGCATATTGTCTAATCTATAGACCAACAGTTCCTAAATCTTTTGAACCACTTTTACTACTTTTTTAAACTT  
 AACTCAGTTCTAAATACCTTTGTGAGGACCAAAACATAAAGGTTATCTTATAGTCTGACTTTAAACCTTTG  
 TAGACCACAATTCACCTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGCTCTCAAATTAAGTTCTCCAGTAG  
 AGATTGAGTTTGGCCCTGTATATCTATTAATAAATTTCAACTTCCCATATATTTACTAAGATGATTAAAGACTTA  
 CATTTTCTGACAGGTTCTGCAAAAAAATAAATAAATAAAGTCCATCCAAGAACCAAGGTTTGTATAAACAGGT  
 TGTATAGCTTGTGAATGAAATGGAAACATTTCAATCAAACTTTCTATATAACAATTTATATATTACAAT  
 TTGGTTCTGCAATATTTTCTATGTCCACCTTTTAAATAATTTATTTTGAAGTAATTTATTACAGGAATG  
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGATATATTTCAGCTATTGAC  
 TTGTGAATTTAGGAAAAATGTATAAAGATAAAATCTATTAAATTTTCTCTCTTAAAACTGAAAAAATAA  
 AAAAAAAAAAAAAAAAAA

251/615

**FIGURE 250**

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLQQA  
YPCSSDKECEVGRYCHSPHQGSSACMVCRRKKRCHRDGMCCPSTRCNNGICI PVTESILTPHIPALDGT RHRDR  
NHGHYSNHDLGWQNLGRPHPTKMSHIKGHEGDPCLRSSDCIEGPCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL  
EIPQRCDCAKGLSCKVWKDATYSSKARLHVQCQKI

**Signal peptide:**  
amino acids 1-25

205110-93525001

**FIGURE 251**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTGGGATTAC  
 AGGCGTGAGCCACCGGCCCGGCCAACATCAGCTTTTAAAAATTGATTTCTTCAAATTCATGGCAAAATATTTC  
 CTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTCATTCGATAGTAAT  
 ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTATAGATTATAGGTTTAAACATACCTTG  
 AAAATACCTTGATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTTGTTGAGGATTTGTTCTTTATCCCCCTTTT  
 AAAGTCATCCGTCTTGGCTCAGGATTGGGAGAGCTTGACCCACCAAAATGGCAAAACATCACAGCTCCAGAT  
 TTTGGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCAACCCCAAGTACACAGCAGAATAGTACAAGTCA  
 CCTACAACTACTACTTCTTGGGACCTCAAGCCCCAACATCCAGTCTCAGTCCTCAGTCATCTTGACTTCAA  
 ATCTCAACCTGAGCCATCCCGAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACGT  
 TCCTCCTCCTGGTTTGGAGTCCTTTCCTTCCAGGCCAAAACCTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC  
 TGTGAACAAGCTTTGCGAGCTTCCAGCAGCAGCAATGAAAATATCTCTGTGTCGTGCCACAGCCACAGCCCAA  
 ACACATCAAACCTTGCTAAGCGCGGATACCCCGAGCTTCTAAGATCCAGCTTCTGCACTGGAAATGCCTGGTTC  
 AGCAGATGTCACAGGATTAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGTAATTTGG  
 ATCAGCTCCAAGCAGTGAAAAATAGTAATCAGATTTCCATCAGCTTGATTCGAGTCTTTAAGTGAGCCTTTGAA  
 TACATCTTTATCAATGACAGTGACAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTGCACTTGAC  
 AAGCTCATCACTGAATTCGTGCTAGTCCAGTAGCAATGTCTTCTTATGACCAAGTTCGTGCATAACAGGAT  
 CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCAAG  
 TCAGCAGACATAGACAGTAAGTATAGCAGCAAGCTACTCTGTATGGCTGGTGCCAAACCAAACAGAGGAAGAG  
 GATAGCTCAGCTGATGTGAAAAACACAGTTGGTCAATGGCTCATTCGTTAAAGACAGCCCTTTTGTCTTTTGT  
 TTTTGGACCAAGGTGTGGCTGTGGTGTTATTAGAAATGTCTTAACCAAGCAAGAGGAGGTGGTGGTCTCATA  
 TTCTTGGCCCTAATCAGACTGCACCAAGTGACAGCATACAGTATGCAATTTAAAGATGCTTGGGCCAGGCCGG  
 GTGGCTGATGCCATAATCCAGTGTCTTGGGGGGCCAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACC  
 ACCCTGGGCAACATGTTGAACTCTGTCTCTACTAAATACGAAAACTAGCCGGGTGTGGTGGCGCGCGTGGC  
 TGTAAATCCAGCTACTTGGGAGCTGAGGCACAAGAAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT  
 CTGAAAAGA



253/615

**FIGURE 252**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT  
TTSWDLKPPTSQSSVLHLDPKSQPEPSPVLSQLSQRQQHQSQAVTVPPGLESFPPQAKLRESTPGDPSSTVVK  
LLQLPSTTIENISVSVHQPPKHIKLAKRRIIPASKIPASAVEMPGSADVTGLNVQFGALEPGSEPSLSEFGSAP  
SSENSNQIPIISLYSKSLSEPLNTSLSMTSAVQNSTYTTISVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQ  
SPVSSSESAPGTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**  
amino acids 1-24

253/615

**FIGURE 253**

GGGGCGCCGCTACTACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTGCAGATGTCGGAGCTCAT  
 GGGGCTGTGCTGTGCTTGGGCTGTCTGGCCCTGATGGCGACGGCGCCGTAGCGCGGGGGTGGCTGCGCGCGGG  
 GGAGGAGAGGAGCGCGCGCCCTGCCAAAAGCAAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAA  
 GCAGAAACAATATCAGCGGATTCGGAAGGAGAAGCCTCAACACACAACTTCACCCACCGCCTCTGGCTGCAGC  
 TCTGAAGAGCCACAGCGGGAACATATCTTGATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGCAGA  
 TGATGCAACCATCCGCATCTGGAGCACCAGGACTTCTGCAGCGAGAGCACCAGCATGAGAGCCAACGTGGA  
 GCTGGACACGCCACCTCTGTGCGCTTCAGCCCTGACTGCAGAGCCTTCATCGCTCTGGCTGGCCAACGGGGACAC  
 CCTCGGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAA  
 AAAGCACAGGCGCCTGTCTCATGCATTTGGCATTGTCTAACACAGGGAAAGTTTATCATGACTGCCCTCAGTGACAC  
 CACTGTCTCTCATCTGGAGCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAAACACACGCG  
 TGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTTCAACCCAGATGTGAAGGTTTGGGAAGTCTGCTT  
 TGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAACTAAAGGGCCACTCCGCGCTGTGCACTCGTT  
 TGCTTCTTCCAACGACTCAGCGAGGATGGCTTCTGTCTCCAAGGATGGTACATGGAACATGTGGGACACAGATGT  
 GGAATACAAGAAGAAGCAGGACCCCTACTTGTCTGAAGACAGGCCCTTTGAAGAGGCGCGGGTGCCGCGCCGTG  
 CGCCTTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTATCTCAATAACCCG  
 GCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCAACTTGTCTTTGACATCACTGG  
 CCGCTTCTGCGCTCTCTGTGGGACCGGGCGGTGCGGCTGTTTCAACAACCTCTGGCCACCGAGCCATGGTGA  
 GGAGATGCAGGGCCACCTGAAGCGGGCTCCAACGAGAGCAACCCGCGAGAGGCTGCAGCAGCAGCTGACCCAGGC  
 CCAAGAGACCTGAAGAGCCTGGGTGCCCTGAAGAAGTGACTCTGGGAGGCCCCGCGCAGAGGATTGAGGAGGA  
 GGGATCTGGCCTCCTCATGGCACTGTGCCATCTTCTCCAGGTGGAAGCCTTTCAGAAGGAGTCTCCTGGTT  
 TTCTTACTGGTGGCCCTGTCTTCTCCATTGAACTACTCTTGTCTACTTAGGTCTCTCTTCTTGTCTGGCTGT  
 GACTCTCTCTGACTAGTGGCCAAAGTGTCTTTCTTCTCCAGGCCAGTGGGTGAATCTGTCCCACTGGC  
 ACTGAGGAGAATGGTAGAGAGGAGGAGAGAGAGAGAGAATGTATTTTGGCCTTGTGGCAGCACATCCTCAC  
 ACCCAAAGAGTTTGTAAATGTTCCAGAACAACTAGAGAACACCTGAGTAAAGAGCACTTTTGCANAGATG  
 GGAGACTGGGATAGCTTCCATCACAGAACTGTGTCCATCAAAAGAGCACTAAGGATTTTCTTCTGGGCTCA  
 GTTCTATTTTGAAGATGGAATAATCCTCTCTGTGAACCTCTTGCAAAAGATGATGAGGCTAAGAGAATATCA  
 AGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTCTAAGAGTGGTAAAGTGGGA  
 CAGTGTGCTTTGAAACCAAATTAGAAAACATCTTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTT  
 TATATGGTTGGACTCTCTCTCTGGGAGATGATATCTGTTTAAAGAGACCTCTTTCAAGTTCATCAAGTTCAT  
 CAGATATTTAGTGGCCACTCTGTGCCCAATAAATATGAGCTGGGATTAACAAAAAAGAAAAAAGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

255/615

## **FIGURE 254**

MELSQMSRLMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQKQYQRIKKEKPQOH  
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPPDCRA  
FIVVLANGDTLRVFKMTKREDGGYTFATPEDFFPKKKHKAVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTI  
NTNQMNNTHAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD  
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALS PNAQV LALASGSSIHLYNTRRGEKEECFERVHGEC  
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLLKRASNESTRQRLQQQLTQAQETLKS LGALKK

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

255/615

256/615

## FIGURE 255

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCCAGGAACCTGAGCTAGGTCAAAGACGCCGGGCCAGGTGCCCC  
GTCGCAGGTGCCCTTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCCCTTCTCGGCCGTGCCAACCC  
GCCACCCAGCCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCCTGCCCTTCTGCTGGCCCGCTGG  
GGCCGAGCCTGGGGGCAAAACAGACCACTTCTGCAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC  
AGCTCCGATGGCAACCTGCCTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC  
CTGGCTGTGGGGCTGGCACTGTTGGTGCGAAGCTTCGGGAGAAAGCGGCAGACGGAGGGCACTACCGGCCAGT  
AGCGAGGAGCACTTCTCCCATGCAAGCGAGGCCCGGGCCCTCAGGACTCCAAGGAGACGGTGACAGGGCTGCCCTG  
CCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGAAAGGCAGTGCCCTCTCT  
GGGCAGTCAGATCCACCCAGTGCTTAATAGAGGGGAAGAAGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGA  
GGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

105256.01502

257/615

**FIGURE 256**

MANPGLGILLALGLPFLARNGRAWGQIQTTSANENSTVLPSSTSSSDGNLRPEAITATIVVFSLLAALLLAVG  
LALLVRKLRREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

205K10.98525007

**FIGURE 257**

GCACGGAATAACTAGAGAGGAACAATGGGGTTATTACAGAGTTTGTGTTTCTCTTAGTTCTGTGCGCTGCTGCAC  
 CAGTCAAAATACTTCTCTTATTAGCTGAATATATATGGCTTTGAAGATATGTGATTTGTATAGATCTCTAGTGTG  
 CCAGAAATAGAAAATAATTAATGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTAGTGTGAAGCCACA  
 GAAAAAAGATTTTTTCTAAAAATGTATCTATATTAATCTCTGAGAGATTTGGAAGGAAATCTCTCAGTACAAAGG  
 CAAAAACATGAAAAACCATAAACCTGTGATGTTATAGTTGACACCCTACACTCCGAGGTAGAGATGAACCATAC  
 ACCAGCAGTTTCAGAGATGTGGAGAGAAAGCGCAATACATTCACTTCCACCCCTGACCTCTACTTGGAAAAAA  
 CAAATGAATATGGAACCCAGGCAACTGTGTTCTCATGAGTGCGCTCACTCCGGTGGGGAGTTTGTGATGAG  
 TACAATGAAGATCAGCCTTTCTACCGTGCTAAGTCAAAAAAATCGAAGCAACAGGTGTTCCGCAAGTTCTCT  
 GGTAGAAATAGAGTTTATAAGTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAAGATTTGATTCTACAAACAAA  
 CTGTATGGAAAAAGATTGTCAATTCTTTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAAGT  
 ATTGATTCTGTTGTTGAATTTGTAAACGAAAAAACCCATAATCAAGAAAGCTCCAAGCCTACAAAAACATAAAGGTGC  
 AATTTTAGAGTACATGGGAGGTGATTAGCAATTTCTGAGGATTTTAAAAACACCATACCATGGTGACACCACT  
 CCTCCACCTGTCTTCTCATTTGTGAAGATCAGTCAAGAAATGTGTCTTACTTTCTGATAAATCTGGAAACATG  
 GGGGTGAAGGACCGCTTAATCGAATGAATCAAGCAGCAAAACATTTCCTGTCTGCAGACTGTTGAAAAATGATCC  
 TGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAAATAAAAAAGCAGTGATGAA  
 AGAAACACACTCATGGCAGGATTACCTACATATCTCTCTGGGAGGAAGCTCCATCTGCTCTGGAATTAATATGCA  
 TTTCAAGTGATTGGAGAGCTACATTTCCCACTCGATGGATCCGAAGTACTGCTGTGCTGACTGATGGGGAGGATAAC  
 ACTCGAGTTCTGTATTGATGAAGTGAACCAAGTGGGGCCCTGTTCTATTATTATTTCTTTGGGAAGAGCTGCT  
 GATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTTTCAGATGAAGCTCAGAACAT  
 GGCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCCAAGAGTCCCTCAGCTCGAAAGT  
 AAGGGATTAACTGAATAGTAAATGCTGGATGAACGCACTGTCTATAATTGATAGTACATGGGAAAGGACAGC  
 TCTTTCTCATCACATGGAACAGTCTGCCCTCCAGATATTCTCTCTGCGGATCCAGTGGAAACATAATGGAAT  
 TTTCAAGTGGATGCAATCTCCAAATGGCTTATCTCAGTATTCCAGGAATCGCAAGGTGGGCACTTTGGGCATAC  
 AATCTTCAACCCAAAGCAACCCAGAACATTACTATTACAGTAATCTCTCAGCAGCAAAATCTCTCTGCGCT  
 CCAATCAGCTGAATGCTTAAATGAATGAATAGGACGTAACAGTTTCCCGAGCCCAATGATGTTTACGCAAGAAAT  
 CTACAAGGATATGATCCTGTTCTGGAGCCAATGTGACTGCTTTTCATTGAGTACAGAAATGGACATACAGAAAT  
 TTGGAAGCTTTTGGATAATGTGTCAGGCGCTGATTCTTTCAAGAAATGATGGTCTACTCAGAGTATTTTACAGCA  
 TATACAGAAAAATGGCAGATATAGCTTAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTATAAATTAACGG  
 CCTCACTGATAGAGCCGGTACATACAGCGCTGGGTAGTGAACGGGAAATTTGAAGCAAAACCGCAAGACCT  
 GAAATTTGATAGGATATCTCAGACCCTTGGAGGTTTCAGCCAGACATCTCGGAGGTCTATTGTGTATCA  
 CAACTCCCAAGCTTCCCTTGCTGACCAATACCCACCAAGTCAATACAGACCTTGATGCCACAGTTTCAATGAG  
 GATAAGATTATTCTTACATGGACAGCACAGGAGATAATTTGATGTTGGAAAAATTTCAACGTATATCATGAAGA  
 ATAAGTGAAGTATTTCTGATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACA  
 AAGGAGCGAACTTCAAGGAAGATTTGCAATTTAAACAGAAAAATATCTCAGAAGAAAAATGCAACCCCATATTT  
 ATTCCATTAAGATATATGAGGCAATTTGACATCAAAAGTATCCAAATTTGCAACAGATATCTTTGTTATC  
 CCTCAAGCAATCTGATGACATTTGATCCTAACCTATCTCTACTCTCTACTCTCTGATGAAGATCTAAT  
 TCTGGATTAAATATTCTACGCTGGTATTGTCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTAATTTAAGTACC  
 ACCATTGGAACCTTAACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAAAACAATGTAA  
 GTAAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAATTAATTTAAGATGTCG  
 GAAAGGATCACTTTGATTAATAAAAAACCTCATGATATGTAAAAACCTGCAAGATTAAATTTAATAGTTTCA  
 TTTATTGTTTATTATTGTTGAAGAAATAGTATGACAAAGATCTTTTCTATCTGATCACTGCTGTGATATT  
 ATTTGATGCAACAGTTTTCGTAATGATATTTCAAATTCATCAAGAAATTAATATCTATCTGATCTGATCTCAA  
 AATACAGTAAAGGAGAGCAAAATAACACACTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 258**

MGLFRGFVFLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFATEKRFPPFKN  
 VSLIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTCEGEGEYIHFTPDLLLGKKQNEYGPPG  
 KLFVHEWAHLRWGQFDEYNEDQPPYRAKSKKIEATRCAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQF  
 PPKVQTEKASIMFMQSIDSVVVEPCNEKTHNQEAPSLQNIKCNEFRSTWEVISNSEDFKNTIPMVTPPPPPVVFSL  
 KISQRIVCLVLKSGSMGGKDRLRNMQAAKHFLLQTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLMAGL  
 PTYPLGCTSCISGKIYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVQKSGAIVHFIALGRAADEAVIEMS  
 KITGGSHFVVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNANMNDTVIIDSTVKGDTFFLITWNS  
 LPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLITITVTSRAANSVPPITVNAKM  
 NKDVNSFSPMIIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGRYS  
 LKVRAGGGANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLTLEDFSRASGGAFVVSQVPSLPLP  
 DQYPPSQITDLDATVHEDKIIITWTAPGDNFVGVQRYIIRISASILDRDSFDDALQVNTTDLSPKEANSKES  
 FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL  
 VLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,  
811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 259**

CGCCGGAGGCAAGCGCGCGTGGCGCAGCGGCGCA**CATG**SCCGTGTCTCAGAGGACGACTTTCAGCACAGTTCAA  
 ACTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACCCAGGAGGCACTGCTTGAGAACTGCTGGACCGCC  
 CGCCCTTGGCTCGAGAGGCCCGAGGACCGCTCTTGCGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA  
 GTCTACTGCCATGGAACCTTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCCAATCTCCAGCCCA  
 CCACCGGGGAGGACCTCGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC  
 CCTCCATGCTGTGCTCGTGGCCAACTTCTGCTTGTCAAAGGGTTGCAGTCCACATCCGTTCTCTGGCCTCAC  
 TGACGGTCATCTGGCCATCTTCACTGGTGATAAATGCACCTGGTGAAAGGTGGACACTTCTCTGGACCCGTGGTT  
 TTTTTCGGGTCAACATTGCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA  
 TGACCGGCTCCTTTCTATGAGGAATCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGACGGTCAGCGCCG  
 TGGCCTCATTTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA  
 TCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCGAGGTACTACATGAGGCTCG  
 TTCTTGGCGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCAGGACTCCCTCAGTGCCCTTTCGGTGGCCTCCA  
 GATTTCATTGATTCCACACACCCCTCTCCGCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACT  
 ACGTCTTCTTCATCACCAGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT  
 CACTGTGGACCAACAGTTTTCATCCCCCTCACTACTTCTCTCTGTACAACCTTTGCTGACCTATGTGGCGGGC  
 AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGGTTCTGTGCTCTCCGGAACCTGCC  
 TCATCCCCCTCTTCTGCTCTGTAACTACAGCCCCCGCTCCACCTGAAAGACTGTGGTCTTCCAGTCCGATGTGT  
 ACCCGCACTCCTCAGCTCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCTA  
 AGATTGTGCCAGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTTGGGCTTAAGACTGG  
 GCTCAGCCTGCTCTACCGCTCTGGTGGCACCTCATCT**AGA**AGGGAGGACACAGGACATTGGTGCTTCAGAGCCTT  
 TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCTAGGAGGAAAGGCTTAAGATTTCATTGGGGACAGAGAG  
 CAGAGCACACTCGGCTCATCCCTCCAAAGATGCCAGTGAAGCACTCCATGCCATTCCGTGCAAGGCAGATA  
 TTCCAGTCATATTAAACAGAACCTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTTCACA  
 GCTGATGGTTAAACATTCCACCTTCTTCTAGSCCTTCAAAGATGCTGCGAGTGTTCGCCCTAGAGTTAATACAA  
 GCCAGTGCCAAACCCAGCCATGGGCTCTTTCAGCACTCCAGCTGCGCTCATTCAGCTGACAGCGAGATGCAA  
 GCAAATGCTCAGCTCTCTTACCTGAAGGGGCTCCCTGGAATGGAAGTCCCTGGCATGGTCAGTCTCAGGGC  
 CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACTGCCACTAACCCAGACTGGAAAAACCCAG  
 AAGATGGGCTTCCATGAATGCTTCATTCCAGAGGGACCCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCT  
 GGCCTGGGTTTTCAAAAAAAGAGGGATCTCATGACCTGGTGGTCTATGGGCTGGGTCAAGATGAGGCTTTTCA  
 GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCATATCAAAAA



261/615

## FIGURE 260

MAVVEDDFOHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYIIFPSLIGISLLPWNFFITAK  
EYWMFKLRNSSSPATGEDPEGSDILNYPESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAI FMVIT  
ALVKVDTSSWTRGFFAVTIVCMVILSGASTVVFSSSIYGMTGSPFMRNSQALISGGAMGGTVSAVASLVDLAASSD  
VRNSALAFFLTATIFLVLCMGLYLLSRLEYARYYMRPVLAHVFSGEEELPQDLSAPSASRFIDSHTPPLRP  
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGFN  
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSLTLALLYGFKIVPRELAEATG  
VVMSEYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,  
448-472

261/615

AGGACGCGTGGGCTGCTGGTGGGAGGCCCTAAAGACATGGAAAGCCACTCTCTTGGAAACCAACCTCGTTTAA  
AGAACTGAGGAGCACCATTAAAGCAAGCTAGGAAATTTGTGTTCTAGCTGTTGTGGGTGAAATAAGGAGGGCAGAAAT  
GGATGATTTTCATCTTCCATTTAGCCTGCTGCTCTCTGGGTATGTTTGGTGGGAATGTACGTGGGCGGAATACCTCCCTT  
CGCTGTTAATTTCTCAGAGAAACAGCATGAGCTGTGTACTGTTTGGGTGTCTGGCCCTTCTCTGTGGAAAGCTGTCT  
GGCAGTCATCTGTCGCTGAAGGAGTACATGGCTTTTGTAGAAGTATTTCTGGAGGGAAACACCAACAGCAGATGCA  
AACAACAATAATGTGATTCGATCAGCAAAAGCAGGAAAAATACAGTTGTCATGAACATGAGCAGACAGCAGCA  
ACAACAGCTGCATGCCATTATTTGGTGTGTTCCCTGCTTCTGGGCTTGCTTTTCAGTGTGCTGTGGACAGAGT  
TAACTCCCATGTGCATTCTACTGACAGTGCAGAAAGCAGCAAGCTCTAGACAAATCCAAAATCAGACACAGCTGGG  
TCTGGTGTTCGATCGTGCAGCTGATGTGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGCCAGGTGTCCAGTT  
AATTTGGTGTGTCATGTCATCATGTGCTACATAAGAGCCAGCAGCTGTTTGGAGCTGTTTCTCTTTTGATGTCATGCTGG  
CTTTAGAGCGGAATCGAACTCGAAGAACCTGTGGTGTCTTTGCATTGGCAGCAGCAAGTATGTGCTACAGGTGATCACT  
CTTAGGATCGTAGTAAGAGCAGTAAGAAGGCCCTTTCCAGAGGTGAACCGCAAGGAGTGGCCATGTGTTCTCTGTC  
CGGGACAATTTCTTATTTGTGCCACAGTACATGTCTCCCTGAGTGGTGGGGAATAGGCCACGCCCAACAGCCGGA  
TCCAGCAGGGAGGAGAGGCTCAGCGCGCTGGAAGTGGCAGCCGTGTTCTGGGTGCTCTATCCCTCTATCTCT  
GTCACTAGGGAACACAGCACTAAATGTTTCAAGTGCAGCCTTGCTCAGGGCCGTTGTCATCCAGTGAAGAACGCG  
CGCGCATGTCAGACATCTCACTTCTCAGTCTCTGTCTGCACCTTCGCGCATCTCATATGCTTCTAGATGCCA  
GAGGGGAGGTGAGGTAAACCTGAGTATGTGAAAAGTTTTAGAGTAGAAACCAACTTAGCTTGCAGTTAGCTA  
TAGACATCCCAATGTGTATATCTTTTAAAGAGCCCTTGACATTTTGGCTTTTAAATATTTCTCTTAACCTCATTTCTC  
AGGGAAGATGGAAATTTAGTTTAAAGAAAGAGGAGGAACCTTCATCACTCACAATGAATAGTAGTATAGAAATAC  
AGTGTGTTGTAATTAAGCTATGTCTCTTCTCTTAGTTTTAGAGGCTCTGCTCATTTTATCCATTGATTTTAAACA  
TGTTGTCACCAATGTAAGACTGGGTGCTTTAGCATCTATGCCACATGCGTGTATAGTGAAGGTGTAGGACCCCACTA  
CTTAGATAGCTAAAGGTGATCTAGTAACTAGGATAGGGTAGGGAGAAATAGTAGCAGACACATGAAAGGCTCT  
TCTTTATATCAAAAGAGATATCCATTGAAAAGGGATGTGTAGAGGAAATTAAGACAGCTCTTGGCAGCGCCCT  
CTCTGAATCAGCCCTGCACTTCCATCAAATGAGACAGGAGAGGTGGGAGGAGCTCTTAAGAGAGTCACTGTGATAT  
TTGTAGATCTCCCTGTCAAGTTCTGTTTTCGACAGTACCTGTCTCCACTTCTTAGAGGAGGACGAGTTCTAGT  
AGTTTTCAGTCTCAGGCTTTCTCTCAGAAACAGCTCAGATCAGAAAGTCTTTCTTGAAATTAAGGGAATATAAATTT  
TAAGTGAATTTTGTGAGTTATTTAGTATCTTTGTAGTAGCTTTTATAAGAGACACAAATGTATGTTGTGCTC  
TTTTTTTGTGTTTTTTTTTTTTTAAATATTTCTCTTAGCAGTACAGCAATCCCTCTAGGGACCTTAATATACCTAGG  
TCAGCTTTGGGCACACTGTGCTCTCTCACATAACCACTCTAGCAGAGATGATATAAATAGAAAGTGTGTTGCCCT  
ATGATTTTAAAGCTTATTTGGAATCATGTGCTCTGTGCTCTGCTCTTTTCTTGTGCTTTCTCTTCAACTTTCCCTC  
TAGGCTCTCTCGCCACAAATTTGCTGCTACTGTGGTGTATAATTTGTGGGGATGAATTTCTATCAGGACAA  
CCACTTTCTCGAAGCTGAATTAATGAAGATAATATATCTTTATCTTATCCCTCTCAAAGAAATATCTCTTTGTG  
TCAAATGCCGCTTTGTGAGCCCTTAAATACCACTCTCATGTGTGAATTAGACAACTCACTAATCTGTGATAT  
TAAACAAATGAGATAGCAAAAGTGTTTAACAGCATAGGATAATTTTTTTTCATATTGCCCCAAATTTTGTGAA  
ACCTGTCCTTGTCAAATAGGTGTATAATTTGTATTAATTTATTTTACTTTCTATACCTTTCAAACAAACA  
CTATACATGCGGGGAACCAAGCATAGTTTCTCAGGGCAGCTGGACGTAGTAGTTTGTAAACAGCTTTTCTATGAC  
CAATAAGCTAGCATGCTCATGATTATTTTCCCTCTAGTAATTTGTCACTGATCAGCAGCTGTGGAAATTAAGCTT  
GTGAGCCCTCTGCTGCGCCACAGTGAAGGAATGACAAATAGGATACAGTTGTATGTAGTCACTGGCAACAAT  
GCATACATCTTCTACCAAGAGAGATAGTAGTAGGAAGTCCAAATGACTCTCTCTGTGTGATGTGTTAACAGCT  
GACTGGTGTGAGACTGTGAGTTCTCATCTAGCTCTTCAAACCTATAGGTTGCTGCTAGTTCTCTCTGGAACCTGAC  
TTTGTGTCAAATTAAGTAGCAGTTGTAGTGTCAAATAAAAA

263/615

## **FIGURE 262**

MDDFISISLLSLAMLVGCYVAGIIPAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS  
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQIGNSHVHSTDDPEAARSSNSKITTTTL  
GLVVHAAADGVALGAAASTSQTSLIVFVAIMLHKAPAAFGLVSLMHAGLERNRIRKHLVLFALAPVMSMVT  
YLGLSKSSKEALSEVNATGVAMLFSACTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI  
LSVGHQH

**Signal peptide:**  
amino acids 1-18

**Transmembrane domain:**  
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

263/615

**FIGURE 263**

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCTCCCGG  
 GCAGGGGTGACCAACAGGTGCATCTTTTGATCTCGTGTGTGGCTGCCCTTCCTATTCTAGAGGAAGAC  
 GCCAAGTGAATTTTGACCCAGAGGACCAATGATGTAGCCACCTCTCAACTCTCCCTTCTTGAAACCCCC  
 AGTTATGCCAGGATTTTACTAGAGAGGTGCACTCAACACGACAGCGGCTCCTTCGGCTTAACTTTGTGG  
 TTGGAGGAGAGAACCTTTCTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCTGAGGCTG  
 GACCAGAAAGAAAGGAAAGGTCCCTCTTGCTGTGTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA  
 GGTGAAACCTTGAGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTCTTAAAAAGTAGAGA  
 AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC  
 TCCGGGGGCCCCAAACGCATGCTTCTGTGGCTAGCCCCAGGGAAGCCCTTCCTGGGGGGCCCCGGCT  
 TTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATCTCTGAATGATGATGGTTCGCCGGGGGGCTGCT  
 TCGGTGGATTTCCCGGGTGGTGGTTTGTGTGGTGCTCCTCTGCTGTGCTATCTCTGTCTGTACATGT  
 TGGCTTGACCCCAAAGGTGACGAGGAGCAGCTGGCACCTGCCAGGGGCCAACAGCCCAACCGGGGAAG  
 GAGGGGTACCGGCTCCTTCAGGAGTGGGAGGACGACACCGCAACTACGTGAGCAGCCTTGAGCGG  
 GCAGATCGCACGCTCAAGAGGAGCTGACAGAGAGGATGAGCAGCTCAGGAATGGCAGTACCAAG  
 CCACGCTATGCTGTGCTGGCTGGTCTGGACAGAGGCCCCCAAGAGAAACCCAGGCCAGCTCTCGGCC  
 TTCTGCTGACTCGCAGGTGGACAGGCAAGGTGAATGCTGGCTCAAGCTGGCCACAGAGTATCGCAGC  
 AGTGCTCTTCGATAGCTTTACTCTACAGAAGGTGTACAGCTGGAGACTGGGCTTACCCTGCCACCCCG  
 AGGAGAAGCCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACC  
 CTGAACAATCCTGCAGAGAACCGCCCAATCAACCGTCTTACACCGGCTCTGATTTCATAGAGGGAT  
 CTACCGAAGACAGAAAGGACAAGGGACATTTGTATGAGCTCACCTTCAAAGGGACACAAAACGAAT  
 TCAAACCGCTCATCTTATTTCGACCAATCAGCCCCATCATGAAGGTGAAAAATGAAAAGCTCAACATG  
 GCCAACGCCTTATCAATGTTATCTGTGCCTCTAGCAAAAAGGGTGACAGTTCGCGCAGTTTCATGCA  
 GAATTTCAAGGAGATGTGCATGTAGCAGGATGGGAGAGTCCATCTCACTGTGTTGTTTACTTTGGGAAAG  
 AAGAAATTAATGAGTCAAAGGAATACTTGA AAAACCTTCAAAGCTGGCAACTTCAGSAACCTTTTACC  
 TTCACTCAGCTGAATGAGGAATTTCTCGGGGAAAGGGACCTTGATGTGTGAGCCCGCTCTGCGAAGG  
 AAGCAGCGCTCTCTTTCTGTGATGTGGACATCTACTCACATCTGAATCTCTCATAGCTTA  
 GCGTGAATACACGACGAGAGAAAGTATTTTATCACTTCTTTTCAGTCACTGACATCACTCTGGCAT  
 ATATACGGCCACATGATGCAGTCCCTCCCTTGGAAACAGCAGCTGGTCTATAAGAGAGGAACTGGATT  
 TTGGAGAGACTTTGGATTTTGAGTTGAGCTGTCAGTATCGGTGACACTCTCAATATAGGTGGGTTTG  
 ATCTGGACATCAAAGGCTGGGGCGGAGGAGATGTGCACCTTTATCGCAAGTATCTCCACGACAACTC  
 ATAGTGGTACGGACGCTGTGGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAGCT  
 GACCCCGGAGCAGTACAAGATGTGCATGCACTCAAAGGCCATGAACGAGGCACTCCACGCGCAGCTGG  
 GCATGCTGTGGTTCAGGCGACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAACAGTAGCAAA  
 AAAACATGAACCTCCAGAGAGAGGATGTGGGAGACATTTTCTTCTTTTGGCAATTACTGAAAGATG  
 GCTGCAACAGAGAAAGACTTCCATAAAGGACGACAAAAGAAATTTGACTGATGGGTGAGAGATGAGAA  
 AGCCTCCGATTTCTCTGTGTGGGCTTTTACAAACAGAAATCAAAATCTCCGCTTTGCTGTCCAAAGT  
 AACCGCTTGCACTGGTGTGAAGTCTGACAAAAGGAGAAATGCTTGTAGAGTATAAGGCTTAATGGTG  
 TGGAGGTTTTGATGGGTGTATCAATACATGAGCTTGTGTTTGTGTGTCAATGAAATTAATCATG  
 ATTTAAGAGCAGTTTTGTAAAAAATTCATTACATGAAAGGCAAGCATTTCTCTCATATGAATG  
 GCCTATCAGCAGGCTCTAGTTTCTAGGAATGCTAAAAATCAGAAAGGAGGAGAGGAGATAGGCTTA  
 TTATGATACTAGTGAGTACATTAAGTAAATAAAATGGACAGAAAGAAAGAAACATAAATATCG  
 TGTCAATATTTCCCAAGATTAAACAAAATAATCTGCTTATCTTTTGGTGTCTTTTATGCTGTCT  
 CCGTTTTTTCTTTTATTTAAAAATGCATTTTTCCTTGTGAGTATATAGTCTGCTTATTTAATTA  
 CCATTTTGAAGGCTTACAAGAGGACAAAGTTGGCTACATTTTATATTTTAAAGAAAGTACCTT  
 GAGATGCATTTATGAGAACTTTCAAGTCAAAGCATCAAAATTTAGTGCATATCAAAGGACATGCGAAATG  
 CTGATCTGTGAGGCACTGAATGTGAGGCAATGAGACATGAGGAAGGAATGGTTTTGATCATATACAGA  
 CGTACAGATATTTCTCTGAAGAGTATTTCAAGAGGAGGCAACTGAAACACTGGAGGAGAAAGAAATG  
 ACACCTTTCTGCTTTACAGAAAGGAAACTCATTCAGACTGGTGATATGCTGATGATACCTTAAAGGTCAG  
 AAACCATTTTCTCTCAGAGTATGGGACGCTTTCTTACCTGTTTAAATAAACCAAAGTATACCGT  
 CTGAACCAAACAATCTCTTTTCAAACAGGCTGCTCTGCTGCTTCTGCTTCTCATATAGAAATG  
 GAGAAAAATATATATATATATATATTTGGAAGATCAATCATCTGCCAGATCTAGTGGGATG  
 GAGTTTGTCTACATGTTATGCTCCACCCAGGCGAGGTGGAAGTAACTGAATTTATTTTAAATTAAGC  
 AGTTTACTACTCAATCAAGATGCTTCAAAATTCGATTTTATTAACATTTCAAATCTTTTAAAA  
 AATAAATACAGTTTAACTAGAGTGGTTCTTCATTTCATGTGAAAAATTTATGCGACGACAGATGCAT  
 GAGCTAATTTATCTTTTGTGCTTCTGCTTCTGTTTGTCTCAGATAAATCTGTTTAAAAAGCTCAA  
 GAACATTTCAAGCTGTTGGTGTGTTAAAAAATGCAATGATGATTGTTGTACTGGTATTTATGAAATTT  
 AATTTAAACACAGGCTCAAGTGGAAAGGTGGTATTTGCAAGCTATAAATAATGATTTGTGGATATGAA

265/615

**FIGURE 264**

MMMVRRGLLAWISRVVVLLVLLCCATSVLYMLACTPKGDEBQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL  
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPPDS  
FTLQKVYQLETGLTRHPPEKPPVRKDKRDELVEAIESALETLNPNPAENSPNHRPYTASDFIEGIYRTERDKGTYE  
LTFKGDHKEHFKRLILFRPFSPIMKVINEKLNWANTLINVI VPLAKRVDKFRQFMQNFREMCLEQDGRVHLTVVY  
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTRCLNT  
QPGKKVFYPVLFQYNPGI IYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED  
VHLYRKYLHSNLIIVRTPVRGLFHLWHEKRCMDELTPQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ  
KTSSKKT

1002556.072502

**FIGURE 265**

GGATG CAGAAA GCGCT CAGTGT TGTCT CTCTGG CCGTGG GTCTG CTCTCTCT TCTAC GCTGG CATTG GCGCTCTTCA  
CCAGTGGCTTCTCTGCTCACCCTGTTTGGAGCTCAACCACTAGCAGCTGCCAAGAGCCCCAGGGCCCTGGGTCCC  
TGCCATTGGGGGAGCCAAAGGAAACCTCGGGCCCTGCTGGATGGCTTCCGATTTTTCGGGGTGTGTGGTGGCTGTA  
TGATGCTCTCCGATTTGACTTTCGCCCAGCGCCAGCATTACACGTGCCATAGAGAGGCTCTGCTCTCCCTACCTCT  
TCTTGGGCAAACTAAGCTCTCTTGCAGAGGATCTCTGGAGATTACAGCCCCACCATGCCCGGCTCTACCGATTCCAGG  
TTGACCTCTCTACCAACCAACATGCAGCGCTCAAGGCCCTCACCAGTGGCTCAGTCTACCTTTATTGATGCTG  
GTAGTAATCTCGCCAGCCAGCCATAGTGAAGACAACTCTCATTAAAGCAGCTCACCAGTGCAGGGAAGCGGTGTAG  
TCTTCATGGGAGATGATACCTGGAAAGACCTTTCCCTGGTGTCTTCTCCAAAGCTTTCTCTCTCCATCTCTTCA  
ATGTCAGAGACTAGACACAGTGGACCAATGGCATCTCGGAACACCTCTACCCCAACCATGGACAGTGGTGAATGGG  
ACGTGCTGATTGCTCACTTCTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA  
AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAAATGACACACTGCTGCTAGTGG  
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTCT  
TGATAGCCCCACAGCAGTCTTCCCGACACCCACAGAGGAGCCAGAGGTGATTCCTCAAAGTTAGCCTTTGTGC  
CCACGCTGGCCCTGCTGCTGGGCCCTGCCCCATCCCATTTGGGAATATCGGGGAAGTGTAGGCTGAGCTATTCTCAG  
GGGTGAGGACTCCAGCCCCACTCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTCGACAACCTCT  
TCTCAAGGCTCTGCTGACTACCAAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCAGCTGTGA  
TTGCTGAGCTCGACAGTCTCTGGGGGAGCTCGGGCCATGTGCATCGAGCTCTGGGCTCTGTTCTCTCTGCTGCTC  
GCATGGCGGGGGTACTGCTCTCTCTGCTGCTCTCTGCTCTTATCTGCTCTGTCGATCTCAGTGGGCAATATCCC  
CAGGCTTTTCACTTTGCGCTCTACTCTGACACCTGTGGCCCTGGGGCTTGGTGGGGCCATGCGTATCTGTGGAC  
TCTGTGGAACTATTGGCTGAAGCTAGATCTAGTGTCTCTAGGGGCTGTGGTCTGGGCTGAGCTCATTCTCTCCCTT  
TTCTGTGGAAAGCTCGGCTGAGCTGAGTCCGAAGAGGCCCTGGGCAACCTGTTTCCATCCCTGGGCCCTGCC  
TGTACTCTCTGCTGTTCTGCTGTGCTGTCTCTCTGTAGTATTTGTGTAGCTGAGGCGAGGGCCACCCCTCT  
TCTTTTGGGCTCATTCACTCTGCTCTGTTGTGTCAGCTTCACTGGGAGGGCCAGGCTGCTTCCAGCTCAAGCTAC  
TCACAATGCCCGGCTTTGGCACTTCAGCCACAACAAACCCCCACGGCAATGGTGCATATGCCCTGAGGCTTG  
GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCACT  
CTCTCTCTGGCTGAGTCTCTCGGCATCCATGGTGGGTGGTCCAGCCAAAGAAATTTATGGTTAGGAGCTTGTGTGG  
CGGCGCTGGTGGCCCTGTTAGCTGCGCTGCGCTTGTGGCTTCCGCCCTATGGTAATCAAGAGCCCCAGCCAC  
CCATGCTCTTTGTGGCTGGGAGCTGCCCTAATGGCAATGGGTACTGCTGCCCTACTGGGCATTGGGCTCGGGGG  
CAGATGAGCTCCCCCGCTCTCCGGCTCTGGTCTCTGGGCACTCCATGTGCTGCCCTCGGCTCGGCTAGCAGGGC  
TGCTGCTCTTCAAGGCTCGGCTGCTGCTCTCGGAAGCCTGTGACAGTGTCTGGTGAAGGCTGGGGCAGGCGCTCCAA  
GGACCAAGACTGTCTCACTCTCTCAGGGCCCCCACTTCTCAAGCTGACTTGGATTATGTGTGCTCTCAAA  
TCTACCGACACCTCGAGGAGGAGTTCGGGGCCGTTAGAGAGGACCAAAATCTCAGGGTCCCTGACTGTGGCTG  
CTTATCAGTTGGGAGTGTCTACTCAGCTGTCTAGTGTTCACAGGCCCTCACCCTGTGGGCTCTCCACTCTGTGCTGT  
TTCATGTCGGAGCGCATCAGCTGTGTGTTCTCTGCTTCTGTGTTCTGACAGAGCTTCTCTCTCACTACTGCTTGTGCT  
CTGGGATACCGCTCACCACCCCTGGTCTCTTACTGTGCCATGGCAGGCGAGTCTCGGCTTGGGCCCTCATGGCCA  
CACAGACCTTCTACTCCACAGGCCACAGCGTGTCTTCCAGCCATCCATTGGCATGGGATCTGTTGGGATTTC  
CAGAGGGTCTATGCTCTGTACTTGGCTGCTGCTTGTCTAGTGGGAGCCAAACACTTTGCTCTCCACCTCTCTCT  
TTGCAGTAGGTTGCCCATGCTCTGCTCTGCGCTTTCTGTTGTGAGATCAGAGGCTCGCAAGAGCAGGCTCAGCAG  
CCCCAGGAAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCGGG  
ATGCGCTCAGCATCTCTATGACAGCACTGCTGCACTGGGCTCAAGTACTCTTATCTCTGTTATTCAGATT  
TGGGCTGTGCTGTGGCAGCTCCATCTCTCGCAGGCATCTCATGCTCTGGAAAGTGTGTGCCCCCTAAGTTTCATAT  
TTGAGGCTGTGGGCTCATTTGTGAGCAGCGTGGGACTTCTCTGGGCATCTTGTGTGATGAGATGGATGGGTG  
CTGTGAGCTCTGGTTACAGGCAGCTATTCTGGCCAGCAGAGGTAGCCTATGCTGTGATTACTGGCACTTGGCT  
ACAGAGAGTCTGCTGGAGAACAGTGTAGCTTGGCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
CTTACTATCTCAGCAGCAGGGGCGCTGACATCTAGGACTTCATTATTCTATATTCAGGACCAACAGTGGAGTA  
TGATCCCTCACTCTGATTTTGGATGATCTGAGGGACAAAGGGGGCGGTCTCCGAAGTGGAAATAAATGAGCCGG  
GCGTGGTGACTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATGCTTTGTGCTCCAGGAGTTCA  
AGACCAGCTGTGGACATAACAGACCCCGTCTCTACTATTTAAAAAAGAGTGAATAAAATGATAATAT

267/615

## FIGURE 266

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQIASVLLFLAWVCFIFYAGIALFTSGFLLTRLELTNHSSCQEPFGPSLPGWSQKPGACWMAFRFSRVVLVI
DALRFDFAQPHSHVPREPVSLLPPLGKLSLQRILEIQPHHARLYRSQVDPPTTTMQRLKALTTCGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMSDDTWKDLFPGAFSKAFFFPSPNVRDLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGPHPHPEMAKKLSQMDQVIQGLVERLENDTLVVGADHGMTTNGDHGGDSELEVSAAFL
YSPTAVFPSPTPPEPEEVI PQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAAQASALHNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFCICLLASQWAISPGFFPCPLLLTPVAVGLVGAIAYAGLLGTIELKLDLVLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVILLLLFRLAVFFSDSFVVAERATPFLGSGFILLVVLVQLHWEGQLLPKLL
TMPRLGTSATTNPRHNGAYALRLGILLCTRLAGLPHRCPEETPVCHSSPWLSPPLASVMVGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLSVGASMLPRAVAGL
AASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGLRLERTKSGQPLTVAA
YQLGSVYSAAVMTALTLLAFPLLLLHAERISLVFLLFLQSFLLHLLAAGIPVTTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVPFAIHWHAFAVFGVPEGHGSCWLPALLVVGANTFASHLLFVAGCPLLLWPFCLCSQGLRKRQOP
PGNEADARVRPEEEEEFLMEMRLRDAFQHFYAALLQLGLKYLFI LIGIQILACALAASILRRHLMVWVKVFAKPIFI
EAVGFIVSSVGLLGLIALVMRVDGAVSSWFRQLFLAQQR
```

### Important features:

#### Signal peptide:

amino acids 1-16

#### Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

#### Leucine zipper pattern.

amino acids 843-864

#### N-glycosylation sites.

amino acids 37-40, 268-271

1053536.011500

[illegible]



269/615

## **FIGURE 268**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVINILAADGGQHWTYEGPHGQDHWHPASYPECGNNAQSPIDIQTDSVTFDPLPALQPHGYDQPGTE
FLDLHNNGHTVQLSLPSTLYLGGLERKYVAAQLHLHWGQKSGPGGSEHQINSEATFAELHIVHYDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAIEHILSHLHEVRHKDQKTSVPPFNLRLLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLQGTILFSTEEEPKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKRRLENRKSVVFTSAQATFEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

269/615 "FASTA" format

**FIGURE 269**

GTGGCGCTGGCGGTTGCTGTACGCTGATTCGCGGGGTTGGTGGCAGCGCGGTAGCAGCAATGGACTTTCTCCTG  
GGGAACCCGTTACGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG  
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG  
AAGAGAATCGTGGGGAATAAGAATTCCACGAGGTGATGCTGGCTCTCACAGTCTAGAAACCTGTGTCAAGAAC  
TGCGGGCACCGCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCTCGCCC  
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCTCTGGGCTGACGCGTTCCGCGAGC  
TCGCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCTGGAGTTCCCCATGACTGAC  
CTGGACATGCTGTCACCCATCCACACACCAGAGGACCGGTGTTCAACTCAGAGACACAATCAGGACAGGATTCTG  
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGTGCCCCCTGTGCCGCCGCCCCATACTCTCCG  
GTGACACGCCCAATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG  
TGAGGGTGATGTGGAGATGCTGACGGAGCTGGTGCCCCACCCAGGCCGAGCCCCGAGACTGGAGCTGCTGCAGG  
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGCTCCTGAGTGATACCTGTCTCCGGGCCCATGCCCAAGGA  
GCCCTTCAGAGCCCACTGCCAGTCGAGGCCCTGGCTGGAGGCTGGCCACAGTGGAAATTCGTGCCGAGCCTATTG  
TCCTTACCTGTCTGTGCTGATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG  
CCCCCTGAGGAGCTGCGGCGGCCAGGTACGAAGCTGCAACTGTGCGCGCAGTGGGCGAGATCTCATAGCCCCA  
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCTCCATCCTTCTCTGT  
TCCTTCTGGCCGGGCACCAAGCACTGGGGCTCACCTCTTGGTTGATCCTTTGTACTGGGAGAGGTGCGCTTTTG  
TATCCCCAATTAAAGGTAGAAAAAC

271/615

## **FIGURE 270**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSFVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGRHFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTTIYEDLRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSFVTRP
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-15

#### **N-glycosylation site:**

Amino acids 41-45

#### **N-myristoylation sites:**

Amino acids 6-12;23-29

**FIGURE 271**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGCGGAGACGCCAGCCTGCGTCTGCCATGGGGC  
 TCGGGTTGAGGGGCTGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCGTGAAGCCCCCGCAG  
 GCTCCTGGGGGGCCAGATCATCGGGGCGCACGAGGTGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT  
 TCGGGGGCCAAACATCACTGCGGAGGCTTCTGTGCTGCGAGCCCGCTGGTGGTCTCGGGCCGCCACTGCTTCAGCC  
 ACAGAGACCTCCGCACTGGCTGGTGGTGTGGGCGCCACGTCTGAGTACTGCGGAGCCCCACCCAGCAGGTGT  
 TTGGCATCGATGCTCTCACCACGCACCCCGACTACACCCCATGACCCACGCCAACGACATCTGCTGTGCGGC  
 TGAACGCGCTCTGCTGTCTTGGGCCCTGCAGTGGGGCTGTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCCACAG  
 CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGG  
 CCAAGGTCCGAGTGTGGAACCCGACGTCTGCAACAGCTCCTGGAAGGGCCACTGACACTTACCATGCTCTGCA  
 CCCGAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGACAGGAACCGGG  
 CTCACGCGCTCGTTCTCTCTCGGGCCTCTGGTGGCGCGACCCCAAGACCCCGACGTGTACACGAGGTGTCCG  
 CCTTTGTGGCCTGGATCTGGGACGTGTTCTGGCGGAGCAGTCCCGAGCCGGGCCCTGCTGGGACCAACAGGC  
 CCCAGGAGAAGCCGCTGAGCCACACCTTGGCGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG  
 TGGCTGGGCCCCACGGGAAGCCTGATGTTACGGGTTGGGGTGGGACGGGCAGCGTGGGGCACACCCATTCACAC  
 TGCAAAGGGCAGAAGCAAAACCCAGTAAATGTTAACTGACAAAAAAGAAA

272/615

273/615

## **FIGURE 272**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATLMLFVKPPAGSWGAIIGGHEVTPHSRDPYMASVRFGGOHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSAEFTQQVFGIDALTTHPDYHPMTHANDICLLRINGSAVLGPVGLLRLPGRRARP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGLTLTLMCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVVSFGLWCGDPKTPDVYTQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**

amino acids 1-30

2052556-031507

**FIGURE 273**

GAAGTTCGCGAGCGCTGGCTATGGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTGGGACAG  
 GAGACCCAGAAAGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAAGCGTGGCGGCGGCCCTGGCGCCCG  
 AGCGCCGCTGCTGGGCTGCTGAGGCGGTACTTCCGCGGGAGGAGCGCGGCTGCGGGACCTGACTACATTCT  
 ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTACTCTCATCA  
 AACGCTCGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG  
 GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGCCCTGATGCGGCTGC  
 AGGACGTGTACATGTCTAATGTGAAAGGCCCTGGCCCCGAGGTGTCTTTCAGAGAGTCACTGGCTCTGCCATCACTG  
 ACCTGTACAGCCCCAAACGGCTCTTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA  
 TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCAGGAGTCTTACGGAGAGTGGA  
 AGACAGAGGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGACAGGAATGTTT  
 CGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAAAGAGGATGGCCAGGAATGTCTTGA  
 AATATGAAAGGCTCTTGGCAGAGAGCCCAACCACTGGTAGCTGAGGCTGTCTCCAGAGGCCAATATACCCC  
 ACCTGCAGACCAAGACCTACGAGGGGCTATGTACAGCCCTGGGTTCCAGCCCACTCTCTACAGATCCCTA  
 GCCTCTACTGTTCTTATGAGCAAACTTCCAACGCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACC  
 TGGAGCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC  
 CATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAAGTGGAGTACCGCATCAGCAAAAGTGCCCT  
 GGCTGAAGGACACTGTTGACCCAAAATGGTGACCCCTCAACCAACCGCATTGTCTGCCCTCACAGGCCCTTGATGTCC  
 GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG  
 CTACGTCAACCAAGCAGCCCCCTCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCT  
 CGGTGGAAGCTGAGGAGCCACAGCCTTCTATGATGCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT  
 TTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCACTGCTGGCTGTCTGTCTGTCTGGTGGGAG  
 ATAAGTGGGTGGCCAAAGTGGATACATGAGTATGGACAGGAATCCGAGAGCCCTGCAGCTCCAGCCCTGAAG  
 ACTGAAGTGTGGCAGAGGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAGCTGGGGTA  
 GGAGAGGAGAAAGCAGAGCAGCCTCTGGAAGAAGGCCCTTGTGAGCTTTGTCTGTGCTCGCAATCAGAGGCAA  
 GCGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCAGGAAGTCAGATAGGATGC  
 ACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAGTTTCTGGAGTTACAGATACCTCTGTGTGGGACAGG  
 ACATCTCAACAGCTCTCAGGTCGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCAAGGAGCCAAAGAGTGG  
 CAATGAGGACACTGAGGAGGGGCTAGCCTGACTCCAGAAGTTTAAGACTTTCTCCCACTGCTCTGTCTGC  
 AGCCCAAGCAGGAGTGTCCCCCTCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA  
 GTTGAACAACACTTTCTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTAATAATGTTTATAAATCAAAA

275/615

## **FIGURE 274**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 61126, pI: 6.40, NX(S/T): 2  
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLRRLRGEAA  
RLRDLTRFYDKVLSLHEDSTTPVANPFLAFTLIKRLQSDWRNVVHSLSEANIRALKDGY  
EKVEQDLPAFEDLEGAARALMRLQDVIMLNVKGLARGVFRVTGSAITDLYSPKRLFSLT  
GDDCFQVGKVAYDMGDY YHAIPWLEEA VSLFRGSYGEWKTEDEASLEADALDHLAFAYFRA  
GNVSCALSLREFLLYS PDNKRMA RNVLYK YERLLAESPNHVVAEAVIQRPNI PHLQTRDT  
YEGLCQTLGSQPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA  
QKIRELAEPWLQSRVSVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP  
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPL YRMKSGNRVATFMIYLS SVEAGGATAFIY  
ANLSVFVVRNAALFWWNLHRSGE GSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSS  
SPED

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-19

#### **Leucine zipper pattern:**

Amino acids 34-56;41-63

#### **Ribonucleotide reductase small subunit signature:**

Amino acids 340-356

#### **N-glycosylation sites:**

Amino acids 242-246;482-486

#### **Cell attachment sequence:**

Amino acids 27-30

#### **Tyrosine kinase phosphorylation site:**

Amino acids 189-198

#### **N-myristoylation sites:**

Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;  
457-463;473-479

275/615, 275/615

**FIGURE 275**

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAGAATGGACTTGTAAATTGCATCCTGGTGATCAC  
 TTACTCCTGGACCAGACCACAGCCACACATCCAGATTAAAGCCAGGAAGCAGCAAAACGTCGAGTGAGAGAC  
 AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACACAAGTCAATGCCTTGAAGGAAATTCAGCCCTG  
 CAGACAGTCTGTCTCCGAGGCCATAAAGTTCAAGAAGATGCTACTTGGCTTCAGAAAGTTTGAAGCATTCCAT  
 GAGGCCAATGAAGATGCAATTCCAAAGGAGGAATCCTGGTTATCCCAGGAACTCCGACGAATCAACGCCCTC  
 CAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTGGCTGGGCATCAATGACATGGTACGGAAGGC  
 AAGTTTGTGACGTCAACGAATCGCTATCTCCTTCTCAACTGGGACCGTGACACAGCCTAACGGTGGCAAGCGA  
 GAAAACTGTGCTGTCTCCTCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCCTGTCGACGAGCAAGAGATAC  
 ATATGCGAGTTCAACATCCCTAAATAGTCTTTCTCCAATGTGTCTCCAGCAAGATTTCATCATAACTTATAGG  
 TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTACTTTATTAATAAATTCGAACACAAGATCAATGTCCAT  
 AGCAATATGATAGCATCAGCCAAATTTGTCTAACACATTTCTTTGGGATTTTGGCCCTTCTGGGGTATAGGGGATC  
 AGAAATATTGATCCATGTGACGCGAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTAGTCTTTC  
 TCACTTGTACAAACCCAGTTTGTCTTCAAAAATCAGTAGCAATGCAACTCATCACTAGAAAAAGCAAGCTT  
 AGGCTACCTGAAAGATTTTCCCTTGGAAAGTTTAGCGTATGTTTGACTAAACAAAAATCCCTACATCAGAGACTCT  
 AGGTGCTATATAATCAAAAACTTTTCAGCTGTGTGCTCATTCTGCTCCATGCTGGCAATATACCTTGTGACGC  
 CATTAACCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACAACAAACCC  
 TGAAGAGGTTCTGATTGATTTTTTTTTTCTTCATGCCCTACCTTTTGGAAAGTTCCAGCCGCAATTTGA  
 AATGAAATGACAAGGTGATATTTTGTATCAATTTTCATTCCACCATTTGCATTCAACCTCTAACCTTAAATGGGTA  
 ACCCTAAGGCATATCAAGAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTT  
 TAGCATCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTTTCGTATATTTAT  
 TTTTTTTAGCCATCATTTATGTTTAAAGTTTATGAGGCAACCAATCTTTGGAAGCTGAAACCTGAATTTAAAG  
 AATGCTATCTTGGAAAAATGCATACGTCTGTGCAATTTTTATTCTGCTAGTGCTATTCTGCTGTGTTTAACTAG  
 ATTGTACAAAATAACCTTATTGCTTAAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTGAAG  
 CAAACRAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACATATCC  
 CACTTTGCAAACTTTAACTACACATGCTTGGAAATTAAGTTTAGTGTGTTTTCATTGCTCAATAATAAGCCTGAA  
 TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



277/615

**FIGURE 276**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRVRDKDGDLDKTQIEKLWTEVNALKEIQALQT  
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLEGVNDFWLGINDMVTECKF  
VDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGKWSDEACRSSKRYICEPTIPK

205770: 99255001

**FIGURE 277**

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAGGAAGCCACCAGAC  
 TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC  
 GGAGAGCCCCGGAGCCCCGTAAACCGCGCGGGGAGCGCCACGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT  
 ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG  
 CCTGGTCTGTCTGTTGGGCATCTATGAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCTTCTCTGG  
 CTCAGCCATCATCCTCATCCTCCTGGGCGTGTATGTTTCATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC  
 GTGACAACTGTACCTTCTCCAAGCATTTCATGTACATCTTGGGATCTGCTCATCATGGAGCTCATTTGGTGGCG  
 TGGTGGCCTTGACCTTCGGGAACGAGACCATTGACTTCCTGAACGACAACATTGGAAGAGGAATTGAGAACTACT  
 ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACC  
 GAGATTGGAGCAAGAATCAGTACCACGACTGCACTGCGAGTGCCTTGGACCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT  
 GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATACGACAAGGAGCGTTTCAGTGTGC  
 AGGATGTCTATCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTTCATGGACAACATACACCATCATGGCGT  
 GCATCCTCCTGGGCATCTGCTTCCCCAGTTCTGGGGGTGCTGCTGACGCTGCTGTACATCACC CGGGTGGAGG  
 ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCGTGCCAGCCAGCGTGGAGGCGGCAGGCA  
 CGGGATGCTGCTTGTCTACCCCAATTAGGGCCCGAGCTGCCATGGCAGCTCCAAACAGGACCGTCTGGGATAGC  
 ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACTCAGTACTGACCAAAGCCAGG  
 GCTGTGTGTGCTGTGTAGGTCCCACGCCCTCTGCTCCTCCCGAGGAGCAGAGCTGGGCTCCCCTAAGAGGC  
 TTTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCTGGGGAAACAGGCCCTCCTTTCTCAGGCCCTGGG  
 CTACAGGGGAGGGAGGCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCTTGGCGGTGGTATTCA  
 AGGCAGTTTGTAGCACTGTAAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGGGCATCTGGGGAA  
 GAGCAGGAGGGAAGAGCTGTCCATGCAAGCCACGCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCAGGTTGCCCTT  
 GTACAGATAACAGAGTTTCTGACTAATCAAAGCTGTATTTCCTCCCGCATGCTTATTCTTGGCCCTCCCCCAAC  
 CAGTTTGTGTAATCAACAATAAAACATGTTTTGTTTTGTTTTTAAAAAAA

# THE JOURNAL OF THE

**FIGURE 278**

Signal peptide:  
amino acids 1-4

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

AGAGGACGGCGCCGAGGACATGAGCTGTGCCAGTCTGGCAGCTCTGCTGCCCTCTGACACCTCTGGGAAGATAGCGCGCCGCGTGGACCTCTCACTCTCTCTGTGTGTCTGGCAGCACCTGTACTCAAGACGACCCCTCAGCTCCACCTGCAGTTCTCTATCTCGGCCCGCAAAAGTCACTCAAGAAAGACTGACACAGGAGCTGAAGGACACCAACGCTACACGATCCTCTGACAGAGCTGTGGCTCTCAGTGTGCTCAGTGACCTGCGGAAAGCTGAGGAGCTCTGTGTCTGGGACGCTGGTGAACACCGTCTCTGAGACCATCATCTGGTGAAGGTTCACTCAGACTAACATCTCCAGCTTGCAGTGTGAAGCTCTCGGCCAATGACAGGAGCTGCTATGCTCAAGATCCCCCTGGACATGGTGGTGGATCAACAGCCCCCTGTGTCACAGCCATCTGTGGAGTTCACATGACGATCTAGGGCCGACCTCAATCCGATCGGACAGGACCTGCAAGTGTGAGGCCCCACCGCTGTGCTCAGTAGACTGTGTGCCACCACTGGAGGCTCTGCATCAACACTGCTGTATAAGTCTCTCTCTCTGGTGAACCGCTCTAGCTTAAGACGAGTCAATGAACCTCTCTAGTGCCTCTAGTGAAGAAACACGCTGTGTCTCCGCTGTCTGAGGCTCTCTTCAATGCGATGTATGACAGACTCTCTGAGCTGGAGGAGTGCCCTATCTCTCAGCTACAGCTGTCTGAGTGTGACCTTCTCTGTATCTGCCATCAAGGTTGACACCACTCAGCTCTACTCTGGGGGCGCAATTGTGTGAGACTCAAGGAAAGGTGACCAAGTGTTTAAATACTCTGACGCTCTCCGCAAGTGGCCACCTGGAACATCACTCCGTTCCAGCTCATCTGTAGTCTGAGTGTGTGAAAGCTGCAAGTGGCTGTGTGCTCTCTCCAGAAATATCTCATGCTCTGTGGACTCTGTGCTCTCTGTAGAGTGCCACTCGCTCAGGTCTCAGACTCTCGGGCTGATCAATGAAGGCTCGGATATGAGTCTGGGATCTACCCGATCTCGTAAGATCTCTAATCAGGACACTCCCGAGTGTTTTATAGACAACGAGCCATCGAAGTGGCCCAACTGATGTGTGTGAAGTGTGTTCCCTCAGTGAAGCCCTCGGCCCTGTGTTCACTCTGGGCACTGGAAGCCAGCTCGGAAAGCTCAGTTTATACACAAAGGTGGACCACTATATCACTATCACTGATATCACTCAGTGTCTCTGCTGTGCGGAAGCAAGTGGCAATTAAGATCTGGGGTCTCCAGGTGTCAAGTGTGATGGAGGCTGGGATGAGGACGCTAGTGTCTCACTGACCAAGGATGCTCTGTGCTCTCTCAGCTCTCTGTGTGAACAAAGCTCTGAGTCTCTGCAATCACTCTCTGCAATCAATAAACACTTGCCTGTGAAAAA

281/615

## FIGURE 280

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVILGPKVIKEKITQELKDHNATSILOQLPILLSAMREKPAAGGIPVLGS
LVNTVLKHIINLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTEAQATIRMDTSASGP
TRVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPKIGDITQLYLGAKLKLDSDGKVKTKWFNNSAASLTWPTLDNIIPFSLIVSQDVVKAAVAALVSP
EFMVLLDSVLPESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNITETIHSILLPNQNGKLRSQVPSL
VKALGFEEAASSLTKDALLVTPASLWKPSSPVSQ
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-21

#### N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

#### Glycosaminoglycan attachment site.

amino acids 412-415

#### LBP / BPI / CERP family proteins.

amino acids 407-457

281/615: FIGURE 280

282/615

## FIGURE 281

CCCACGGCTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCCTTCCCGCGTTCT  
CTTTCACCTTTCTCTTCTCCACCTTAGACCTCCCTTCTGCTCCCTCTTCTGCTCCACCGCTGCTTCTCTGGC  
CCTTCTCOGACCCCGCTCTAGCAGCAGACCTCTGGGGTCTGTGGGTGATCTGTGGCCCCCTGTGCTCTCCGTCTC  
CTTTTCGTCTCCCTTCTCTCCGACTCCGCTCCCGGACGAGCGGCTGACCTGGGGAAAGGATGGTTCCCGAGGT  
GAGGGTCTCTCTCTCTTGTCTGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCAGAG  
CATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT  
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCTGTCCA  
TGCCCCCAGCCTGTGA CGGAGCCA CAGCAATGCTGTCCCAAGTGTGTGGAACTCACACTCCCTCTGGACTCCG  
GGCCCCACCAAAGTCTGCCAGCAACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT  
CCCCCTCCGCTGTCCCAACAGTGTGTCTCTGCACTGCA CAGAGGGCCAGATCTACTGCGGCCCTCACAACTG  
CCCCGAACCAAGGTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA  
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC  
TGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCCATGGCCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCACAAGGGAGCAGGCAGCAACTGTCAAGATCGTCTTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG  
CGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCCTTCGCTGCCCTTCGGCCCTTGCCCTGCATCCTATG  
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCGCTCACCCGAGAA  
AGTGGCTGGGAAGTGTGCAAGATTGCCCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAG  
GTGTCCCAAGGCACCGGGCGGGTCTCGTCCACACATCGGTATCCCCAAGCCACAGCAACCTGCGTCTCGTTTGC  
CCTGGAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCA  
GAGAGGTGAAGTACCTGGCCCAAGGCCACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC  
AAGACTTCCAGAAAGAGGCCACAGCACTTCCGACTGCTCGCTGGCCCCCAAGAGGTCACTGGAACGCTCTTCTAG  
CCCAGACCTGGAGCTGAAGGTACAGGCCAGTCCAGCAAAAGTGACCAAGACATAACAAAGACTTAAAGTGTGCA  
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTAACCTCAAAAAA

10055556.34502

283/615

## **FIGURE 282**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSLLGLALLNFPILDSHARAPDMFCLFHGKRYSPGESWHFYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPOPVTEPQCCPKCEVHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFP SRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDDEEDSVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSF
IPRHRFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGFLPCILCTCEDGRQDCQRVTCFTEYPC
RHPEKVAGKCKKICPEDKADPGHSEISSSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLVKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERG TALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

**Signal peptide:**

amino acids 1-25

205K10-0022502

**FIGURE 283**

GCGATGSGTGCGCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCAACGAGGAGAAGAT  
 GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCTATGAGGAGGCTGCCGAGCCTGGGCG  
 GCCTCGCCCTGTTGTCTGCGCCGCCGCCGCCGCCGCTCGCCTCAGCCGCTCGCGCGGGGAATGTCAACGGTG  
 GCGGCGGGGCGCGGGCGAGGTGGACGCGCTCGCCGGGCCCCGGGTGCGGGGCGAGCCACGCCCTTCCCTA  
 GGGCGACGGCTCCACGGGCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACGACCCCTGGCTGCGA  
 CTTCTCCAGCCCGAGTCCCGGGAGACCAACCCCTCTTTGGGGAGCTGCTGGACCCCTCTCCACCACTTTTCAGGCGC  
 CGCTCGGCCCTCGCGACCAACCCCTCGGCGGGCGGAACGCACTTCGACCACTCTCAGGCGCGGACGAGACCGG  
 CGCCGACCACTTTTCGACGACCACTGGCCGGGCGCGACCAACCCCTGTAGCGACCAACCGTACCGGCGCCACGA  
 CTCCCGGAGCCCGACCCCGATCTCCCGAGCAGCAGCAACAGCAGCGTCTCCCAACCCCACTGCCACCGAGG  
 CCCCCTCTTCGCTCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC  
 AGACCACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGGCTTTTACC  
 TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT  
**AAGCAACAGAGGGTGGAACTGAAGTTTATTTTATTTTAGCAAGGGGAAAAAAAAAGGCTGCTACTCTCAAGGACCA**  
**TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTACAAAATATTTTATATACTTTTATTCTTTACTTTAT**  
**ATGTTATATTTAATGTCAAGATTAAAAACATCTAATTTACTGATTAGTTCTTCAAAGCACTAGAGTCGCCAA**  
**TTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATATTGAAGAATAAATCTGCTTTCTGGAGGGGCT**  
**TTCAAGCATGAAACCTGCTAGGAGGTTTGAATATGTTCTTATGTTTATTAATATACCATTTGGAGTTTGAGGAAAT**  
**TTGTTGTTTGGTTTATTTTCTCTCTAATCAAATTTTACATTTGTTTCTTTGGACATTAAGCTTAACCTGGG**  
**GGTACCCTAATTTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTACCACTACATTTTGAAGCAAAA**  
**GTAGATTAAAGCAGGAATTACTTTAACTATTATGTTATTGGAGGTAATTTAATGTAGTGAATAATGTACTGT**  
**TATCTAAGCATTTGCGTTTACTGCACTGAAAGTAAATTTCTTTGACCTTATGTGAGGCACTTGGCTTTTGTG**  
**GACCCCAAGTCAAAAACTGAAGAGACAGTATTAATAATGAAAAAATAATGACAGGTTATCTCAGTTGAACC**  
**TGGGTATAACCCAGATCTGCTGCCACTTACGAGCTGTGTTCCCTGGGCAAGTAAATTCCTTTCACTGAGCTTGT**  
**TTCTCTCAAGGTTGTTGTGAAGATTAATGAGTTGATATATATAAATGCCTAGCACATGTCTCACTCAATAAAT**  
**CTGGTTGTTTAAATTTCAAAGGAATATATGAACTGAAATGAGAGAATATGTTTAAAGAACTTTTAGCTCCTTG**  
**ACAAAGAAAGTCTTTTAACTTTAGCACTAAATATTTTAAATGCTTTTAAATGATATTTACTGTTATGGAATAT**  
**TGTATCATATTGTAGTTTATTAATAATGTAGAAGAGGCTGGGCGCGTGGCTCACGCCGTGAATCTTAGCACTTT**  
**GGGAGGCCAAGCGCGGTGGATCACTGAGGCCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGTCT**  
**CTACTAAAAATACAAACAAATAGCTGGCGGTGGTGGCACACAGCTGTAGTCCCACTACTCGGAGGCTGAGGC**  
**AGGAGAACTCGTTGAACCCGGAGGTGGAGGTTGCAGTGAGCTGCAGATCGCGCCACTGCCTCCAGCCTGGTGAG**  
**AGAGGGACACTCTGTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAA**



285/615

## **FIGURE 284**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLGGLALLCCAAAAAASAAAGNVFGGGAAGQVDASPGPGLRGEPSHPFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPETTPLMATAGESSTTFQAPLGPSPITPPAAERTSTTSQAPTRPAPITLSTTTGPAPTTPV
ATTVPAPITTPRTPTPDLFSSSNSSVLPTPPATEAPSSPPPEYVNCNSVVGSLNVNRCNQTIGQCECRPGIQGLHC
ETCKEGFYLYNTSGLCQPCDCSPHGALSIPCNR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

285/615: FIGURE 284

**FIGURE 285**

AACAGAGCTTCCCTCGCGGCCCTGGCACTTAACCCAGAGCA**ATG**CTGCTGCTGCTGCCCTGCTCTGGGGG  
 AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCTGACGGTGAGGAAGGCCTGTGT  
 GTCCATGTGCCCTGCTCTCTTCTCTACCCCTCGCATGGCTGGATTACCTGGCCAGTAGTTTCATGGCTACTGG  
 TTCCGGGAAGGGGCCAATACAGACCCAGGATGCTCCAGTGGCCACAACAACCAGCTCGGGCAGTGTGGGAGGAG  
 ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGA  
 AGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAGGAAGTATAAATGGAATTATAAACATCACC GGCTCTCT  
 GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCTTGGAGTCCGGCTGCCCCAGAAT  
 CTGACCTGCTCTGTGCCCTGGGCCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCC  
 CCCCTGGACCCCTCCACCAACCCGCTCCTCGGTGCTCACCTCATCCCAGGCCCCAGGACCATGGCACCAGCCTC  
 ACCTGTCAAGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTACCCGCCCT  
 CAGAACTTGACCATGACTGTCTTCCAAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA  
 CTCCACAGAGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGC  
 CTGAGCTGGAGAGGCCCTGACCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCTTGGGTGCAC  
 CTGAGGGATGCAGCTGAATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC  
 CTGCAGAGCAAGCCACATCAGAGTGACTCAGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTGGTCTTCTCTG  
 TCCTTCTGCGTCTATCTTCTGTGTAGTGAGTCTCTGCAGGAAGAAATCGGCCAAGGCCAGCAGCGGGCTGGGAGAT  
 ACGGGCATAGAGGATGCAAAACGCTGTGAGGGTTGAGCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGAC  
 AGTCCCCAGACCGAGCTCCCCCAGCTTCTGCCCGCTCCTCAGTGGGGGAAGGAGGCTCCAGTATGCATCCCTC  
 AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCATGACACCGAGTACTCGGAGATCAAGATC  
 CACAGAT**G**AAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCAAGAGGC  
 TGATTCTGTAGAAATTAACAGCCCTCAACGTGATGAGCTATGATAACATATGAATTATGTGCAGAGTGAAAAGC  
 ACACAGGCTTTAGAGTCAAAGTATCTCAACCTGAATCCACACTGCGCCCTCCCTTTATTTTAACTAAAAAG  
 ACAGACAAATTCCTA

287/615

## **FIGURE 286**

MLLLLLPLWGRERAEQGTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA  
TNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVLTALTHRPNILI  
PGTLESGCPQNLTCSPWACEQGTTPMISWIGTSVSPLDPSTTRSSVLTLIPOQPDHGTSLTCQVTFPGASVTTN  
KTVHLNVSYPPQNLMTVFQGDGTVSTVLGNSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS  
NPGVLELFWHLRDAAEFTCRAQNPLGSSQQVYLVNLSLQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCKR  
KSARPAAGVGDGTGIEDANAVRGSASQGPLTEFWAEDSFPPDQPPASARSSVGEGLQYASLSFQMVKPWDSRGQE  
ATDTEYSEIKIHR

**Signal peptide:**  
amino acids 1-15

**Transmembrane domain:**  
amino acids 351-370

2025 RELEASE UNDER E.O. 14176

**FIGURE 287**

CGCGAGCTGAGAGGAGCAGGTAGAGGGGACAGGGGGGACTGTCTGTGGGGGAGCCGCCAGGAGGCTCCTCAG  
 GCCGACCCCGAGACCTTGGCTGGCCAGGATGAAGTATCTCCGGCACCGGGGCCCAATGCCACCTCATTTTGGCC  
 ATCGGCGCTTTACCCCTCCTCCTTCACTCTGTAGTGTACACACCACCTGCAAGGTTCCAGGAGCAGCCACCG  
 GCGATCCCGGAGGCGCTGGCTGGCCCCACTCCACCCACCGGCCAGCCCGGGCCCGTGCATGCCAACAACCTCT  
 ATGGTCAACCAACCGGACTTGCACGCGAGCCGACGATTCAGAACTCTCTCTGTACAGACACTGCCGCCAC  
 TTTCCCTCTGTGCAGGACGTGCCCCCCCTTAAGTGCAGCGCGCTCTCTGTCTGTGGTATCAAGTCTCTCC  
 CCTAGCAACTATGTGGCGCGAGCTGTGGGGCGACGTGGGGCCCGGAGCGCAAGGTACGGGGTTTGCAGCTG  
 CGCCTCTCTTCTGTGTGGCGACAGCTCCAAACCCGACGAGGCCCGCAAGGTCAACCGGCTGTGTGGAGCTGGAG  
 GCACAGACTCACGGAGACATCTTGCAGTGGGACTTCCACGACTCTTCTTCAACCTCACGCTCAAGCAGGTCTGT  
 TTCTTACAGTGGCAGGAGACAAGGTGCGCCACGCCAGCTTCTGTCTCAACGGGGATGATGACGTCTTTGCACAC  
 ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCTTGGCGGCCACTCTTCTGTGGGGCAACTGATCCAAAC  
 GTGGGCCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAATGAGCGGTACCCACCC  
 TATTGTGGGGGTGGTGGCTCTTGTGTCCGCTTACGGCCGCTGCCCTGCGCCGTGTGCCATGTCTTGGAC  
 ATCTTCCCATATGATGATGTCTTCTTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCACAGCGGC  
 ATCCGACGCTGGCGTGGGGTCCATCGCAACACCTGTCTCTTTGACCCCTGCTTCAACGAGACCTGCTG  
 CTGGTGCAACCGCTTCTACCTTATGAGATGTGTCTATGTGGGATGCGCTGAACAGCCCAACCTCACCTGCGGC  
 AATCAGACACAGATCTACTAGTCAAGTCAAGGTCCCGACCTCTGGGCTCTGTCTTCCATAGGAAGGGGCGAC  
 ACCTTCTCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAAGGAGTGCAGGGGAAGGTTTGAAGTTTATGA  
 GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACTGGTACTGTCCAGCATCTTCCCTGGAT  
 GGCTGGAGGAATCCAGAAAATATCCATCTTCTTTTGTGGCTGTCTAATGGCAGAAGTGCCTGTGTAGAGTTCC  
 AACTGTGGATGCATCCGTCCTTTTGGTCAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA  
 AGCAGTGCACCTGCAGTGGTTTAAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCGCAGCCAGAACTCCTGTGT  
 CACATAGAGCTGACGTGAGAAATATCTTTGAGCCAGGAGAGAGGGGTCTGTATCTTAACCCCTTCTGGGTCTC  
 AGACAACTCAGAAGGTTGGGGGATACAGAGAGGTGGTGAATAGGACCGCCCCCTCTTACTTGTGGATCAA  
 ATGTCTGTAATGGTGGAGGTGGGCGAGGAGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG  
 GGGTCTCATTAGGAGCCCCATCCCTGTGTTCCTAAGAAATCAGAGAACAGCACTGGGGCTGGAATGATCTTG  
 AATGGGCCCAAGGCCAACAGGCATATGCTTCACTACTGCTGGAGAAGGGAGAGATTCAAGTCTCCACAGCCCT  
 CCTCACCCAGTATGTTTACAGATTACGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTTCAGG  
 CCTCAGTGTCTGCCAGTCAAGCTTTCACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

289/615

## **FIGURE 288**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413
<subunit 1 of 1, 372 aa, 1 stop
<MW: 42515, pI: 8.92, NX(S/T): 6
MKYLRHRRPNATLILAIGAF TLLLFSL LVS PPTCKVQE QPPAIP EALAWPT PTPRPA PAPHCHAN TSMVTHP DFAT
QPQHVQNFLLYRHCRHP LLLQDV PPSKCA QPVFLL LVIKSS PSNYVR RELLRRTW GRERKVR GLQLRLL FLVGTA
SNPHEARKVNRLLLEAQA THGDIL QWDFHDS FFNLTL KQVLFL QWQETRC ANASFVL NGDDDDV FAHTDNM NVFYLQ
DHD PGRHLF VQG LIQNVGPI RAFWSKY YVPEVVTQ NERYPPY CGGGG FLLSRFTA AALRRAA HVLDI FPI DDVFL
GMCLELEGLKPASHSGIR TSGVRAPS QHLSSF DPCFYR DLLL VHRFLP YEMLLM WDALN QPNLTC GNQTQIY
```

### **Important features:**

#### **Type II transmembrane domain:**

Amino acids 15-34

#### **N-glycosylation sites:**

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

#### **TonB-dependent receptor proteins signature 1:**

Amino acids 1-32

#### **N-myristoylation sites:**

Amino acids 308-314;316-322

**FIGURE 289A**

CGCGCTCCCGCGCGCTCTCTCGGCTCCACGCGTCTTGCCCCGACAGGCGAGCTCTCCAGGAGCGGGGCCCT  
 GCACACCACTGCCCCCGGGTGGGACAGGGTTCGGCGCGCGCTGGCGCCCGCTGGCGCTGGCTTGGCGCTGGC  
 GAGCGTCTGAGTGGGCTCTCAGCCGCTCGCGCTGCCCAACCAAGTGTACTCTCTCGCTGCCACGCTGGATGCGA  
 CGGGCTGGGCTCTCCGCGCGCTCTCTCGGGGCATCCCCGCAACGCTGAGCGCTTGAACCTGGACAGAAATAATAT  
 CACAGGATCAACAAGATGGACTTGGCTGGGCTCAAGAACTCCGAGTCTTGCACTGGAAGAACAACAGCTCAG  
 CGTCACTGAGAGAGGCGCTCTCCAGGACCTGAAGCAGCTAGAGCGCTGCGCTGAAACAGAATAAGCTGCAAGT  
 CCTTCCAGAAATGCTTTTCCAGAGCAGCGCGAAGCTCACAGACTAGATTTGAGTGAACACAGATCCAGGGGAT  
 CCGAGGAAGGCGCTCCGCGGCTACCGGATGTGAAGAACTGCAACTGGACAAACAACACATCAGTCGCTGATTGA  
 AGATGGAGCCTTCCGAGCGCTGCGCGATTGGAGATCCTTACCTCAACAACAACAACATCAGTCGCTCTGGT  
 CACAGCTTCAACACATGCCGAAGATCCGAACCTCTGCGCTCCACTCAACACCTCTACTGGGACTGCCACT  
 GGCTGGCTCTCGGATTGGCTGCGACGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT  
 GAGGGGCTTCAACGTGGCGGATGTGACAGAAGAAGGAGTACGTGTGCCAGCCCCCACTCGGAGCCCCCATCTG  
 CAATGCCAACTCCATCTCTGCCCTTCGCCCTGCACTGTGACGAATAACATCGTGGACTGTGAGGAAGGGCTT  
 GATGGAGATTCCTGCCAACTTGC CGGAGGGCATCGTGAATAACGCTAGAACAGAACTCCATCAAAGCCATCCC  
 TGCAGGAGCCTTACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC  
 AGATGCCCTTCCAGGCTGAAATCACTCACTCGCTGGTCTGTATGGGAACAAGATCACCGAGATTGCCAAGGG  
 ACTGTTTGATGGGCTGGTGCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCACTGCGCTCGGGTGAACAC  
 GTTTCAGGACCTGCAGAACTCAACTGTCTCTCCTGTATGACAAACAGCTGCGAGCAATCAGCAAGGGGCTCTT  
 CGCCCCCTGCGAGTCCATCCAGACACTCCAATTAGCCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT  
 GGCCTGACTACTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCGAGCGCCGCGGACTCGCCAAACA  
 GCGCATCAGCCAGATCAAGAGCAAGAAGTCCGCTGCTCAGGCTCCGAGGATTAACCGCAGCAGTTTACGACGGA  
 GTGCTTCATGGACCTCGTGTGCCCGAGAAAGTGTGCTGTGAGGGCACGATTGTGGAATGCTCAACACAGAAGCT  
 GGTCCGCTCCCAAGCAGCTCCCTGAATATGTACCGACCTGCGACTGAATGAACAATGAGGTATCTGTTCTGGA  
 GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTCGGGAATAAATCTGAGTAAACAATAGATCAAGGAGGTGGC  
 AGAGGGAGTTTCCATGGAGCAGCGCAGCTGCGAGGCTGATGCTGACAGGGAAACGATGGAGACCGTGCACGG  
 GCGCTGTTTCCGTGGCTCAGTGGCTTCAAACCTTGTATGCTGAGGAGTAACATTGATCAGCTGTGTGAGTAAATGA  
 CACTTTTCCGGGCTGAGTTTCGGTGAGACTGCTGTCCCTCTATGACAATCGGATCAACCATCACCCCTGGGGC  
 CTTTCAACACGCTTGTCTCCTGTCTCACCATAAACCTCTCTGTCAACCCCTTCAACTGCAACTGCCACTGGCCCTG  
 GCTCGCAAGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTTAGGTGCGAGAAGCCATTTTCTCAAGGA  
 GATTCCCATCCAGATGTGGCCATCCAGGACTTCACTGTGATGGCAACAGGAGAGTAGTCTGCCAGCTGAGCCC  
 GCGCTGCCCGAGCAGTGCACCTGTATGGAGACAGTGTGCGATGCAGCAACAAGGGGCTCCGCGCCCTGCCAG  
 AGGCATGCCCAAGGATGTGACCGCTGTACCTGGAAGAAACCACTTAAACGCGCTGCCAGAGAGCTGTCCGC  
 CTTCCGACACCTGACGCTATTGACCTGAGCAACAACAGCTACGCTACCAATTAACCTTCACTGATTAACAT  
 GTCTACCTCTCACTCTGATCTGAGCTACACCGGCTGAGGTGATCCCCCTCCAGCGCTTCAACGGGCTCGG  
 GTCTTGGAGTGTCAACCTTCACTGGCAATGACATTTCCAGGCTTCTGAAGGCTCTTCAAGACTCCACATC  
 TCTTTTCCATCTGGCGCTGGGAAACCAACCACTCCACTGTGACTGCACTCTTGGGTGGCTGTGAGTGGGTGAA  
 GGGGGGTACAAGAGCTGGTGCATCGCCGCTGCGAGTAGCCCTGAGCCATGGCTGACAGGCTCTCTGCTCACCAC  
 CCACCCACCGCTTCCAGTGCACAAAGGGCCAGTGGACATCAAAATGTGGCAATGCAATGCTGCTCTCCAG  
 CCGGTGCAGAAATAACGGACATGCACCCAGGACCTGTGGAGCTGTACGCTGTGCTGCCCC

1052536\_01502

TACGATCTACCAAGGCGACATCTGCTCAGTCTGCCATCAACCACTGCCATCCGAAGAACCCTTGCTCAGCATGAGGAGCCAT  
TGCCACTCTGAGTGTACGACCCACGACAGTGGTTCAGCTGCTCTCGCTCTGGGCTTTGAGGSGGACGGGTGTGAG  
ATCAAGCCAGATGACTGTGAGGACAAAGACTGCGAAAAAATGCCACTTGGCTGGACGGGATCAACAACCTACAGCTG  
TGATATCTGTCTCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTTGTCGTGAGCTGAACTCT  
TGTGACATGAGGGCCAGGTGTCATCCCCCTGCAGAAAGAGTTCAGTGCAGAGTGTGCTGGTGGCTACGCGGAA  
CTCTCTGTAGACAGCAATGATGACTGTTGTGCCCCACAAGTCGCCGACGGGGCCAGTGGCTGGAGCAACAATCAAT  
GGCTCAACTGACCTCTGCCCCCAGGGCTTCAGTGGACCTTGTGAAACCCCCACCATGGTCTACTTACGAC  
ACACGCCCATGCGACCAAGTACGAGTGCAGAAACGGGGCCAGTGCATCTGGTGTGACAGACGGCCACCTCGCGCT  
TGCCCAACAGGCTTTCGGCGGGCCAGATGCGGAGAGGCTCATCTGTCAACTTGTGGGCAAGAAGCTCCTACGTG  
GAACTGGCTCCGGCCAGGTGCGAACGGGCGCAACATCTCCTCTGAGGTGGCCACTGCAAGAAGCAACCGGCTAT  
CTTCTCTACAAGAAGACCAATGACCCCTGGCCTGGAGCTGTACGAGGCTGAGCTCGCGCTGGTCTATGACAGC  
CTGAGTTCCTCTCCAACTCAAGCTGTACAGTGTGGAGACAGTGAATGATGGGCAAGTTACAGTGTGGAGCTGTGTG  
ACGCTAAACCAAGCTCTGAAGCTACTGATGGACAAGGAATCTCAAAGAGCTCGGGGAGCTCCAGAAGAGCCACA  
CGATGGGCTACCAACGAGCCCTCTACTCTGGAGGCTATCCCCACTCACCGGCTCTCCGCTCTGGCCAGGGG  
ACCGACCGGCTCTTAGGGCGGCTTCCACGGATGCATCCATAGAGTGGCCTACAACAAGAGCTGAGAGTCTCAAG  
GCCCTCCCAACAGTCCCTGGSGGTGTGACGAGCTGCAAGTCTGCACCTGTGTGACGACAGCGCTCTGCGC  
TCGCTGGGAAGGACAGCTGTGTGTGCGATGCGCCGACCTGGACCGGCCCATCTGCGACCGAGGCGGCTCC  
GACCCCTGGCTCGGCCACAGATGCCAATGGAAATGTGTGGCACTGGGACCTCATATGTCAGAGTGTGCC  
GAGGCTATGGAGGGAGCTTGTGTGACAACAGAACTGACTTGCACATGCTTGCTCAGCTCTCAAGTGTCCACAT  
GGGCACTGGCACTCTCAGACAAAGGGGAGCCTACGCTGTGCGACCGCGGCTTTGTGGCGGAGCACTGGCCA  
CAAGAGAAATCCGTGCTTGGGACAAAGTAGTCTGGAGAGGTGATCGCCGCGACAGAAAGTTATGTCATCATGTGCCA  
GCTCCAAGTGGCCATCTGAAATGTGCTGGGGGCTTGGCGGCCAGTGTGCAGCAACCCGACAGCAAGCGG  
CGGAAATGCTCTTCAGGTGCACGCGGCTCTCTCTTGTAGAAGAGTGGAGAGACATTAGAGTGGCGCTCT  
CTCGGTGTCTG**TAA**AGGCGCGCGCTCGCTGCCACTCTCGGACTCAGGCTTGTATGAGGAGTGGGACAGCAT  
GTGGGACCCCTTGATGATTCAGCATGAGGAAGATAAGCTGGAGAGGAAGTAAAGAAGAAGAGAAATTAAGTA  
TATTGTAAATAAGAAAAAATGAACAATAAAAAAAATAAAAAAATAAAAAA

**FIGURE 290**

MAPGWAGVGA AVRRLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVFRGIPRNAERLDLDRNNITR  
 ITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVPELLFOSTPKLTRLDSENQIQGIPR  
 KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLIELTLNANNISRLVTSFNHMPKIRTLRLHSHNHYCDCHLAW  
 LSDWLRQRRTVQGOFTLCMAPVHLRGFNVDVQKKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME  
 IPANLPEGIVEIRLEQNSIKAI PAGAFQYKKLRIDISKNQISDIAFDAPQSLKSLTSLVLYGNKITHAKGLF  
 DGLVSLQLLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTSIKGLFAPLQSIQTLHLAQNPFVDCDCHLWLAD  
 YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDRSRFSSECFMDLVCEKRCCEGTIVDCSNQKLVR  
 IPSHLPEYVTDLRNDNEVSVLEATGIFKKLPNLKINLNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV  
 FRGLSGKLTMRLSNLISCVSNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG  
 KWLKRKRRIVSGNPRCQKPPFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRLALPRGM  
 PKDVTLEYLGNHLTAVPRELSALRHLTLIDLNNISIMLTNYTTFSNMSHLSLTLLSYNRLRCIPVHAFNGLRSL  
 RVLTLLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLITPT  
 HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGDCTVPTINTCIQNQCQHGCTCHLSDS  
 HKDGFSCSCLPGPEGQRCEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPFLNLCQHEAK  
 CIPLDKGFSCCECVPGYSKGLCETDNDCCVAHKCRHGAQCVDITNGYTCTCPQGFSGPFCHEHPPMVLQTSPCDQ  
 YECQNGAQCIIVQOEPTCRCPGFGAGPRCEKLITVNFVGKDSYVELASAKVRQANISLQVATDKDNGILLYKGD  
 NDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHSVELVTLNQTNLNVVDKGTPKSLGKLQKQPAVGINS  
 PLYLGGIPTSTGLSALRQGTDRPLGGFHCIEHVRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDS  
 VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCCKAEGYGGDLCDNKDNSANACSAFKCHHGQCHIS  
 DQGEPIYCLCQPGFSGEHCQENPCLGQVVREVIRRRQGYASCATASKVPIMECRGCGCGPCCQPTRSKRRKYVPQ  
 CTDGSSFFVEEVERHLECGCLACS

Signal peptide:  
 amino acids 1-27

1002556-01502



**THE UNIVERSITY OF CHICAGO PRESS**

GATGTCAGAGACGCTCCCTCAGCTGCGCTCTCACCGACTAGGTGGAGCAGTGGTCTTCCCGACAGTCAACTGAGA  
AGTCAGCTCTTGGGGGACAGCCAGCAAGGATCTGCTTTTCAGTTCTGTCTCCGGACGGATTTTGGAGTGAAGGCTG  
GGGCAATTCTCAGCCTCATTTGGCTGCTGTGTCAAGCGGCGCGAGTCCAAATATGCATCTGTGTGCAAACTGGCA  
AAATATTTCCGAGGCTGGCTGGACAAATCTGGGGCTTACGCTTGGAAATCGAGTCTGCAATGGCGCATATATG  
AGAGCGGCTACAACCAACAGCAAGCTCGAGCTCTGGATGAGCGGACAGATCGACTTGGCATCTTCCAGATCAACA  
GCTTTCGGTGGTGCAGACGGGAAGCTTAAGGAGGACAACCACTGTCATGTCCGCTGCTCAGCTCTGATCACTG  
ATGACCTCCAGATGTGAATTTATCTGTGCCAGGAAATTTGTTAAAGAGACAGCAAGGATGAACATTATTGGCAAGCT  
GGAGGAACATCTGTGAGGCGGACAGACTGCTCCGAGTGAAGGAGGCTGTGAGGTTCTCTTAAATCTGGAACGTGGAC  
CGAGGATGCTTTGGACGACCGCTCTAGGATTTGCAGTGAATTCGCAATGGCTGTGTGCTCATCTTGTCCGCTGCTCTCT  
CCCAATATCTCTCTCAAACTGGAGGAGGAAAATTAAGCTATATCTTTAAGAAATAAATAATTTCAATTTAAATGT

294/615

**FIGURE 292**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYVESGYNTTAPTVLDDGSIDYGIF  
QINSPAWCRGKLENNHCHVACSAITDDLTDAIICARKIVKETQGMNIWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**  
amino acids 1-19

294/615

**FIGURE 293**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAAGGAAAG  
 TGCAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACACCAGAGGA  
 TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCTGCTCCATCTCTGCCCAGAAGCTGC  
 AAGGAAATCAAAGACGAATGTCCTAGTGCAITTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTAC  
 CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATCGGT  
 GGGAAAGTGACCGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC  
 TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGACGATGACTACAAGAACCTGGCTACTACGAC  
 ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGGAGAAAACAGCTCCCTG  
 CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAAGAAATATCCA  
 GTGAAATATGGAGAAGGAAAGTGTGGACTGACAAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC  
 CAGAAAACAGCATCTTATTACTCACCCTATGGCCAGCGGGAATTCAGTGGCGGATTTGPTCAGTTTCAGGGTATTT  
 AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCAACGGATGTAACTAGCATCACTGCATT  
 GGTGGAGGAGGATACTTTCCAGAGGCGAGTCCCCAGCAGTGTGGAGATTTTCTGTTTGTATGGAGTGGATAT  
 GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTT**GAG**AGTTT  
 TGTGGGAGGGAAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCAGTAGCTAGA  
 ATGTTAATGGCAGAAGAGAAAAAATAAATCATATTGACTCAAGAAAAAAA

205710-98525011  
 105556-01500

296/615

**FIGURE 294**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG  
GGGWTI.VASVHENDMRGKCTVGDRWSSQOGSKADYPEGDGNWANYNTFGSAAEATSDDYKNPGYDIQAKDLGIW  
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFPGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSP  
YQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCCGDFSGFDWSCYCTHVGYSSS  
REITEAAVLLFYR

10052586.011502  
202510.9825001

**FIGURE 295**

CAGGCCAATTGTCATCCCACCTGTCCTTGTGTTCCGAGCCAGGCCACACCGTCTCAGCAGTGTGTCATGTTGTTAAAAA  
 CGCCAAAGCTGAATATATCATGCCCCCTATTAAAACTTTGTACATGGCTCCCCATTTGGTTTTTGGAGAAAAGTTCAAG  
 CTTTTTACCTTGGTGTCTGCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT  
 CACTTCCCAGATCTGCTTCTACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA  
 GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAAACA  
 TTCAAGTCCCTGTCTCACATAGACCCCTGATGTCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT  
 CCTGAAAAGCTGGTAGCCTAGTCCCAAGGGGAAAAAATTCCTGCTGCTCTCCATCAACAGATACGAAAGGAAG  
 AAAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTT  
 CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG  
 GTCCAAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAAATCTCCTCCTC  
 CACAGCTGCACGTGTGTGCTTTACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG  
 CAGTGCCCACTCATTGCTGTTAATTCGGGTGGACCCCTGGAGTCCATTGACCAAGTGTGACAGGGTTTCTGTGT  
 GAGCCTGACCCGCTGCACCTCTCAGAAAGCAATAGAAAAAGTTTATCCGTTGACCTTCTTAAAGCCACCATGGGC  
 CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACC  
 AAATGCTGGTATATCAGATGTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACCCAGTTTGA  
 AACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA  
 CTTTCTATATACACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTATGCTATAATCATCCAAATTT  
 TGCCAGTGTAAAGTTACAAATGTGGTGTCAATCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTAT  
 TGCTCTTCTGTCTATAAAATTTGAATGATACCTGTGCCTTAATTTGGTTTTTATAGTTTAAAGTGTGTAATCATTA  
 AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCCGAAGTGT  
 TCACCTGTCATCTGTTAGGGAATTTTGTGTTGCTGCTTTGCTGGATCCATAGCGAGAGTGTCTGTTATTTT  
 TTTAAGATAATTTGTATTTTTCGCACTGAGATATAATAAAAGTGTTTATCATAAAAA

298/615

**FIGURE 296**

MPLLLKLVHGSPLVFGEKFKLFTLVSACIPVFLARRRKKILFYCHFPDLLLTKRDSFLKRLYRAPIDWIEEYTTG  
MADCILVNSQFTAAPVKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGGKFLLLSINRYERKKNLTALA  
LEALVQLRGRLLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQOSDLGQYVTFLRSSFSDKQKISLLHSTCV  
LYTPSNEHFGIVPLEAMYMQCPVIAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRAR  
VKEKFSPEAFTEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

298/615

**FIGURE 297**

AACTACGCCGATCCGAGAGTGGCTCCCTGGGGCGGCAGAACATGTGTGGAAGCTTCGCGATCTTCGCCGTACCTCTC  
 TTGCTGGCGTGTGGTGGGAGCCGTGCTCTACCTCTATTCGGGCTCCAGACAAGCTGCAGGAATCCAGGGTAATTCT  
 CCAACTTGAAGAAAAGATGGTAATCTCCAGATATGTGAATAGTGGAAAGTTGCATAGTTCCTGGTAAATTGAT  
 CTAGAGATGATATGGGCTGTGCTCTCTCTGGTTTGGCAGCGCCTCGTGGTATGTTTGGGCACGTGTGATGTA  
 TGAAGCAGCATATCAATCCCAATAAGACATCGGACCCCTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA  
 TCTGGTGTGTGGCAGTGTGAGTGAAGAACACCATATGATGAAATAAAATTGATGAAATGGTGTGACATGATTCTCTGAAG  
 AGTAAGTTTGGCCCTCCTCTAAAGCTTTCAGAAGAAATATTAGATAAATGGGCTCTCTACCGAGAGCCACGAC  
 GTCGCCCTTCGCGCAGCATATGCTGGTTTGTGCTGAAGTCTGTACACAGATGGTAATGGGTAGTACATTTGAA  
 GATGATCAGGAAGTCATTGCTCTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGAAAAAGGCTTCTAGAT  
 GGGTCACTTGTATAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAATCGGAGTCGTGTTAAGG  
 AACATCATAAAGAAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTCCTTAGTACAGGGAAGCT  
 AATGCAACCAAGCATCTCAGAAGACAGTATGATATTTCTCTGGCCAGTTGTCATATAAATCGCAAATATGGTACC  
 TTGGGCAACTCTGTTTTTAAACCATCTCGAAGAAAGTTCAAAAAAAATATATGAAGAGATAAAACCAAGTTTGTGA  
 AATGTGCTCTGTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTGACGATGTGCTTTGTGAAACTGTTCCGAAC  
 GCCAACTGCTCAGTTTCTCGCCAGCTCAAGATATTGAAGAGAAAATTGACCGATTATTTATTCCTAGAGAG  
 ACCCTCGCTCTTTATGCCCTTGGTGTGATCTTCAGGATCTCAATACTTGGCCACTCTCCACCAAGTTTGTACA  
 GATCGGTTGTATGATGAATAGTAAATGAACACTTTTCTCCATGGATTCTCAGGCACACAGAGAGTCCAGAG  
 TTGAGGTTTGATATATGTGTGACCAAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAG  
 GGCACGGTTATTGTAAACAAAGTATGAATCGGTAACTCATCAAGGGAAAGAGCTTGGATCACTGTCTCAAAGAGA  
 TATTTAAAATTTTATACATTTAAACATGCTGTAATTTGATTGAGGAAGAAACCACTTATAAAAAAATCTATGTG  
 TAATCCTTTTATAAACCAAGTATCACTTTGTAATTAAACCACTTATTTGACTTAA

300/615

## **FIGURE 298**

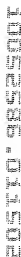
MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR  
RLVVS LGTV DVLKQHINPNKTSDFP ETMLKSLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLLKSEELL  
DKWLSYPETQHVP LSGHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGT VWSEIGKGF L DGS LDKNMTRKKQYE  
DALMQLESVL RNI I KERKGRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSZEVQK  
KLYEEINQVFGNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVLQDP  
NTWPSPHKFDPRFDDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS  
REEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290





301/615

**FIGURE 299**

CTAGATTGTGCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCAGCCTCAGAGACCGCGCCCTT  
GTCCCCGAGGSCCAATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT  
CGTCATCACCTTATTCTGGTCCGCGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTCACCCCGAGGAGTA  
TGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCTCTGTCAACCTGGGCCTCTTTGCAGTGGAGCTGGCGGTTT  
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC  
CCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCC  
AGCTGTCACTGAAATGGCTTTATTTCGTACCGTCTTTGGGCTGAAAAAGAAACCTTCTTGATTACCTTCATGACG  
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTT  
TTCCCTCGGAAACGCTCTCTGCTGGAGGATATGTGTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT  
GTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggacaattaaa  
AAAAAAAA

10052556.011502

302/615

**FIGURE 300**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV  
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALEFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

202110-0825001



304/615

## **FIGURE 302**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLLYLICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA  
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP  
PSKAVEFHQBQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF  
YSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

305/615

**FIGURE 303**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT  
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTCTGGTTGGTGTCTCTACTGA  
TTTCGTCCCTTGTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA  
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTGTCATATTATAAACTCTTAAAAAAGCCA  
GTGAAGGTTTGAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG  
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA  
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTACGCTTTCATGACGCTGGTCATTATCTTGCTGCAATGATTCT  
GGGGCATTGTATTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC  
TGGTGTGAGCCAGACCTTCATAAGTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTCA  
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCTGTCTGCCAAGACAAGA  
ACTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA  
GAGGAAGCACAACTGTGCCTTTCTGAAAATCCCTTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

10052535.01500

306/615

## **FIGURE 304**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTTATIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSNPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIHG
DSPQFFLYSAFMTLVIILLHVFVGIVFFDGCCKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFPLAAGGSCRSLKCLLCQDKNFLLYNQRSR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

Downloaded from www.sagepub.com at UNIV OF CALIF SAN DIEGO on June 11, 2015

**FIGURE 305**

[illegible]

**WILEY**

**FIGURE 306**

MRSTILLFCLLGSTSLPQLKPALGLPPTKLPADPGQTLNQQQSNQVFPSSLISLPLTQM  
LTLGFDLHLHLPNPAAGMTPGTQTHTPLTLGLGNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLLIHSLFPGGILFSLTSQAGNPDVQDGLSPAGGAGVNPATQGTTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHATEARATESPANGQL

Signal peptide:

amino acids 1-16



**FIGURE 307**

CCGGGGCAATGAGGTTGGATACTGTTTCATTGGGGCCCTTATTGGGTCAGCATCTGTGGCCAAAGAAAAATTTTGTG  
 GGGACCAAGTTTTTGGAGATTAAATGTCAGAAATGGAGACGAGATCAGCAAAATTGAGTCAACTAGTGAATTCAAACA  
 ACTTTGAAGCTCAATTTCTGGAAATCTCCCTCTCTCTCATCGGCCCTGTGGATGTCTCTGCTCCATCTGTCAATC  
 TGCAGGCATTTAAATCCTTCTGAGATCCGAGGGCTTAGAGTACGCAGTGACAAATTGAGGACCTGCAGGCCCTTT  
 TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACCGAGGACAGTAATACTTCAACTACGGGGCTTT  
 ACCATTCCTCGGGAAGCTATTTTACACGAGATGGACAACATTCGCCGACAGCTTTCTCGACCTGGCGAGGAGGGTGA  
 AGATTGGACATTCGTTTAAAAACCGGCCGATGTATGTACTGAAATTCAGCACTGGGAAAGGCGTGAAGGCGGCCGG  
 CCGTTTGGCTGAATGCAGGCATCCATTCGCGAGATGGATCTCCAGGCCATGCAATCTGGACGGCAAGGAAGA  
 TTGTATCTGATTACAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAAATGGATATTTCTTGTGTGCTGTGG  
 CCAATCCTGATGGATATGTGTATCTCAAATCAAAACCGATTATGGAGGAAGACGCGTCCCGAAATCCTGGAA  
 GCTCCTGCATTTGGTGTACCCAAATAGAAACTGGAAACGCTAGTTTTCAGGAAAGGGAGCCAGCGCAACCCCTT  
 GCTCCGAAGTGTACCATGGACCCCAAGCCAATTCGGAAGTGGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC  
 ATGGGAATTTCAAGGGCTTCATCGACTGCACAGCTACTCGCAGCTGCTGATGATCCATATGGGTACTCAGTCA  
 AAAAGGCCCCAGATGCCGAGGAACCTGCACAAGGTGGCGAGGCTTCGGGCCAAAGCTCTGGCTTCTGTGTCGGGCA  
 CTGAGTACCAAGTGGGTCCCACTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA  
 ACGGCATCAAAATTTGCAATTCACATTTGAGTTGAGAGATACCGGGGACCTATGGCTTCTCTGCCAGCTAACCGA  
 TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGCAACCTCTACTAGG  
 CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCAGCACTGAGGCCATTTGTTAAAGGAGCTCTTT  
 CCTACTGCTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG  
 TCGTGTCTCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTGGTCTCTGCTGTTTTGTATG  
 AGCCTTTGTCTCTCTCTCTCTCTCTCTCCCTTCAACCTCTGGCTGGCGGGCTGCACTCAGCATCACCCCTCTCTGGGTGGAT  
 GCTCTCTCTCAATTTATTTAGAACCAAGAACATCTGAGATGATCTCTCACTCCCTCCACATCTAGCCAGG  
 CAGTGACCTTGGCTGTGGCACTGTGGGAGACACCCTTGTCTTTAGGTGGGTCTCAAGATGATGTAGAATTT  
 CTTTAAATTTCTCGCAGCTCTCTCGAAAAATTTTCTTTGAGCAGCAAACTCTGTAGGGATATCAAGTGAAGGT  
 CTCTCCCTCTCTCTCTCTCTCTTTTCTTTTGTAGACAGAGTTTGTCTTTGTGGCCAGGCTGGAGTGTGA  
 TGGCTCGATCTTGGCTCACCAACCTCTGCCTCTGGGTTCAAGCAATTTCTCTGCCCTCAGCCTCTTGAATGAC  
 TTGGTTTATAGGCGCATGCCACCATGCTGGCTAAATTTGTGTTTTAGTAGAGACAGGTTTCTCCATGTGTGT  
 CAGGCTGGTCTCAAACTCCCACTCAGGTGATCTGCCCTCTTGGCTCCAGAGTGTCTGGGATACAGGTGTG  
 AGCCACTGTGCCGGGGCGTCCCTCTTTTGGGCTGAAACAAAGTAGAAGATCACTTTCTCTCACTGTGC  
 TGAGAATTTCTAGATACTACAGTTCTTACTCTCTCTCTCTCTTTGTATTGAGTGTGACAGGATGCGCGGAGGG  
 GATCTGTGTCACTGTAGGATCTGTGCCAGGAAGGCTGGGTGAAGTGACCATCTAAATGCAAGGATGGTGAAT  
 ATCCCATCTGTCTAATGGGCTTACCTCTCTTTTGGCTTTTGAATCACTTCAAAGATCTAGGCTCATCTAC  
 AGGCTCTAAATCACTCATCTGGCTGGATAATCTCACTGCCCTGGCACATTCCTATTGTGCTGTGGTGTATCTCT  
 GTGTTCTCTGTCTGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
 TTTGTATCTGTGACCAAGTTCCTAAGTAGAGCAAGAAATTCATCAACCAAGCTGCTCTGTGTTTCAATTCACCT  
 CAGCAGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
 TCTTAACTCTGCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAGCCAATAAATTAATCAATGTGAAAAA  
 AAAAAAAAAA

310/615

## **FIGURE 308**

MRWILFIGALIGSSICGQEKPFQDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA  
FKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNNEGQERSNNFNFGAYHSLEAIYHEMDNIAADFPDLARRVKIG  
HSFENRPMYVLKFTCKGVRPFAVWLNAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP  
DGYVYTQTQNRLLWRKTRSRNPGSSCIGADPNRNWNASFAKKGASDNPCSEVYHGPHANSEVEVKSVVDPIQKHGN  
FKGFIDLHSYSQLLMYPYGYSVKIPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNIGI  
KFAFTFELRDTGTGYGFLLPANQIIPTAETWLGLKTIMEHVRDNLV

**Signal peptide:**

amino acids 1-16

2024-09-25 10:00:00

**FIGURE 309**

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAAACCCAGGCATCCAGCTGCCACGCCTGAGTCCAAGAT  
TCTTCCCAGGAACACAAACGTAGGAGAGCCACGCTCTCTGGAAGCACCAGCCTTTATCTCTTCCACCTTCAAGTCCC  
CTTTCTCAAGAACTCTCTGTCTTTTGCCTCTTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC  
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCTTATGTTTGGTCTACTATTGCAITTAGAAGCTGC  
AACAAATTCCAATGAGACTAGCACCTCTGCCAACTCTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC  
CAACTCTGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCAATGG  
GGTCAGCATAGTCACCAACTCTGAGTTCCATACAACTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTTCAG  
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCCACCACTCTGGGTCCAGTGTGACCTCCAGTGG  
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG  
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC  
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG  
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG  
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTTCAC  
CAATCTGAGTCCAGCACACCTCCAGTGGGGCCACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG  
GGCCAAACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
GACAACTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGTCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG  
GATCAGCACAGTCCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCACACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCTCCAGGCTCTGGAAACAGCAGCTCTGACTGGAATGCACAACTTCCCATAGTGCATCTACTGCAGT  
GAGTGGGCAAGCCTGGTGGGTCCCTGGTGGGGAATCTTCTCATCAGCTGGTCTCGGTTGGGCGGC  
CGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCTGTCCCTGAGAAACACTTTAAACACAGCTGT  
CTACCACTCTCATGGGCTCAACATGGCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCAGAGGCCAG  
GTGGAGTCTCAACTGTTCTGGAGGAGACAGTATCATGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC  
CTGAGCAGCCCCGGAAGCAAGTGGCGCATCTCTCAGGAAGGAAGAGACTGGGCACCAAGACTGGTTTCTTT  
CATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGAGATCTGAAATCTTGAAAGGTATTCTCTCACTTTCT  
TGCTTTTACCAGACACTGGAAGAGAAATATATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACAC  
ACACGACAAAGAGAAGCTGTGCTTGGCCCGGGTGGGTATCTAGCTCTGAGATGAACCTCAGTTATAGGAGAAAAC  
CTCCATGCTGGACTCCATCTGGCATTCAAATCTCCACAGTAAAACTCAAAGACCTCAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

312/615

# **FIGURE 310**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVSSGASTATNSGSSVTSSGVSTATIS  
GSSVTNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS  
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS  
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA  
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA  
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS  
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS  
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS  
LVPWEIPLITLVSVVAAGVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP  
HRPRWSPNWFRRPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

2025.03.25.01.00.00

## FIGURE 311A

CTAAGCCGCGAGGATGTGCAGCTGCGCGCGCGCGGCCGCTACGAAGAGGACGGGGACAGGCGCGCTGCGAACC  
 GCGCCAGCCAGCCGAGGAGACGCGCGCAGGGCGGGAGCGGAGCCCGGACTCGTCTGCCGCCGCCGCTCGTCCGCGT  
 TGCCGCGGCCGCGCTCCCCGCGCGCGAGCGGAGGAGCGGCCGCCACCTCGCGCCGAGCGCGCGCTGCGCGCGC  
 CGGGCATGGTCCCCCTTTAAAGCCGCGAGCCGCGCGCGCGCGCGGGTGTGCGGAACAAAGCGCGCGCGCGGG  
 CTTGCGGGCGGGCTCGGGGCGCGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCTGCCGCGCGCGCGCTCG  
 CGCGCTAGGGCGGGCTGGCTCTCGTGGCGGGGCGAGCGGCTGAGCGCGCGGAGCTGCGCGCGCGCGCGCG  
 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGCTGC  
 TGCTCGGGCTCTGCTCGGGCTTCGTGCTGGCTCGCGGCTCGTCTCGCCCGGGCTTCCGAGCTGAAGCGAGCG  
 GCCACGCGCGCGCGCGCGAGCCCCGAGGGCTGCCGCTCCGGGCGGGCGCGCGCTTCCGCGCGCGCGCGCGCG  
 GCGATGCGCGCGCGCGCGAGCTTGGCGCGCGCGCTCGGACCCAGATGGCGCGCGCGCGCGAGGAACTTTCTCT  
 TCGTGGGAGTCATGACCGCCGAGAAATACCTGCAGACTCGGGCGCTGGCGCGCTACAGAACATGTTCCAGACAA  
 TTCTGGGAAAGTTCACTTCTCTCAAGTAGGGTTCTGCACATCTGTACCAATTCAGTAGTGCCATACGCG  
 GTGTGGACGACTCCTACCGCGCCGAGAAAGTCTTCTATGCTCAAGTACATCACGACCCACTATTGGACA  
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGCTTGGAGAACTTCTCGAGGAGTT  
 TGAAACGACGCGAGCGCTCTTCTTTGGGCGAGCAGGCTTGGGACCCAGGAAGAAATGGGAAAACTGGCCCTGG  
 AGCTTGGTGAAGAACTCTGCGATGGGGGGCGCTGGCGTGTATCATGAGCGGGAGTGCTTGGAGAGTGGCGCCG  
 ACATTGGCAAGTGTCTCGGGAGATGTACACACCCATGAGGAGCTGGAGTGGGAGGTGTGTCGAGGTTTG  
 CAGGGGTGCGATGTGCTGGTCTTATGAGATGCGGCGAGCTTTTATGAGAAATTACGAGCAGACAAAAAGGGGT  
 ACATTAGAGATCTTCAATACAGATAAATTCACCAAGCTATCACATACACCCCAACAAACCCACCTCAAGAT  
 CAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGCAACAATACAGCTGCCCGCGAAA  
 TTGCTCTGAGGACAAATACGACACACAGAAATTCATAAAGAGGAGCTTCTGAGTGGAACTCGCCCTCTCTCA  
 TGAAGTTTCAAGCCCGCGCGAGCGGAGGAGATTTGGAATGGGAGTTTCTGACTGGAAATCTGTATTGCGCAG  
 TTGACGGCGCGCCCTCGAAGAGGAAATGGACTCCGCCAGAGGGAAGCTTGGACGAGCTTGTGATGAGCTCA  
 TGAGATGATCATTAATGCCAACGACCAAGGCGCATCATGACTTCAAAGAGCTCAGTAGCGGCTACCGCC  
 GGGTGAACCCCATGCTGAGTACATCTTGACCTGCTGCTTCTGACAAAGAGCAAGAGGGAAGAAA  
 TGACGGTCCCTGTGAGGAGGCGACGCTATTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
 TGGATGCGCAAGAGTTGGCCAAAGAAATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACCTCCCTGAAGA  
 AGCTCGTCCCCTTTCAGCTCCCTGGGTGGAAGAGTGAGCACAAGAACCCAAAGATAAAAAGATAAACATATGA  
 TTCTTTTGTCTGGCGCTTTCGACATGTTTGTGAGATTTATGGGAAACTTGGAGAAGCGTCTTATCCCCAATC  
 CCTGGAAGTAGGATCTCCAGCTTTAAACATGAATCTTTGCTCTTCTTCTCGGAGCGTGACCTCTGTGTTACTA  
 CAGAATCTCTTCAGCATGTGCGAGCAATACAGTTCTGGGCCAACAAATATATTTTCCATCATCTTCAGCCAGT  
 ATGACCCAAAGATTGTTATAGTGGGAAAGTTCCGAGTGACACCACTTTTGCCTTTTACCTACGAAAATCGCTCTT  
 GGAGAACACTATGGGTTTGGCATCAGTGATTTATAAGGGAGATCTTGTCCGAGTGGTGGCTTTGATGTTTCCA  
 TCCAGAGCTGGGGCTGGAGAGATGTGCTTTCAGCGAGTGTGTCAGCGAGTTTGAAGACGTTTAGGAGCGT  
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTGTGATCCCAATTCGAGCCCAACAGCATACAAATG  
 GCTTGGGGCTCAAAGCATCGACTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCGGAAAAAATGATCCAA  
 GTTACAGTAAAGCAGCAATAAATAGGCTCAGTGAGGACAGCGTAAATGTCGAGCTTGTCTGGAAAGACGTTT  
 TAATTATCTAATTTATTTTCAAATATTTTGTGATGATCAGCTTTTGAAGTGGATACAGGATGATGAAACAACTT  
 AAGTGGTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAGGAAGGTGATCAGTGTTTGCCCTTGAA  
 ACATCTCTTGTGTAACATTTATGTAGCAGACTGCTTAACTTGAAGTGAATGTACCTGATGAAACAACTTTTAC  
 TTTAAAAAAATGTTTCTTTTGAAGCCCTTTGCTCCAGTCTTATGGCAGAAAGGTGACATCTCTGCAAGATGT  
 TATTGTACAAAAACATGTAACCTCTGTAATGTTCTGTGTGATGTTTAACTTCCACATTCACATGCTTCTTGT  
 GTTTTGTTTTCTTTTACATATGTTTAAAGCCATTTATGTTCCAGTGTGAAGATGAAGAAATGTGATAATA  
 GCTGTTTATCATCTTCTCAGGAGGCTTCCAGAGTGTGATCTTCTCTCACTGATGATGATGATGATGATGATGAT  
 CAGTGTAGTTTCTTGTGTTTGTGTTTGTCTTTTGTGAGACGAGTCTCACTCTGTATCCAGGCTGGAAATG  
 CAGTGGCGCAATCTTGTGCTCACTTTAACTCCACTTCCCTGGTTCAAGAGTATCCCTCTGCTCCGAGT  
 AGCTGGGATACAGGACACACACCCACCCAGCTAGTGTTTTGTGATTTTATGAGAGAGCGGGTTTCCACCAT  
 CGAACCGCAGCTGGCCACGTAGTTTAAAGCAAGGGCGTGAAGAGGACAGTGGAGTATGGCTGTCTCTCG  
 TGGTAGTTTAACTCGGCTAAATAGACCTGGCATTAATTTCAAGAGGATTTGGCATTTCTCTTCTGACCCCT  
 CTCTCTTAAGGTTAAATTAATGTTTGAATGACAAAGATGAATTTACAAATAATCTGATGTACACAGAT  
 GAAACATACACATACACCTTAATCAAACGTTGGGGAAAAATGTATTGGTTTGTCTTCTATCTCTGTCTG  
 TGTATGTGGGTGGAGATGGTTTTCATTCTTTCATTACTGTTTGTGTTTATCTTGTATCTGAAATACCTTTAA

[illegible]

TTTATTTAATATCTGTTGTTACAGAGCTCTGCCATTCTTGAGTACTGTAGTTAGTATTATTATGTTGTTATCGG  
GAGTGTGTTTAGTCTGTTTCTTTATGTCGATAACCGATCTCCAAAGATTTCCTTTGGAAACGCTTTTCCCCTCC  
TTAAATTTTATATCTCTTACTGTTTATCAAAATTAGTGTCTTTGACAGATTTGGTGCCTATGGTGTGTTGGG  
GACAAAGGTGAAATGGAATCTGTCATTATACACAGAAAGTTAAATCTCAGATCAAGATGTGCCCTTAATAAATTTGTT  
TCTATTAGATTTCAACACGATGATAGCTTGCATTTTAAATCAGCTCATTTGGAGGTCGCGTATTGTGTGAATAG  
CTTGATGTCATTTTGGAAAAATAAACAGATGAACATATTTTCTTGATCTGTTTGTGCAACCATTTGTCTCATTT  
ATCTCGTTTGTAGCTGAAGAAATTGTATTACATTTGGAGGAGAAAAAATTAACACAGAAAAAA

**FIGURE 312**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLFVGLASRLVLPRASELKRAGPRRRASPEGCRSGQAAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAVRTWSKTIPGKVQFFSSEGGSD
TSVPPIPVVPLRGVDDSYPPQKKSFMMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALPEGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYTTHE
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEONKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREBEILEW
LTGKYLVSADVGGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVPFQLPGSKSEHKPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VVLNFNSDSNPDKAKQVELMRDRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVVGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGDIVRVGGFVDSIQGWGLEVDVLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCGLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

```

Signal peptide:  
amino acids 1-23

**FIGURE 313**

GGCCGGACGCCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC  
 TACGGAGCCCCAGCTTGGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTACACA  
 GGTTGGGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA  
 ACAATGGATGATGTGATATATGTCATTCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT  
 GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT  
 TTGGAATCATGGTGTGCATGGAAGGGATTTACTTTATACTGACTCTGTTTGGGGAAGCTTTT  
 TTGGAAGCATTTTCATGCTGAGTCCCTTTTACCTTTGATGTTTGTAAACCCATCTTGGTATC  
 GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA  
 TGTGTGGTGTAAGAAGTGATTATAAAGTGGGATGCATTTGTTCTCTGGAGAAAGAAGTGTCATTA  
 TCATGAACCATCGGACAAGAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCT  
 ACCTCAGATTGGAGAAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCTCGGATTGGTTGGG  
 CCATGCAGGCTGCTGCCTATATCTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTTCG  
 AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAG  
 GGACTGATCTCACAGAAAAACAGCAAGTCTCGAAGTAATGCATTTGTGAAAAAATGGACTTC  
 AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA  
 GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAAACATTCTTC  
 AATCAGAGAAGCACCTCTCCAAGGAGACTTTCCAGGGAATCCACTTTACAGTCCACCGGT  
 ATCCAATAGACACCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG  
 AAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAGGGGAGAAGAATTTTATTTTACCGGAC  
 AGAGTGTCTATCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC  
 TGTATTGGACCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT  
 GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA  
 TCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG  
 AGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT  
 TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTTATTTGT  
 TAAAGATATTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAACTCTGAA  
 TGTAATTTTCGATACGTGTACATAGCAGGGAGTGATCGGGTGAAATAAATTGGGCCAGAATA  
 TTATTAACAATCATCAGGCTTTTAA



317/615

### **FIGURE 314**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSI FML  
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR  
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF  
CDIHEPLQLLIFPEGTDLTENSKSRSNFAEKNGLQKYBYVLHPRTTGFTFVVDRLRREGKNLD  
AVHDITVAYPHNIPQSEKHLQGDFFPREIH FHVHRYPIDTLPTS KEDLQLWCHKRWEEKEERL  
RSFYQGEKNFYFTGQSVIPPCSELRLVVKLLSILYWT LFS PAMCLLIYLSLVKWYFIITI  
VIFVLQERIFGGLIIE LACYRL LHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

2025-09-24 14:55:01

**FIGURE 315**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCCTGA  
 CCTCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTTCATAGTGTGAGATCAACCCACAGG  
 AATATC**CATGG**CCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG  
 GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG  
 CTCCTCTTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCA  
 TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG  
 AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGCGGTGTCTCTTAAGGCTAAAAAA  
 CATCACTCCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCACAGATTTACGATGAGGA  
 GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATA  
 TGTGTAGCGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCAGCCACAGCCAA  
 GTGGAAGGTTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG  
 CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT  
 CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA  
 GCCCTCACCTTGGCCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT  
 TGTCTATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAATCCAGCGGAACTGGAGTG  
 GAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACCGCAGTGGAGGTGACTCT  
 GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACTGAACCCATAGAAA  
 AGCTCCCCAGGAGGTGCTCCTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA  
 GGGTTTCCAAGCAGGGGACATTACTGGGAGGTGGACGTGGGACAAATGTAGGGTGGTATGT  
 GGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAAATGTGACTTTGTCTCCCAACAATGG  
 GTATTGGGTCTCTAGACTGACAACAGAACATTTGTATTTTCAATTCAATCCCCATTTTATCAG  
 CCTCCCCCCAGCACCCCTCTCTACACGAGTAGGGGTCTTCTGGACTATGAGGGTGGGACCAT  
 CTCTCTTCTTCAATACAAATGACCAGTCCCTTATTATACCTGCTGACATGTGAGTTTGAAGG  
 CTGTGTGAGACCCATATATCCAGCATGCGATGTATGACGAGGAAAAAGGGGACTCCCATATTCT  
 ATGTCCAGTGTCTGGGGAT**GA**GACAGAGAGAAGACCTGCTTAAAGGGCCCCACCCACAGACC  
 CAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTCTCTCTCCGAGCCTGCGC  
 ACAGAGAGTCACGCCCCCACTCTCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA  
 GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAGTCAGAAGCC  
 ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAACCTCCATC  
 CAGCTAAGCGATCTTGAACAAGTCACAACTCCAGGCTCCTCATTGTGCTAGTCACGGACAGT  
 GATTCTTGCCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAAGTTTGA  
 GGGCACAGTGTGTCTAATGATGTGTTTTTATATATACATTTTCCACCATAAACTCTGTTT  
 GCTTATTTCCACATTAAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC  
 CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCAG  
 CATTTACCTGATACCAAAACAGGCAAGAAAAAGAAAGAGGAAGGAAAAACTACAGTCCA  
 TATCCCTCATTAACACAGACACAAAAATTTCAAATAAAATTTTAAACAAATTAACATAAACAT  
 ATATTTAAAGATGATATAAATACTACTCAGTGTGGTTTGTGCCCAAAATGCAGAGTTGGTTTAA  
 TATTTAAATATCAACACAGTGTAAATTCAGCATTAAATAAGTAAAAAGAAACCATAAAAAA  
 AAAAAAAA

319/615

### **FIGURE 316**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGQWQVTGPGKFFVQALVGEDAVFSCSLFPETSABEAMEVRRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSPDGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGGDLSSDSRANADGYSLY
DVEISIIVQENAGSILCSIHLAEQSHVESKVLIGETFFQPSPWRLASTLLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPEAHPKLCVSDLKTVTTHRKA
QEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

2025-01-15 09:22:56

**FIGURE 317**

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC  
TGGGCTTGTCTCTGGCTCTGTCTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA  
GGAGCCGCCCGCGACACCTGAAGGAAAATTGGGCCGATTCCACCTATGATGCATCATCACCA  
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT  
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG  
GCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTATATATACTGTACATTCTATTTAAGGT  
AAGTAGAARTCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAATCATTGT  
CTACATTAAAACTTCTTATAGTTTCATAAAATATTTCAAATCCATCATCTCTTTAAATCCTGC  
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCACTTTACATAAGAATGTTTACTCAA  
TGTTTAAGTGTTTTGCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT  
CTTTTGGTTCCTAATCCAGTGAGTGATACAATTCATGCACTCCCCTGCCA

321/615

**FIGURE 318**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRPPMHHHQAPSDGQTP  
GARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILIIILHQ

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

**FIGURE 319**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG  
 GAAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCCCT  
 GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATT  
 CTATAGCACATTGTCTATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA  
 CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC  
 ATTAAGGGAAGAAATTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGT  
 GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT  
 TGTTCACCTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA  
 CTCAGTTAAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG  
 AACACGAAGAAGTAAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA  
 GGGTGAATGGCCCTGGCAGGCTAGCCTGCAAGTGGGATGGGAGTCACTCGCTGTGGAGCAACCTT  
 AATTAAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG  
 ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAAATGAAACGGGGTCTCCGGAGAAT  
 AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGACAGAGCTTTC  
 TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT  
 TCAACCCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA  
 AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACCTCAAGC  
 TTACAATGACGCCATAAATCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC  
 ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTAGATGCTAGAGATATCTGGTACCTTGC  
 TGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCACAAGCCTGGTGTTTATACTAGAGT  
 TAGCGCCTTGGGGACTGGATTACTTCAAAAACCTGGTATCTTAAGAGACAAAAGCCTCATGGAA  
 CAGATAACATTTTTTTTTTTTTGGGTGTGGAGGCCATTTTAGAGATACAGAATTGGAGA  
 AGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAACTGTTTGTCTGATGCATGTATTTT  
 CTTCCAGCTCTGTTCCGCAAGTAAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA  
 GCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATAACAATATTACATTACAGCCTGTA  
 TTCATTTGTTCTCTAGAAGTTTGTGAGAATTTGACTTGTGTGACATAAATTTGTAATGCATA  
 TATACAAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAAATATCCA  
 TTTTCAAGGTGCAGAACAGGAGTGAAAGAAAAATATAAGAAGAAAAAAATCCCCTACATTTTA  
 TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTATTATT  
 GAAAGGTCAAGCAAGACAGCAGAAATCAACTCATCTCATATTAGGAAGTATGGGAACATAA  
 GTTAAGGAAGTCCAGAAAGAAGCAAGATATATCCTTATTTTCAATTTCCAAACCAACTCATG  
 ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACCTTCATGCAATG  
 TACTTGTCTTAAGCAAAATTAAGCAAAATATTTATTTTAACATTGTTACTGAGGATGTCAACATA  
 TAACAATAAAATATAAATCACCCA

323/615

## **FIGURE 320**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

### **Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 321**

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG  
 CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT  
 AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG  
 CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCCGCAAGGCGGCA  
 TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCCTGGTGATCCCTCCGCTGCAGCTCCTATCCA  
 TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCCTCCAGAGCCTACTCCAAGGCTT  
 CAGCCGACTTTTCTCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT  
 GGACTTCCGGGGCCTCCCTGGGAACCTACCACAAAGAGGAGAACAGGAGCACCAGCTGGGGAA  
 CAACACCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT  
 GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA  
 GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC  
 ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAGCTGCCACGGCGGAGGTCCCACCAG  
 GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCTGCAGGCCATCCGGGAT  
 GGACTCCGCAAGGGGACCCACAAGGACGTCTAGAAAGAGGGGACCGAGAGCTCCTCCCACTCC  
 AGGCTGTCCCCCGAAAAGACCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG  
 TGGGGACCGGGGAGCACCTGCTGTAGCCCCCATCAGACCCTGCCCCAAGCACCATATGAAAA  
 TAAAGTCTTTCTTACATCTAAAAA



325/615

## **FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879  
><subunit 1 of 1, 242 aa, 1 stop  
><MW: 27007, pI: 8.68, NX(S/T): 2  
MGEASPPAPARRHLLVLLLLSTLVIPSAAPIHDAQAESSLGLTGLQSLQGFSLFL  
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS  
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTLHPRVAFWI IKLPRRRSH  
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYILRPSR  
QL

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-30

#### **N-glycosylation sites:**

Amino acids 97-101;112-116

#### **N-myristoylation sites:**

Amino acids 80-86;132-138;203-209;216-222

AGAGAAGAAGACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCT  
 TGCCCCGATGAGCCCCCGCTGGCTGGCCCTGACATCCCCAGGCGGGCGTGGGGCAGCCGGCC  
 CAGCGCCGACGATCGCTGCGGTTTTTGCCCTGGGAGTAGGATGTGGTGAAGAGTATGGGGCTTC  
 TCCCTTACGGGGCTCACAATTGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCTCTAC  
 GCCCTCAATCTGCTCTTTTGTTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGATGAGG  
 GACTACCTTAATAATGTGTTCTACTTTTAATGACAGAAACGAGGGTAGAGGAAGCAGTCATTTTG  
 ACTTACTTCTCTGTGTTTCATCCGGTCATGATTTGCTGTGCTGTTCCTTATCATTTCTGTGGG  
 ATGTTAGGATATTTGTGAACCGGTGAAAGAAATCTGTGCTCTTGCATGGTATTTGTGGAAT  
 TTGCTTGTCATTTTCTGTGTAGAATCTGGCTTTGTGGCTTTTGGACATATGAACAGGAACTTATG  
 GTTCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGAATTA  
 AGATATCGTGCGCTTACTCATGCTTTGGAATTTTTTCAGAGAGAGTTAAGTCTGTGGAGTA  
 GTATATTTCTCATGCTGTTTGTGAAGATCAGAGATGGACTGGCCCCAGAGTCTCTGCTGTGTT  
 AGAGAATTTCCAGGATGTTCCAAACAGGCCACCAGGAGAGTCTCAGTGACCTTTATCAGGAG  
 GGTGTGTGGGAAGAAAATGTATTCCTTTTTAGAGAGGAACCAACAACCTGCAGGTGTGAGGTTT  
 CTGGGAATCTCCATTTGGGGTGCACAAATCTGTGGCATGATTTCTACCAATTA  
 TCTCTGATATATGATAGAAGGAGCGCTGGGACAGCAAAATGATGTCCTTGAAGAATGACAAC  
 TCTCAGCAGCTGTGATGTCCTCAGTAGAATCTGTGTGAACCAAGCTGTCAAGAATCTTTGAA  
 CACATCTCATGTCGAACACAGCTTTAATACACATCTTGAGATGAGGAGATTATAAAAAGAATAT  
 TCACAGAAGAAAACCAAACTGTTTTTATTTGAGACTGTGGAATTTTTGAGTACATATACTATGT  
 TTTTCAGAAATATGTAGAAATTAATAATGTGCCATAAAATACACCTAAGCATATACTATTCTA  
 TGCTTTAAATAGGAGTTGGAAGAGTTTCATGTCATAAGTCAACCTGCACATAAATTTGATGC  
 CCTTAAATGCTGAAGACAGATGATCAACCACTGTGTAGCTGTGTATGACTTTTATGAAC  
 ACAGTTATGTTTTTGGAGCAGCATGTTTGGATTAGCATTTCCGATCTCATGCAACAGAGTCACA  
 TATGTTGGAGCTGGAGCCATAGTAAGGTTGATTTACTTCTCAACCTAGTATATAAGAGTACT  
 AATTAAATGCTAACTAGGAAGTTAGAAATACTTAATACTTTTATTAATCAGCGATCTTATTCT  
 TCTGATGCTCAATAAATAATATATATCAGAAAACTTTCAATATGGTGACTACCTAAATGTGAT  
 TTTTGCTGGTTACTAAATATTTCTTACCACCTTAAAGAGCAAGCTTAACCATTTGTCTTAAGC  
 GATCAGGGATTTTTTGATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT  
 GATAATGTTAAGAAATAACCATTTAGAAAGGAAATTTGCTGTGTATGACATCAATTTTATTA  
 GCCTTCTCGTTTAAATAAGAGCTTTACTATCTGTGCTGGGCTTATATATACATATAACTGTGTA  
 TTTAAATACTTAACCATCAATTTTGAATAATCAGGTTGTATACATAGGAATCAATTATTCAGA  
 ATGTAGTCTGGTCTTTAGGAAGTATTAAATAAGAAAATTTGCACATAACTTAGTTGATTGAGAA  
 AGGACTGTGATAGTCTTTTTCTCCAAATGGAAGACTCTTTTGCACATAAACACTTTTAAAAA  
 AGCTTATCTTTGCTCTTCCAAACAGGAAGCAATAGTCTCAAGGTCAATATAAAATCTACAGA  
 AAATAGTGTTCTTTTCTCCAGAAAAATGCTTGTGAGAATCAATTAACCAATGTGACAAATTTAG  
 AGATTCTTTGTTTTATTTCACTGATTAAATATACTGTGGCAAAATACAGATATTAATAATTTT  
 TTACAAAGAGTATAGTATATTTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTAT  
 TTTGTTTATTTCTCAGAAATATGGAAGAAAATTAATAGTGTCATAAAATATTTTCTAGAGAG  
 TAA

327/615

## **FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV  
HPVMIAVCCFLIIVGMLGYCGTVKRNLALLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQWS  
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGC  
SKQAHQEDLSLDLYQEGCGKMYSFRLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR  
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

1052536-011507

**FIGURE 325**

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA  
 GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA  
 ATCACCATCTGAATTCAGAAGCCCTGTTTATGTGAGAATGCCAGATCCATTCCACGCAACCGTTC  
 CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCCTGAAAAGAATTGCTTATTTCTAT  
 GTCTCTTATCTGCGCTTTTGGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCGG  
 TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCAACCGTTC  
 CTCTGTATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT  
 TTTTATTCACGCCATCGCTGCAGCTCTTGTTATTCACATCGAACTCCTTTGATGTGATCAGTG  
 ATGATGCTTTTATTGGCTCTCCACATCTAGAGTATTTATTTCATAGAAAACAACAACATCAAGT  
 CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAAATCACTTGAGCCTTGCAAAACAACA  
 ATCTCCAGACATCCCAAAAGATATTTTCAAAGGCCCTGGATTCTTTAAACAAATGTGGACCTGA  
 GGGGTAATTCAATTAATTGTGACTGTAACTGAAATGGCTAGTGGAAATGGCTTGGCCACACCA  
 ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCCAGAATACAAGAAGCGCAAAATCAATA  
 GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT  
 ATCAATCATTTGCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCACTCGCTCAGC  
 CTTTTACTGGAAATGCAATTTTCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG  
 ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAAACTCAGCTCTATG  
 TTTATGTGGCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAAAATAAAT  
 TCATAAAAATCCAGGATATTGAAATTTCAAATCCGAAAACCCAATGACATTGAAACATTCA  
 AGATTGAAAACAACCTGGTACTTTGTTGTGTGTCGACAGTTCAAAAGCTGGTTTTACTACCATTTAC  
 AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGCACACTGAT  
 GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAAGCGCTCATTTAATTCTGTCT  
 AGTAGTTCCAGCGCTCCTGTAATTTATCAGTGGAACAAGCAACACAAATTTCACTAACCAA  
 ACTGACATTTCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAGGGGACGTG  
 TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGAGGCTCCTCGTTC  
 CAGGATATTAGAGGATGCCATCGCAGGATCCATGGTGTTCCAGCCTCTTCAAATAAATAAT  
 TACCAATATGCAATTTCTGGAAAGTATTACTCCTTTACTCAAGTGATAACTGGGATGCAGAG  
 AAAGCCAAATTTGTGAAATTTTCAGGAATTAATGTTTCAGGCACCAAGATCATTCACACATGTG  
 TCCATTAATAAGCGTAATTTTCTTTTGGCTTCCAGTTTTTAAGGGAATACACAGATTTACAAA  
 CATGTCATAGTTGACTTAAGCGCATGAGACACCAAAATTTCTGTGGCTGCCATCAGAAATTTTCT  
 ACAGTACATGACCCGGATGAACCTCAATGCATGATGACTCTTCTTATCACATTCGAAATGAAT  
 GCCTTTCAAACATTGAGACTGCTAGAACAAGCACTACAGTATCTCCATCCTTAACTGTCCA  
 GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTTAACTGTTCTTTGCA  
 GTGAAGATGTGTAATAAGCGTTTAATGGTATCTGTTACTCCAAAAAGAAATATTAAATATGTA  
 CTTTTCCATTTATTTATTCATGTGTACAGAAACAACCTGCCAAATAAAATGTTTACATTTCTT  
 TCATA

**FIGURE 326**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESRSRCKMRGNACIPKIRIAYFLCLLSALLLTGKKPKAPKPCPAVCTCTKDNLACENARS
IPRTVPDPVISLSLFRSGFTIEISGFLFTPSLQLLFTSNISFDDVTSDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLYICGLPSLANNNLQTLPKDIFKGLDSLRTNVDLRGNSFCNCK
LKLWLVEWLGHGTHATNATDEYCEHPPEYKRRKINSLSKDDFDITFEFASQDLQYQSLSDID
TFSYLIVDEVVIAQPPFTGKCIFLEWDHVBKTFPRYDNIITGSTVVCVKPIVIETQLYVIVA
QLFGSHSIYKRDSPANKFIKIQDIBILKIRKPNDETTFKIEENNWFYVPVADSSKAGFTTII
KWNNGNFGYSHSLHAWYKTRDVEYLEIVRTPTQLTRPHLILSSSSQRPVITYQWNKATQLF
TNQTDIPNMEDYVAVKHFSVKGDVYICLTRFIGDSKVMKWGSSSFQDIQRMPSRGSMVFQ
PLQNNYQYAILGSDYSFTQVYNWDAEKAFVKFQELNVQAPRSFTHVSINKRNFIFASS
FKGNTQIYKHVVDLSA
```

Important features of the protein:

Signal peptide:

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235; 378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

**FIGURE 327**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGTGATAAAGCCC  
 CTACCAGTGTCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAGTGTCTGA  
 AAGAGAAGGGGACAAAGGAAACACCAAGTATTAAAGGATTTTCCAGTGTCTTGGCAGTTGGTC  
 CAGAAGGATGCTCCTCATTCTGCTTCTACCTGCCTCTTTCATCAGGCACCTCCGTGTACCC  
 CGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA  
 CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA  
 CTTACCGGCATGGCGGGAGATGCCATGCCATCCTTCTGCATACCAGAAAACCACTGTGGAAC  
 CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCCAGGCATTGTGCAACGCCA  
 GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAGTCAAGGCTTG  
 CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCAGCGTCTGCTTCCACGCTACTGTGG  
 TCATTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCA  
 ATGCGCTCCAGGAACGTGTCTAGGCCCTGACAGGCAGACATGCTTTGATGAAATGAATGTGA  
 GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGTGAGTG  
 TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA  
 TAAACAATGGTGGCTGCAGCCACTCTTGCCCTTGGATCTGAGAAAGGCTACCAAGTGTGAATGTCC  
 CCGGGCCGTGGTCTGTCTGAGGATAACCAACACTTGCCAAGTCCCTGTGTGTGCAAAATCAAA  
 TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCCTGGAGCTCTTCTGACCAACAC  
 CTCTCGCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCAAGACATGTGG  
 TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA  
 GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACAGCAAGCTGCTGATCCCGGTGAC  
 CTGCGAGTTTCCACGCCGTGTACACCAATTTCTGAAGGATACGTTCCCAACCTTCGAACTCCCC  
 ACTGGAAATCATGAGCCGAATCATGGGATCTTCCCAATCATCTGGAGATCTTCAAGGACAA  
 TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTT  
 TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAAGCTTGGTGGAGAGCTGCTTTGCCAC  
 CCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCATCCGGATGGCTGTGTTTCAGA  
 TGACTCGGTAAGCAGTACACATCCCGGGATCACCTAGCAAAAGCACTTCAGGTCCCTGTCTT  
 CAAGTTTGTGGGCAAGACCAAGGAAGTGTCTTCTGCACTGCCGGTCTTGTCTGTGGAGT  
 GTTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCATGCGTCTGGGGCAGGAGG  
 AGAGGACTCAGCCGCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGA  
 GGACTAGTTTCTGTAGGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC  
 CCCCCACCGCCTCTAAGAACATCTGCCAACAGCTGGGTTCAGACTTCACACTGTGAGTTCAG  
 ACTCCAGCACCAACTCATCTGATTCTGGTCAATTCAGTGGGCACAGGTACACGACTGCTGT  
 AACAATGTGGCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAATCAAATGTCCACCCAGAA  
 AGACACTCACCCCATTTCCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGAATC  
 AGACCAAAAATCAGAAGCTGGGTATAATTTCAAGTTACAAACCCCTAGAAAAATTAACAG  
 TTACTGAAATATGACTTAAATACCAATGACTCCTTAAATATGTAATATAGTTATACCTT  
 GAAATTTCAATTCAAATGCAGACTAATTATAGGGAAATTTGGAAGTGTATCAATAAACAGTAT  
 ATAATTTT

**FIGURE 328**

MPPFLLLTCLFITGTSVSPVALDPCSAAYISLNPEWRNTDHLQDESQGPPLCDNHVNGEWYHFT  
 GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCCLWNTTVEVKACPG  
 GYYVYRLTKPSVCFHVYCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRTCTCFDENECEQN  
 NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHMNNNGGCSHSLGSEKGYQCECPRG  
 LVLSEDNHTCQVPVLCKSNAIEVNI PRELVGGLELFLTNTSCRGVSNGTHVNI LFSLKTCGTV  
 VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTI SEGYVPNL RNSPLE  
 IMSRNHGIFPFTLEIFKDN EFEEPYREALPTLKL RDSLYFGIEPVVHVSGLES LVESCFATPT  
 SKIDEVLKYYLIRDGC VSDSVKQYTSRDHLAKHFQVPVFKFVKGDKHKEVFLHCRV LVCVGLD  
 ERSRCAQGCRRMRMRGAGGEDSAGLQGGTTLTGGPIRIDWED

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
 522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

**FIGURE 329**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT  
 GCATCGGGCCTCCTCCAGCCAGTGTGACCAAGGACCTTCTGACCTGCTGGCCAGCCAGGACC  
 TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC  
 GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG  
 ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAAGTGGGGATCCCCA  
 TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGATTC  
 TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAGCTGTGTG  
 ACGGAGAGCTGGACTGTCCCTTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG  
 GGCCTGCAGTGGCAGTCCGCCTTCCAAGGACCGATCCACACTGCAAGGTGCTGGACTCGGCCA  
 CAGGGAAGTGGTTCTCTGCTGTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTGA  
 GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGTTGAAA  
 TCACAGAAAAACAGCCAGGAGCTTCGCATGCGGAAGCTCAAGTGGGCCCTGTCTCTCAGGCCTCCC  
 TGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG  
 AGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTGAGCATCCAGTACGACAAAACAGCAGCTCT  
 GTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA  
 CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGG  
 CTGTGGCCAAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC  
 TCATGAAGCTGCAGTTCCCACTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT  
 TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTACGAAGCAGA  
 ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGT  
 GCAATGCAGACGATCGGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCCG  
 AAGGGGGTGTGGACACCTGCCAGGTGACAGTGGTGGGCCCCGATGTATCCAATCTGACCAGT  
 GGCACTGTGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCCGAGCACCCAGGAGTAT  
 ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGTCT  
 GCTGCCCTTTGCAGTGCTGGGAGCCGCTTCTTCTCTGCCCTGCCACCTGGGGATCCCCAA  
 AGTCAGACACAGAGCAAGAGTCCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT  
 GGAGCAGCAAAGGCCCTCAATTCTGTAAAGAGACCCTCGCAGCCAGAGGCGCCAGAGGGAAG  
 TCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACT  
 GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACTACTGAATGGAAGC  
 AGGCTGTCTTGTAAAGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTCGGCCA  
 GCCCTGTCCGTCTTACCCATCCCAAGCCTACTAGAGCAAGAAACAGATGTAATATAAAAT  
 GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCTATTGTTATTACAGCTATGG  
 CCATATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA




 UNIVERSITY OF THE PACIFIC  
 300 UNIVERSITY AVENUE  
 STOCKTON, CALIF. 95211-8800  
 TEL: (209) 941-2000  
 FAX: (209) 941-2000  
 WWW: WWW.UOPACIFIC.EDU

## FIGURE 330

Transmembrane domain:  
amino acids 32-53 (typeII)

Transmembrane domain:  
amino acids 32-53 (typeII)

**FIGURE 331**

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGGC  
 TCCAGGACTTTGGCCATCTATAAGCTTGGCA**ATG**GAGAAATAAGAAAATTCTCAAGGAGGACG  
 AGCTCTTGAGTGAGACCCACCAAGCTGCTTTTACCAAATTGCAATGGAGCCCTTCGAAATCA  
 ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATCTACC  
 TGATCCTGCTCACCCTGGCGCTGGGGTGTGGTGGTCCAAGTTCCTGAATCTGCAGGCGCGC  
 TCCGGGTCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCTCTCT  
 CTTGTCTGCAGTCAGCACACCCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC  
 TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAAC  
 TCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC  
 ACAAGGGGGCCATGGGCATGCCCTGGTGCCCTGGCCCCGCGGACACACCTGCTGAGAAGGGAG  
 CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGGCCACCGGGAG  
 TCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAGGAGCCACTGGCA  
 CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGTCTCATTGGCCCCAAAGGGG  
 AAATCGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA  
 TGAAAGGAGATGCAGGGGTCTATGGGCCCTCTGGAGCCAGGGGAGTAAAGGTGACTTCGGGA  
 GGCCAGGCCACAGGTTTGGCTGGTTTCTTGAGCTAAAGGAGATCAAGGACAACCTGGAC  
 TGCAGGGTGTTCGGGGCCTCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCTTGGCA  
 GTGCTGGCTCCCTGGCGCAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC  
 TGAAAGGAAGCAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG  
 TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGAGCCAGGGCTGGCAGGTCCCAAGGGAG  
 CCCCCTGGACAAGCTGGCCAGAAGGGAGACAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG  
 TAAAGGGAGAAAAAGGTGAAAGAGGTGAAACTCAGTGTCCGTCAGGATTGTCGGCAGTAGTA  
 ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTCGATGACGAGTGGC  
 AAAATTCTGATGCCATGTCTCTGCGCATGCTGGGTTACTCCAAAGGAAGGGCCCTGTACA  
 AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGGGGCACGGAGAGTA  
 CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG  
 GCGTGGAGTGCAGCGT**TGA**CCCCGAAACCTTTCACTTCTCTGCTCCCGAGGTGTCTTCGGG  
 CTCAATATGTGGGAAGGCAGAGGATCTCTGAGGAGTTCCTGGGGACAACCTGAGCAGCCTCTGG  
 AGAGGGGCCATTATAAAGCTCAACATCATTGA

**FIGURE 332**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAPHQIAMEPFPEINVVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPPEGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGD
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPAGKGDQGPGLQGVPGPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKSGSGDTGLQGGQGRKGESGVPAGVKGEG
GSPGLAGPKGAPGQAGQKGDQGVKSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVVYSG
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV
```

**Transmembrane domain:**

amino acids 47-66 (type II)

**N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 432-440

**N-myristoylation sites.**amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

**Leucine zipper pattern.**

amino acids 56-78

**Speract receptor repeat**

amino acids 422-471, 488-519

**Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

**FIGURE 333**

GGGCTGTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG  
 CCTCTGGCATATGCACACACTCACACATTTCTGTACACCCCGTCACACACATACCATGTTTCT  
 CCATCCCCCCAGGTCAGCCGCTCAGTGTCTGCCATCCAGCAGGGGTACCTTGAAGCTCTGGC  
 TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCTCCTTTCTCTCCCAAAGCCCAACTG  
 CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAATGCAGTGCAGCAGGAGTAAGAGTGGGAG  
 GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAAGCAGCCTAGAGAGGGCAGACTA  
 TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAACCCG  
 GGCACCTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGCTACCCAGT  
 CCCCTACACAGTCCCAGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCGGGTGGGCC  
 CAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGAGTGCCCTGGTGGTCTGTGAGCCTGGCCGA  
 GCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT  
 GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGCAATGGCACCACTGGGGCC  
 ATCTACTTCGACCAGGTCTGTGTAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC  
 GTAGCCCTGTCCGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGGTGTACAACCGCCAA  
 ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCATCTCAGCCTTTGCCAATGATCCT  
 GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG  
 TCTCTGCGCATGCTGCGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC  
 CTCATCTTCCCTCTCTGAGACCCAAAGTCTTTCAAGCACAAGAAATCCAGCCCTGACAACTTT  
 CTCTTGCCCTCTCTTGCCCGGAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC  
 CCACCTCTTTGATGGGACCTGTGCCAAACACCCAAAGTTTAAAGAGAAGAGTAGAGCTGTGGC  
 ATCTCCAGACAGGGCTTTCCACCCACCCACCCCGATTACCCCTCCAGCCACCTGTCTGCATC  
 TGTTCCTGCGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCAAGAAGGAAGATCTGCACACTT  
 TGCGGCTCTGTCTCTCCGTTCCCCCACCCAGCTTCTGTCTAATGCTGATCAGGGACAGG  
 TGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG  
 CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCCTCAGAAGCTGAG  
 CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA  
 GTCTGTGGCTGGTAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG  
 CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCTCTATGTCTGGATCCCAGAT  
 GGACTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTTGTCTGGCTGAGAGCA  
 GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGGATCC  
 TCTTGCTTGGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC  
 TCTGACTGCTGCTCCTTCTCTCCAGCTCTCTCACTGAGTTATCTCACTGTACTGTTCTTCAG  
 CATATCCCCACTATCTCTCTTCTCTCTGATCTGTGCTGTCTTATTCTCTCTCTTAGGCTTCTCT  
 ATTAACCTGGGATTCATGATTATCTCTCTCAGACCTCTCTCTGCCAGTATGCTAAACCTCTCC  
 TCTCTCTTCTTATCCCGCTGTGCCATTGGCCACAGCTGGATGAATCTATCAATAAAACAAT  
 AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGA  
 TCGGTGTTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAAATAATATCAAACCTGTATACTAA  
 AATTAAAAA

337/615

**FIGURE 334**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEG GGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGLIFPL
```

**Signal peptide:**  
amino acids 1-32

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

**FIGURE 335**

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCGAGCTCCAGGTGTCCTAGCCGCCAGCC  
 TCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCATGG  
 GCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGCCGTGACTGGGCGGGCTTACGCC**ATGAA**  
 GACCCTCATAGCCGCTACTCCGGGGTCTGCGCGGCGAGCGTCAGGCCGAGGCTGACCCGAG  
 CCAGCGCTCTCACGGAGGACCTGCGCTGTGCGCGCAGGGGTCTGGGAGATGGGGCACTGGATC  
 CAGCATCTCTCCGCCCTCCAGGACCTCTTCTCTGTCACTGGCTCAATAGGTCCAAGGTGGA  
 AAAGCAGCTACAGGTCTATCTCAGTGCTCCAGTGGGTCTGTCTCTTCTTGTACTGGGAGTGGC  
 CTGCAGTGCCATCTCATGTACATATTCTGCACCTGATTGCTGGCTCATCGCTGTGCTCTACTT  
 CACTTGGCTGGTGTTTGACTGGAACACACCCCAAGAAAGGTGGCAGGAGGTACAGTGGGTCCG  
 AAACCTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCTCCATCCAGCTGGTGAAGACACCAA  
 CCTGCTGACCACCAGGAACATATATCTTTGGATACCAACCCCATGGTATCATGGGCCTGGGTGC  
 CTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCAGGCATACGGCCTTA  
 CCTGGCTACACTGGCAGGCAACTTCGAATGCCTGTGTTGAGGGAGTACCTGATGTCTGGAGG  
 TATCTGCCCTGTGAGCCGGGACACCATAGACTATTTGCTTTCAAAGAATGGGAGTGGCAATGC  
 TATCATCATCGTGGTCCGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCCTGGCAAGAATGCAGT  
 CACCCTGCGGAACCGCAAGGGCTTTGTGAACTGGCCCTGCGTCTATGGAGCTGACCTGGTTCC  
 CATCTACTCTTTGGAGAGAATGAAGTGTAACAAGCAGGTGATCTTCGAGGAGGGCTCTGGGG  
 CCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTCGCCCCATGCATCTTCCATGGTGC  
 AGGCCTCTTCTCCTCCGACACTGGGGGCTGGTGCCCTACTCCAAGCCCATCACCACCTGTTGT  
 GGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCCAAGCAGACATCGACCTGTACCA  
 CACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCACAAGACCAAGTTTCGGCCTCCC  
 GGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTTCGGGGCCAAATTCCTGGAGGAACCA  
 CTGCAAAATCACTTTTTTGTCTGTAAATTTGGAAGTGTATGGGTGTCTGTGGGTATTATAA  
 AGAAATTATAACAATTTTGTCTAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

339/615

## **FIGURE 336**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLGRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGGRRSQW
VRNWAVWRYFRDYPFIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLRREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIIVVGAAESLSSMPGKN
AVTLRNRRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVELEVN
```

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 76-97

#### **N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

#### **N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

[illegible]



## FIGURE 338

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
>>subunit 1 of 1, 368 aa, 1 stop
>>MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLAKTLQFVLLHLLGVFFVVFSGELVINFVQLCTLALWPVKQLYRRLNCLRLAYSLSWSQLVLM
LLEWSSCTCTFLTDQATVFERFGKEHAVIILNHNFEIDPLCGWTMCERFGVLGSSKVLAKKEL
LVLEPLIGWTFWTFYLEIVFCKRKKEWDTTVGELRLRSDPEYMFLLYCEGTRFTTBKRVSM
EVAACKGVPVLKYHLLPRTKGFTTAVKCLRGTAAVYDVTLNFRGNKPSLLGILGYKKYBAM
MCVRREPLLEIDPLDEKEAAQWLHKLYQEKDALQEIYNQKMGFPGEGQFKARRPWTLLNFLSWA
TITLSPLEPSFVLGVFASGSPILLITLFLGVFGAAGVGRVRLIGLSELEPGRRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

**FIGURE 339**

GAATATCTTTATTTTAAAGAACTGAAGTACTATGTCATCACTCCCTCCAATGTCCTGGGGCAG  
CCACGAGCATATTCATCTTTGTGTGTGTTTCTTTCTTTAGCATCTGGGGCAGCTTCTTGC  
TATTTCTTTGGTAGGAAGGGGCTCAGTTTGTCTTGTGGGGTGTGGTGAGCGAGCCGCGCT  
TACGCTGTATACGGCCCTGGGTGTAGAAAGGAAGGGAAGATAAACTTTTATACAAATGGGATA  
GCTGGGGTCTAGACAGCTCTTCTCTCACTGAAAATCTCTGGGATCTGCCATACCTTCTTCTT  
TAACCTGGCATACCTCTGCTTAAAGCTCTCAGGGCTTCTCTGTCTTATAGATCAAGATATT  
TAGAGCTACAAGAGCCCTCATGTTCTGCCCCCTGCCCTCGCCAGCTTCATTGTACATGTG  
GTGTCTCTGTGCTTCTCTGTAATGTGGTATGCCATGGGGTCTTGTACAAGAGTCTTCTCTCT  
TGGCTGGACATGTTTCCCTGCCCCCCCCATACCTTCTCTACTTAATATGTAGTCATCTCTGCAG  
ATTTCAATTCTAAACATATTTTCTCAGGAGTCTGCCGCTGACAGAAATCTCATCTTTGTTAAT  
GCTCTACAAGACCACTTGTTCCTTTTGTGACATCTGCCATCAGTTGTATCTTATGTGTC  
GTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTTGCTGCTGCGTGAAGGTC  
AAGGCAATCTGCTGTGCCCTGCAGGTTATAGTGGCTACATGTGGTGGGTGCTCATGTTTATGAGA  
CTAAATGAGGAGGAGATGAGGAAGAAGATTGAAATCTCTCAGTTACACAGATGGTGTAGGCCC  
CAGCATGTCTAAATTCACAGCTTGACTGTGCTTGTGAATTATCTGGGATGCGGCTGCTGATTCT  
AGTAGGCCAGGTTGGGCATCTTAACAAATCCCAGCTGATGCTGATGCTGATGCTGCTTATGAAC  
TATACATAAATAGTAAGATCTATGAGCGAGGCTGGGCATGGTGGCTCACACCTATGATCCCA  
GCATCTTGGGAGGCTGAGGACGGTCTAATCACTTGAATCAGGATTTCAAGATAGCTAGCTGGCCA  
ACATGGTGGAAACCCCATCTGTACTGAATTAACACAAATGACTGGGCATGGTGGCAGCATGCT  
GTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG  
CAGTGAGCGGAGATCAGGCCACTGTATTCCAACCAAGGTTGACAGATGAGACTCTATGTCCAA  
AAAAAAAAAA

343/615

### **FIGURE 340**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCFSPALALGHFLLISLVGKGLSLSCGVGGRQAGLRLLIRPWVRE
GKINFYTNGDSWGLRFPASSVKFLGSAYTFPSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

2025.09.08 10:00:00

**FIGURE 341**

CGCCATGGCCGGGCTATCCCGGGTCCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG  
 CTGTTGGCGCTGCTCGTGTGCCCCGCGCGGGGTCGCGGGCGCCGGGACCACGGGGACTGGGAC  
 GAGGCCCTCCCGGCTGCCGCCGCTACCACCCCGGAGGACGCGGCGCGCGTGGCCCCGCTTCGTG  
 ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG  
 CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCGGGCGCGGGCAGCGCGTGCCCTAT  
 TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG  
 ACCATGACTTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT  
 TGTGTTACATAATGCTGTGAGGAACGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA  
 AAGCATTCTGTTATTTCATTCGACCCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC  
 TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTTGGTGGACAAAAATCGTG  
 ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC  
 TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCTCTGGAAGCGT  
 CCCAGAATATTAGCCAGTTTTCTGTC

345/615

## **FIGURE 342**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 24075, pI: 7.67, NX(S/T): 3  
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR  
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN  
PYATLTMTLAQTNFCKKHGFDPPQSPLCVHIMLSGTVTKVNEMDIAKHSLFIRHPEMKT  
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ

### **Important features of the protein:**

#### **Transmembrane domain:**

Amino acids 11-29

#### **N-glycosylation sites:**

Amino acids 160-164;193-197;216-220

#### **N-myristoylation sites:**

Amino acids 3-9;7-13;69-75;97-103

2025-03-25 10:00:00

**FIGURE 343**

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGAT  
 TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAG  
 GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT  
 AAAATCTGTTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCTTAACACAGAGGATCTGTCACT  
 GTGGCTCTGGCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT  
 CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC  
 TGTCTCAGCTCTGGAGGCACTGACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGGTAGCTGCGG  
 CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGAACAAGCCCGAAGATTTTCATAGGCG  
 ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG  
 GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCAGCTGCCCGCCCATCTAACCTTTT  
 CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACCTGTGCCAAGGAACCCAGAGCT  
 TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA  
 CTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG  
 TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC  
 ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG  
 GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTAACAGCTGCTGAAGGGCAACTGCAGGC  
 CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG  
 GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT  
 CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTTGGCCAGGA  
 GGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAATGCCTCCAGT  
 AAGCACAGGCTGCAAAATCCCCAGGCAAGGAGCTGTGTGGCTCAATTAAATCATGTTCTAGT  
 AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT  
 TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAATCCAAACCTAAGAACCAGGTGCA  
 TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG  
 GGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC  
 TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCAGCTACTCGGG  
 AGGCTGAGACAGGGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT  
 TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT  
 GTAA

347/615

**FIGURE 344**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

**Signal peptide:**  
amino acids 1-15

2025-03-26 10:00:00

CCGCGCCGCGCAGCCGCATTACCGCCGCTGCAGCCGCTTTCCGCGGCCCTGGGCCTCTCGCCGTGAC  
CATGCCACACGCCTTCAAGCCCGGGGACTTGTGTTCGTAAAGTGAAGGGCTACCTCTCACTG  
GCCTCGCCAGGATCGACGACATCGCGGATGGCGCGCTGAAGGCCCCCAACCAAGTACCCCAT  
CTTTTTCTTTGGCACACACGAAACAGCCTTCTCGGGACCCAAGGACCTGTTCCCTTACGACAA  
ATGTAAGGACAAGTACGGGAAGGCCCAACAGAGGAAGAGGCTTCATGAAGGGCTGTGGGAGAT  
CCGAGAACAACCCCGACGCAGCTACAGCGCCCTCCGCGAGTGAAGCTCTCCGACAGCGAGGC  
CCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGGGCTGAC  
GGCCGCTACACGGGTAAACGCCACAGCTGCCGACGACAGGATGGAGAGCGACTCAGAGCTCAGA  
CAAGATGACGACAACACGATGGCTCTGAAGGAGGAAGCCTTGCCTTAAAGATGTTCGTTCTCGAA  
ACGAGCCCCGAAGGCCTCCAGCGACCTGGATCAGGCAGCGGTGTCCCCATCCGAAGAGAGAA  
CTCGGAAAGCTCATCTGAGTTCGGAGAAGACCGACCGAGGACTTCACACCTGAGAAGAAGC  
AGCGCTTCGGGCGCCACGGAGGGGCCCTTCGGGGGACCGGAAAAAAGAAGCGCGCTCAGC  
CTCCGACTCCGACTCCAAGGCCGATTTCGACGCGGGGCGCAAGCCTTGAGCCGCGGATGTGGCGCG  
GTCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCGACTCCGATGTGTCTGTGAAGAAGCC  
TCCGAGGGGCGGAAGCCACGGGAGAAGCCTCTCCGAAGCCCGGAGGCGGAAACCGAAGCC  
TGAACGGCTCTCGCTCAGCTCCAGTCAGTACAGCTGACAGCGACGAGGTGGACCGCATCAGTGA  
GTGGAAGCGCGGGACGAGGCGCGGAGCGCGCAGCTGGAGGCCCGCGCGCGGAGAGGAGA  
GGAGGAGCTGCGCGCCTCTCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGGAGCGGGC  
TGACCGCGGGGAGGCTGAGCGGGGACGCGCGGCGACGAGCGGGGACGAGCTCAGGAGGACGA  
TGCCCGCTCAAGAAGCGGGGACGCAAGGGCGGGGCGGGGTCCCCGCTCTCTCTGACTCT  
CGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGCGAAGAAGCCGAGTCTCTCAAG  
CACAGAGCCCGCCGAGAAACTCTGCCACAGAGGAGAAGAGTGTGGCCCGGAGGAGAAGCAAC  
AGCCAAGCCGCTGAAGGTGGAGCGGACCCGGAAGCGCTCGAGGGCTCTTCGATGGACAGGAA  
GGTAGAGAAGAAGAAAGGCCCTCCGTGGAGAGCAAGCTGCGAAGCTGCCACAGTGAGATCAA  
GTTTGCTCTTAAAGGTGCAGACGCCCGGAGCTGAAGAGGTGCGCTGAATGCCCTAGAGGAGCTGG  
AACCCTCGAGTGTGACCTCTCATGCTCTCCAGAAGAACACAGACGCTGGTGGCCACTTGAAGAA  
GATTCCGCGTTACAAAGCGAACAAGGACGTAATGTGAGAAGCGACAGCAAGTCTATACCCCGCT  
CAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGGTGACAGAAAGTGAACAGGCTGGGATGGA  
GAAGGAGAAGGCCGAGGAAGAGTGTGGCGGGAGGAGCTGCGCGGGGAGGAGGCCCCAGGA  
GAAGCGGAGGACAACGCCAGCAGCATCTCTCAGCCAGTGAATGGCGAGGCCATCACAC  
GAAGGGGAGAGCGCAGGACAAGGACAGGAGCAGGAGGCTGCGGATCCGAGAGAGGGGCCAAG  
GTGTGCTCTCTCTGAAGACCTGCACGACAGCGTACGGGAGGGTCCCGACCTGGACAGGCTTGG  
GAGCAGACCGGAGGAGCGCAGAGGAGCAGCGGGGACTCGAGGAGCCCTTGACGAGGAGAGCTG  
ACGCGCGGCGAGCGAGGCCACAGCCCCCGCCGAGCTCAGGCTGCCCCCTCTCTCTCCCGGCTC  
CGAGGAGAGCAGAGCAGAGAAGCTGTGGGGAACGCTGTGCTGTTTGTATTGTTCCTTGGGTT  
TTTTTTCTCGCTCAATTTCTGTGATTTCCAACCAACATGAAATGACTATAAACGGTTTTTTTA  
ATTTA



349/615

## **FIGURE 346**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYDK
CKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSEEN
SESSSESEKTSQDQFTPEKKA AVRAPRRGRLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSDSDSVVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISE
WKRREARRRELEARRRREQEEELRRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQ
AKPVKVERTRKRSSEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEEKLAGEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLD R PGSDRQERERARGDSEALDEES
```

**Signal peptide:**

amino acids 1-13

**FIGURE 347**

GTTGGTTCTCTGGATCTTCACCTTACCAACTGCGAGTCTTGGGACTCATCAGCCTCAATAATTATATAAATTA  
 ACACACTTTGAAAGAGCAACTGTTTTCATCATGAATGTCTTAATAAGATGAAAGACTTAAGGCCNAGAGCCAAAGA  
 TTTTCACTTTTCTCGCTTTGTGATGTCTTAAGCATGACCATGTGTGTTTCTTCCAGTCACTGGGCATCTTGAAGCA  
 AATATTTCCAAGACTCAAGCTTAACCTCAAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTTGGGTTCATC  
 AGAAGGACTGGATTTTCAAACCTCTTCTTTAGATGAGGAAAGAGGCGAGCTGCTCTTGGGAGCCAAAGACACAT  
 CTTTCTCATCAGTCTGGTGACTTTAAACAAAAATTTTAAGAAGATTTATTGGCCTGCTCGAAAGGAACGGGTGGA  
 ATTATGTAATTAGCTGGGAAAGATGCCAATACAGAAATGTGCAAAATTTTCATCAGAGTACTCAGCCCTATAACAA  
 AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
 GGATATTATATTCAAACTAGACACACATAAATTTGGAGTCTGGCAGACTGAAATGTCCCTTCGATCTCCAGCAGCC  
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAGATACCTGCATT  
 CACTCGATCCCTTGGGCCCTCATCATGACCACACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATTGGAACCTTTCTTCATACAGACACCTACAATCCAGATGATGATAAAATATATTTCTCTTTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGGAAGATTTGTGAAGAATGATGT  
 AGGAGGACAAACGACGCTGATAAAACAGTGGAGCATTTTCTTAAGGCCAGACTGATTTGTCTCAATTCCTGGGAAG  
 TGATGGGGCAGATACCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCCAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTTTACTACAACAGGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGATAGCATGGCTGACAT  
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGACAGCCATCGTTGGGTGCAGTATGATGGGGAAT  
 TCTCTTATCCAGCGGCTGGTGCATGCTCAAGCAAAAACCTATGACCCACTGATTAAAGTCCAACCGAGATTTTCGAGA  
 TGATGTCTCATCTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGATCCGATCTGCAGGAGGACCAACGTT  
 CAAAGAGATTAATGTGGGATTCAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAAGAGATGGCCAGTACGA  
 TGTATGTTTCTCAAAGACAGACTTTGGAACTGTCTCAAAGTTGTGAGCATTTCAAAGGAAAGTGGGAATATGGA  
 AGAGAGTATGCTGGGAGAGTTGACAGATATTCAGGCACTCATCAATCATCTTGAACATGGAATTTGTCTCGAAGCA  
 GCAACAAITGTCTTATGGTGTCCGAGATGGATTAGTTTACGCTCTCCTTGACAGAGTGCGACATTTATGGGAAAGC  
 TTGCGCAGACTGTTGCTTGGCCAGAGACCCCTACTGTGGCTGGGATGGAATGATGCTCTCGATATGCTCTCTAC  
 TTTCTAAAGAGGAGCTTGCAGCAAGATGTAANAATATGGCGACCCCAATACCCCACTGCTGGGAACATCGAAGACAG  
 CATTAGTCAATAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAAGCTCAACCTTTCTGGAATGTATACC  
 TAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGGAGGTGAAGCGGTGA  
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAGAAGAGGATTTCTGGATGTATTTACTG  
 CAAGGCCAGAGGCGAGACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTTCATGAGAATGAACAGATGGA  
 AATAACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCAAGTTGAGATACAAAGA  
 CTACATCCAAATCTTTAGCAGCCCAAACTTCAGCTCTGACCACTATGCGAAGCAGATGCGCACAGGGAAGCG  
 GAGACAGAGAAAACCAAGGGGGCCCAAAGTGGAAAGCATGACAGGAATGAAGAAGAAAACAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACAGTAGTTTTTCTACTTAATTTAAAGAAAAGATTCCTTACC  
 TATAAAAACATTTGCTTTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG  
 CACAAGACAAATAATCTGAATAAGACAAATATGTGATGAATATAAGAAAGGGGCAAAAAATTCATTTGAACAGATTTT  
 CCAAGAAAACAAATCTTGCAACAGCAAGATATAAGAAATTTATCTAAAAATAGGGGGTTTACAGTTTGAATTTGTTTA  
 TGTTTGTAGTGTGGAAATTTATGTCTATGAATAAGTTGAGCTTAAGCAAGCCCGAATTTGATAGTGATATAGGT  
 GCTTTATCTCCGATGTCCATTAAGCATTGAAGATGGAATTTACCATGAGTTGTGCTATGTTCTTGAAGACAGATATC  
 CATTTCTATTGAGAACACGCTACTCTTGGTAGGGAATAAGAGGTCAGACAAAAATGAGAGCAACTCCCATTATC  
 AACAGGAACCTTTCTCAGTGAGCACTCATCTCCGGAGAAATGGTATAGGAATTTGGAGAGGTGCATTTTCTTCT  
 TGCGCACTGGGGTTAAATTTAGTGATCTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGGAGTAAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTAGTGTTTTATAGATATATACTAA  
 GCTCTACAGGACAGAAATGCTTAATAAACTTTTAATAAGATATGGGAAAAATTTTAATAAAACAGGAAAAACA  
 TAAATGATGTATAAGTACTCTGATGGGAAGGCATGCGATGGGATTTGTTAAGAAGCAGAGGAAGACAGCCAT  
 AAAATCTGGCTTTGGGAAAACTCATATCCCATGAAAAGGAAGAACATCACAAATAAAGTGAGAGTAATGTAA  
 TGAGACTCTTTTCTACAGGATTAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAAATCTAGATATATAACA  
 AACTGCTAGCAAAATCTGAGAGAAACATAAATTTCTCTGAAGAATCATAGGAAGAGTAGACATTTTATTAAC  
 AATGATTTCTCAGTATATATTTTCTCTCTTTAAAAAATATTTATCATCTCTGTATATATTTCTTTTCTGTCG  
 CTTTATTTCTCTCTGATATATGGATTTGTGATATATTTAGTGAATAGGAGAAAACAAATATATATACACACAGA  
 GAAATTAAGAAAATGACATTTCTGGGGAGTGGGATATATTTGTGAAATAACAGAACAGATGTAAATTTTAAAC  
 AACGGAAGGGTTAAATTAATCTTTTGACATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTTTGTAAT  
 GTAGTATGTTTGTGTAATTTAACAATAATTAAGCCTGCTACATGT

351/615

## **FIGURE 348**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883  
><subunit 1 of 1, 777 aa, 1 stop  
><MW: 89651, pI: 7.97, NX(S/T): 3  
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFLG  
SSEGLDFQTL LLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT  
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFPDPQQ  
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNAGAKFIGTFFIPDT  
YNPDDDKIYFFRFRESSQEGSTSDKTIILSRVGRVCKNDVGGQSRSLINKWTTFLKARLICSIPGS  
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKES  
ADHRWVQYDGRIPYPRPGTSPSKTYDPLIKSTRDFDDEVISFIKRHSVMYKSVYPVAGGPTFK  
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEELQIFKHSS  
IILNMELSLKQQQLYIGSRDGLVQLSLHRCPTYGKACADCCCLARDPYCAWDGNACSRYAPT SK  
RRARRQDVKYGDPIITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSSQATIKWYIQRSG  
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTNLNVIENEQMENTQ  
RAEHHEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRQRNRKGGPKWKHMQEM  
KKKRNRHRHRLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

2025-10-28 15:02

**FIGURE 349**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGACAGGTCATCTTGGAGCATGCCACCGCGGGGAGCAGA  
 CAACTCCCGAGTAAAGCTGGGAGCAGGACCTGAAGCTGTTCTTCAGGAGCTGGTGATTTTCCCCACCACCA  
 CTCAAGCTTTTCAGCCAGCAGGAGCATGATCAGGTTGCTGTCCCTGGAGTGGGGAGCAGAAAGCGCTGGCTGGCAAGA  
 GTGGCTCGGAGAAAGAGGTTGAGCGCTTGACCGCTTGACCAGCCGAGCTGCCGTGACTACAAGACTCAGAAACCTAGGCACTC  
 GGGTGAAGTGGGGGGGACAGGTTGCTCATGTGCACTTCTTGCTCTCAGCAAGAAAGACTGAGAGAGGGGATCTTGG  
 AGCCATTGAGGGTGTGATGGAGCTACAGAGGGGAGGGAAAGGATTTTAAAGTAAACAGTGTGGCACTAGATGTTAA  
 GAGCACAGCTTTTGGAGCTAGACGCATAGACTAGGTTCAAATTTCTCTTCTGTGCTTCTTAAGTAACTAGTAACTAGTAACT  
 AAGGAGTGACTTTAACTCTCTGGAGCTTCAAATTTCTCTCATCACTAAAGTAGGGCCAAATAAGACCCACCTCAT  
 AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAATAAGTATGCCCCACAG  
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACAGAGTACTGCAACGACGTGGAGCAGAGGCGGACAGGAGCTT  
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCCGCGGACAGGTTAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAGGCCAGCCA  
 TGACCCAGGCGCAGGATGAGGTGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTTCTC  
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTAGGAGACGGGAGAGCTCTTTGAGGAGCTCGCC  
 CCCAAGCCTTGCCACAGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTGCTATCAGGCGAGGCGTGAAGATG  
 AGCTGACAACTACAGGAGGTGAGTGGCTGGAGTGCATAGAGGAGGAGATGCTGACGAATGGCTCAAGGCTCGGA  
 ACCAGCAGCGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAAATTTCCGGAACCTCTAAGCTCCAGAGAGCAGC  
 AAGACAGTGACAACTCCCTCGGGGACAGGCCACAGCATCTCTGGCAGAGGCGCTGTACAGTACAGCCGACAGA  
 GTGACAGGAGCTGAGCTTCCCTGAGGGGCACTCATCCCTGCTGCTGCCCGCAAGATGAGATGAGATGAGCG  
 GCTTTCTGAGGGGAGGTTGTGGGGCGGTGTGGGGTCTTCCCTCCCTGCTGGTGAAGAGCTGCTTGGCCCCC  
 CAGGGCCGCTGAACCTCTTGACCTGAAACAGATGCTGCCGTGCCCTTCTCTCCCTAGCTTCCCCACCTGCAC  
 CTACCTTGTGTTGGATGGGCCCCCTGCACCTGCTCCTGCCGTGGGCAAGGCCCTGGACTTCCCTGGGTTCTTGG  
 ACATGATGGCACTTCAGTACGGCCGATGCTGCACCACTCCCGCGCGCTAAGGCCCGGATCTGGCCACC  
 CAGATCCCTCACTGAGAGGCCAGGGAGCTTGAACCCCAAGTATGCTGTGTTCCCTATTCTCAAGCTCTGAGA  
 CCAACCATCAATGATCCAGCAACACAGCCCAAAGCTGGAATGCCCTTATTCCACCTCAGCTCCAAGGGT  
 GGAACCTTGCCTCTCCATTTCTAGAGCTGGAACCCACTCCCTTTTTCCTTGTGTCTATCTCTAGGACC  
 GGAACCTAAGCTCTCTAGTAGTGTCTGGCCCACTCTTCCCAACCTGGCTCATGACCCACCCCACTCTGGATG  
 CCAGGCTCAGTGGGCTTGGGCTGGGAGAGGAACAGGCTTGGGAATCAGAGACTGGAGCCAGGATGCCAAGCAG  
 CTGTAATGGTCTAGAGCGGATTTATGACAAATGAATAAAGGACACAGAGGCCAGGCCAGGCGCTGGGCTTTGTG  
 CTAAGAGGCGAGGGGCTACAGGTGCTATTGCTTTAGGGGCCACACAGCGGACCGGCTGCTCCAGCTGCCAC  
 GCTCTATCATATGAGCGAGGCTTGGGGAGCGGGGACAGCAGCTGTTCAGGCGAGGGAAGGAGAGAGAC  
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCACTTCAAGTGGAACTAGAGCTGTCCCTC  
 AGCTGGGGGCGATGCTGTCCAGTGGAGGGGAGGGCTTTTCAAGCCACCCCTGGCCCTGCCAGCTGGTATG  
 TCCATCAGCACAATGAAGGAGACTTGGAGAGAGGAAGAATAACACTGTTGCTTCTGTTCTCAAGCTGTGTCAGC  
 TTTTCCCTTGGGCTCCAGGACCTTTCCCTACTCCACCAACCAAGGGATTATAGCAAAAGCTAAGCTTGC  
 AGTTTACTCTGGGGGTTGAGGAGCGCAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAGATGAGATTACCTCA  
 TTTAGGGCTCAGGCACTACCTCACAATCTCCCTGCTCCTGTGTGGTAGAGACACTGAGAGGAAGGGAGGGG  
 TCAACAATGAGAGACAGGAGTAGGTCTTATCAGTGGCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC  
 AGTCCCGCTGTGTTTCTACTGCTGGTATCAGAAGTGTGTTGCTTGGCTGGCTCAGAGTGTGAGTGG  
 GCAGCCTTGGGCTTGGGCCCTTCCCTCCGCGCTCAGTGTGCTGCTGCAAGAGCTCTGGGTTCCCTCAAGT  
 CAGAGGGGTTAGGCTGCTGCTCTGAGTCTCCATTCTGTACTGGGGGCTAGGCTAGGACTGGGCTGTGGCC  
 TCTCAGGGGCGAGCTCTCTCAGGAGGACTCCCTGCTTGGGCTGCCCTCCCGACGCTGACACCCCTGCTG  
 GGTCTGTGCCCTCAGCAGGCACTGCTGCTGTCTGTGGGGAGCCATCACGGTCTTCTGTGAGTGCATGAGGCT  
 TCTCAATGTGTGTCACCCGGAACCTGGGAGGGGAGGGAACACTGGGCTTTAGGACCACTCAGAGAGCTGTGCT  
 GCCCTCCCTCTGACACAGGACATGCTGAGTTGTGTGCTACTTCCCTGTGGTAGAGGCTAGGGGAGGCTCTC  
 AGATTGTGGGGCACAATTGTGAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAGAGGCCACTT  
 TTGGATCAGGTGCTGATGCTGGGCCCTTACTCAGCCCCCTTCCCTGGAGAGCTGCCCACTGCCCA  
 CAGCAATCAGGTGCTTCCCTGTCCGGGGGCGGCTTTTCTCTCTTGTGAGCGCTCCCTGACCGCAAGTGGAG  
 GCTCTTGTCTGGCTGCAATGATGCAAGGGGCTGACAGAGCCAGGTGCATCTGTGATGTGGGAGGGGCTC  
 CGTCTGACAGGCTGGAGGTGGCACTCCACTGGACAGGAGGAGGGAGTGAAGGTAACTATTCAATTTCCCT  
 TCAATGTTTGTGTTCTTCACTGTTCTGACGTGCTCTTAAACCCAGAGGCCCAATTTCCCAAGGCCCATTT

353/615

**FIGURE 350**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPFPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTEADAELSDF
EECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESQSDSNPCGAEPTAFLAQALYSYTGQSAEELSFPPEGAL
IRLLPRAQDGVDDGFWRGEGGRVGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPSPSPSPPA
PTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

[illegible]

**FIGURE 351B**

TGTGAGCCACCCAGCCCGGTACATATTTTTAAATTGAATTCTACTATTTATGTGATCCTTTGGAGTCAGACAG  
ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTGGCCAATAATAACCTCCCTTAGAAG  
TTGTGTTGTGAGGATTAAATAATGTAAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAA

356/615

## FIGURE 352

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492  
><subunit 1 of 1, 837 aa, 1 stop  
><MW: 90167, pI: 8.39, NX(S/T): 1  
MSQTGSHFPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLIASLLPSARLASPLPREEEIVF  
PEKLNGSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPPELLGGAEPGT  
YLTGTINGDPESVASLHWDGGALLGLVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSPASG  
QGPNCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAAKA  
FKHPSIRNPVSLVVTRLVLGSGEEGPOVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL  
FTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHAELGHVFNMLHDNSKPCI  
SLNGPLSTSRHVMAPVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK  
DYDADRCQQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMG  
RCLHMDQLQDFNI PQAGGWGPWGPWGDSCRTCGGGVQFSSRDCTRPVPRNGGKYCEGRTRFR  
SCNTEDCPTGSALTFREEQCAAYNHRDRLFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY  
YYVLEPRVVDGTGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDSGCSKQSGSFR  
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSTIYLALKLPDGSYALNGEYTLMPSPPTDVVLPGA  
VSLRYSGATAASETSLSGHGFLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPDWLH  
RRAQILEILRRRPWAGRK

### Important features of the protein:

#### Signal peptide:

amino acids 1-48

#### N-glycosylation site.

amino acids 68-71

#### Glycosaminoglycan attachment site

amino acids 188-191, 772-775

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

#### Tyrosine kinase phosphorylation site.

amino acids 730-736

#### N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

#### Amidation sites.

amino acids 560-563, 834-837

#### Leucine zipper pattern.

amino acids 17-38, 24-45

#### Neutral zinc metalloproteases, zinc-binding region signature.

amino acids 358-367

1052536-01502



**FIGURE 353**

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCCC  
 GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCTCTGC  
 TCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACTTCTGCGCACTGGCGGAGGACAG  
 CGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAGTGTG  
 TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG  
 ACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCTGCTGCTCTCGGGCATAGCCTGCGCCT  
 GCGCCGTTCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTG  
 CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCTTGGA  
 CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGTGCCCAGCGGCATGAAGTTTGAGA  
 TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCTGC  
 TTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAAGGCCCGCCAGGGCCACCA  
 CGACCCTGCAAAACCCGCACCTGCCTACCAGCCACCAGCTGCCACAAAGACAATCGGGCCC  
 CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGTGAACGACTACGTGTGAAGTCCCCACAG  
 CCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG  
 TTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATAATGTGAATGCGAGGA  
 AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA  
 GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATATATATTTATGTGGGTGATTGTA  
 TAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGTTGGTTTGTGATCCAGGAA  
 TAAACCTTGGCGATGTGGCTGT'TTATGAAAAAAAAAAAAA

358/615

## **FIGURE 354**

MASTAVQLLGFLLSFLGMVGTLTITLILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ  
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTLFI  
LAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSLSLIGGTLCLSCQDEA  
PYRFPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

2025-03-25 10:00:00

**FIGURE 355**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC  
 AGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGGTTCTCTCC  
 TGTCCATCTCGGGGCTGGCGGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG  
 ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTCGGTGA  
 GGCAGAGTTCAAGGCTTCACCGAATGCAGGCCCTATTTACCATTCTGGGACTTCCAGCCATGC  
 TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCTGGTAT  
 CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA  
 CACTGACCTCCGGGATCATGTTTATTGTCTCAGTCTTTGTGCAATTGCTGGAGTGTCTGTGT  
 TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG  
 GGATGGTGCACTGTTTCAGACCAGGTACACATTTGGTGC GGCTCTGTTCTCGTGGGCTGGGTG  
 CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCA  
 AAGAAACCAACTACAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTGGCTACAAGCCTG  
 GAGGCTTCAAGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAATATACGATGGAG  
 GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGT**TA**ATGCTCTA  
 AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA  
 TCTAGATTTCTTCTGCTTTTGA**CT**CACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG  
 GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTTCCACCATAAAACAGCTGAG  
 TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTCTTTTTTAAATATAA  
 CTTTCTACTCTGATGAGAGAATGTGGTTTTAACTCTCTCTCACATTTTGATGATTTAGACAG  
 ACTCCCCCTCTTCTCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCAAG  
 AAAACTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTCTGCTGTTTGAATTTTGTCTC  
 CCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATT  
 TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAGTTACCAAACCA  
 AAGTCATTTTCAGTTTGAGGCAACCAACCTTCTACTGCTGTTGACATCTTCTTATTACAGC  
 AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTTCTGTGCGGGGTGAGAAA  
 TTGTCCTTAGATGAATGAGAAAATATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAATATA  
 ATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG  
 AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA  
 GTACAAATTCATGAAAAGCTCACACCTGTAACTAGCACTTTGGGAGGCTGAGGAGGAAGG  
 ATCACTTGAGCCAGAGTTTCGAGACTAGCCTGGGCCAACATGGAGAAGCCCTGTCTCTACAAA  
 ATACAGAGAGAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG  
 GCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGTGGGGCTGCAGGTGAGCCATGATCACACC  
 ACTGCATCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAATAAAAAATAAATAATGGA  
 ACACAGCAAGTCTAGGAAGTAGGTTAAACTAATTTCTTAA

[illegible]

## FIGURE 356

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
```

```
><subunit 1 of 1, 261 aa, 1 stop
```

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTTCQVVAFLLSIIGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRWSCVRQSSGFTFC  
RPYPTILGLPAMLQAVRALMIVGIVLGAIGLVSI FALKCTRIGSMEDSAKANMTLTSGIMFI  
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG  
VMMCIACRGLAPEATNYKAVSYHAGSHSVAYKPGGFKASTGFGSNKKKIYDGGARTEDEVQ  
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

**FIGURE 357**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG  
 AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAAAATCGCTGGG  
 CTGTTTCTTGGTGGTGGTGGAAATGGTGGGCACAGTGGCTGTCACTGTATGCCTCAGTGGAGA  
 GTGTCCGCCCTTCATTGAAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATG  
 AATTGCGTGAAGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTCTGCTGGCTCTT  
 TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT  
 TTCTATGATGGCCATCCTTGGCATGAAATGCCACGAGTGACACGGGGGACAAATGAGAAGGTGAAG  
 GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCT  
 GTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCCAA  
 AAACGTGAGCTTGGAGAAGCTCTCTACTTTAGGATGGACACGGCAGTGGTGTGATTGTTGGGA  
 GGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA  
 CCTTCCCATCGCACAAACCAAAAAAGTTATCACACGGGAAGAAGTCAACGAGCGTCTACTCC  
 AGAAGTCAGTATGTGTAAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAAATGACA  
 AAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAACTGC  
 CTAATCTTAATTACAGGAACGTGTGCATCAGCTATTATGATTCTATAAGCTATTTCAAGAGAA  
 TGAGATATTAAACCAATGCCTTGTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG  
 TTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT  
 ACTACTGTAATTTCTCCAGGACATAGCATTATGTACATAGATGAGTGTAAACATTATATCTCA  
 CATAGAGACATGCTTATATGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT  
 AGAACTCAACTATTGCTTTTCAAGGAAATCATGGATAGGGTTGAAGAAGGTACTATTAAATTG  
 TTTAAAAACAGCTTAGGGATTAATGTCTCCATTATAATGAAGATTTAAATGAAGGCTTTAA  
 TCAGCATTGTAAAGGAAATGAATGGCTTTCTGATATGCTGTTTTTAGCCATAGGAGTTAGAA  
 ATCTTAATCTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTTCTGTGTATTAAATTAACATT  
 TTTAAACGCAGATATTTTGTCAAGGGGCTTGCATTCAAACCTGCTTTTCCAGGGCTATACTC  
 AGAAGAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT  
 GTTTTTGTATTGGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT  
 TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATAT  
 GTCTTGGTTTTTCAATTGCTTACCAAAAAACAACAACAAAAAGTTGTCTTTGAGAACTTC  
 ACCTGCTCCTATGTGGGTACCTGAGTCAAAATGTGATTTTTGTCTCTGTGAAAAATAAATTTT  
 CTTCTGTGACCATTTCTGTTTGTAGTTTTTACTAAAACTGTAAAACTAGTATTTTTCTGTTTATT  
 CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGACGCTCTGTCTAGCTTAAAT  
 GAAATGTGTTCTATTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

362/615

**FIGURE 358**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735  
><subunit 1 of 1, 225 aa, 1 stop  
><MW: 24845, pI: 9.07, NX(S/T): 0  
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQ  
CKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF  
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVFCCN  
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

363/615

**FIGURE 359**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC  
GCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCTGCTGCCCTGACCGGGCTGGCGCTGCTC  
CTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAAA  
CGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC  
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGCAGCAG  
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT  
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACATATGAT  
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC  
GATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT  
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC  
TACTTTGTGTGATCAAAAAAGAAGATTAAAAAACACATGTAAATGCCTTTGGATATTTCAT  
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC

364/615

**FIGURE 360**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKLLKMLQKREAPVPTKTKVAVDENKAKEFLG  
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDDYQRHYDED  
SAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

RECEIVED  
JUN 10 1988  
FBI - NEW YORK



365/615

**FIGURE 361**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA  
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC  
AGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT  
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG  
GACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAGC  
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG  
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC  
TGTC AAGATCTGCTGAATCCCAACCTTCTTG CAGGCATCCACTGCGCAAAAAGGATTGTGTCC  
GGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTT CAGGCCGGCCACTCTCC  
TACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTG CACCGTGGAGTCATTCCA  
AGACTCCTGTCTCTACTCAGGGATTCCTTCATTCTTCTTCTCTACTGCCTCCACTTCATGTTAT  
TTTCTTCCCTTCCCATTTACAAC TAAACTGACCAGAGCCCCAGGAATAAATGGTTTCTTGG  
CTTCTCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTGTAAACTGAGG  
ACCACAATAAGAAATCTTTATATTTATCG

366/615

**FIGURE 362**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKIN  
ENADGSFDYGLFQINSHYWCNDYKSYSENLCBVDCQDLLNPILLAGIHCARIVSGARGMNNW  
VEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

U  
S  
E  
R  
S  
E  
Q  
U  
E  
N  
C  
E

**FIGURE 363**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCAC  
 CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTTGAGCA  
 GAATGGAATCATTAATTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT  
 TTGAAGTCCCTGTGATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGACTTGG  
 GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACAGCTGTTT  
 GCAAATGTGAGGACCAAGGTTAAGTGACTGGCAGAAAAAATCTCCAGGTGGAACAAGCAACCCAT  
 GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC  
 ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC  
 AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGTTGCACCTC  
 CCCACCACACCTGCACAGACTGTGACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT  
 ACCGCTTGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT  
 ACAGCCCTCTGAGAGGCCTGCCACCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG  
 TGGCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA  
 TCAAGCAGCCCAAGGAGGCAGGATAAGGAAGCCCAAAGAGGGACTGGGGGGCTGATGAGGACG  
 GCGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGACCCCTGACCCACAGTGGCCCTCAGGAGG  
 CACTAGTGGCCCGCATCCCTCCAGAGGGCTCTGCGGAGGTGCGGCACCCAGCTGTGTGTCG  
 AGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCACTCTGTTTCCATGATGAGGCCCT  
 GGTCCATCTCTGCGGACTGTACACAGCATCTCGACACAGTGCACAGGCCCTTCTCTGAAGG  
 AGATCATCTCGTGGACGACCTCAGCCAGCAAGGACAACTCAAGTCTGCTCTCAGCGAATATG  
 TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC  
 GGATGCTGGGGGCCACCAGAGCCACCGGGATGTGCTCGTCTTCATGGATGCCACTGCGAGT  
 GCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT  
 CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTATTACCCCTCAAAGGACCTGCAGC  
 GTGGGGTGTGGACTGGAAGCTGGATTTCCTAGTGGGAACCTTTGCCAGAGCATGTGAGGAAGG  
 CCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTGCTGCCGAGAGGTTGGTGGCCATGG  
 ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTTGGTGA  
 AACTCGAATGTCTTTCAAGGCCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGTCTC  
 GGTAGGACACATCTACAAAATCAGGATTCCCATTTCCCCCTCGACAGGAGGCCACCTGA  
 GGAACAGGGTTGCGATTGCTGAGACTGGCTGGGTCATTCAAAGAAACCTTCTACAAGCATA  
 GCCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC  
 AAAGGAGACTGGGTGTGCGACATTCCTACTGTTTCTGGCTAATGTCTACCTGAGCTGTACC  
 CATCTGAACCCAGGCCCAAGTTTCTCTGGAAGCTCCACAACTGGAACCTTGGGCTCTGTGTCAG  
 ACTGCCAGGCAGAAGGGACATCTGGGCTGTCCATGTTGTTGGCTCTTGCAGTGACAGCC  
 GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC  
 TGTGCTTTGCTGTGAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCCTGGCCA  
 TCCACAGCAGCAGCTGGGACTTCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT  
 GCATGGAAGCTGTGGTGCAAGAAACATAAAGATTGTACTCGCTCCGTGTGATGGAAGG  
 CCCGCCAGCAGTGGCGATTGTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTGAG  
 AAGGAAAGAGAAATTTGGCCATCAAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT  
 TCATGAAGCTGATCTTTTGTGTGTGCTCTTGTGTAGGAGAGAAAAGCTCTATGAAA  
 GAATATAGGAAGTTTCTCCTTTTACACCTTATTTCACTGCTGCTGGCTGCTTA

368/615

**FIGURE 364**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTQAASKHSPEARYRLDFGE  
SQDWVLEAEDEGEFYSPLGLPPFISLREDQLLVAVLPAQRNQSQGRRGGSYRLIKQPRRQ  
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS  
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQLQQLKSALSEYVARLEGV  
KLLRSNKRGLGAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVSPVIDVI  
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN  
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNDSHSPLDQEATLRNRVRIA  
ETWLGSFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLGCRTFHWFLANVYPELYPSEPRPS  
FSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ  
EQVILQNCTEEGLAIHQQHWFQENGMIVHILSGKCM EAVVQENNKDLYLRPCDGKARQQWRF  
DQINAVDER

**Signal peptide:**

amino acids 1-28

2025-10-27 10:00:00

## FIGURE 365

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGCGG  
AGCCAGACGCTGACCAGTTCCTCTCCTCGGTCTCCTCCGCTCCAGCTCCGCGCTCCCGGC  
AGCCGGGAGGCCATGCGACCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCCTCTGC  
TGCTCCTGCTGCTGCAGCTGCCCGCGCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAA  
AGGCGCAGCTCCGGCAGAGGGAGGTGTGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG  
CAGGAGTGCTCTGGTCGAGACGGGAGCCCTGGGGCCAAATGTTATTCCGGGTACACCTGGGATCC  
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTT  
GGACACCCAACTACAAGCAGTGTTCACTGGAGTTCATTGAATTATGGCATAGATCTGGGAAAA  
TTCGCGGAGTGATCAATTTACAAGATGCTGTTCAAATAGTGTCTAAGAGTTTTTGTCTAGTGCT  
CTGCTCGGCTAAAATGCAGAAATGCATGCTGTGCAGCGTTGGTATTTACATTCAATGGAGCTG  
AATGTTCCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA  
ATTCAACAATTAAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTTGGTGTG  
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTA  
CTGGATGGAATTCACTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTTAATTTT  
CATTTGCTACCTCTTTTTTTATATGCTTGGGAATGTTCACTTAAATGACATTTTAAATAAG  
TTTATGTATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAAGGTGTGATTTC  
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTT  
TAGTTGGTTAGAATTTTCTTCTCATAGTCACATTTCTCAACCTATAAATTTGGAATTATTTG  
TGCTCTTTTGTCTTTCTCTTAGTATAGCATTTTAAAAAATATAAAGCTACCAATCTTTG  
TACAATTTGTAAATGTTAAGAAATTTTTTTTATATCTGTAAATAAAAAATATTTTCCAACA

370/615

**FIGURE 366**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393  
><subunit 1 of 1, 243 aa, 1 stop  
><MW: 26266, pI: 8.43, NX(S/T): 1  
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP  
GRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC  
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTI  
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIII EELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

2025 RELEASE UNDER E.O. 14176

371/615

**FIGURE 367**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC  
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT  
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC  
GGGAGAAGGCCCGTGGAGAGCACCAGCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC  
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCCG  
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGCT  
GCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG  
CGCCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAA

2025.03.15 10:22:56

372/615

## **FIGURE 368**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAFAVLTDVFPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTGP
PAPTVA PGPEDSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 91-110

#### **Glycosaminoglycan attachment site.**

amino acids 44-47

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

#### **N-myristoylation site.**

amino acids 91-96



GGCGCTTGGTTGGTGCTCGCGGCTGAAGGGTGTGGCGCAGACAGCGTCGTTGGTTGGCCGGCGCGC  
GGGCGGGAGCGGGCAATGGCGCCCTGCTGCTGTCTGGCTGTGTCGCTGACGGCGGGCGCTGCCCAACG  
GCTGTCTGCATCTGCCACAGCAACTTCTCCAAAGATTTCTCCTTTACCCGACCACTGTGAACAT  
TCAAGTCTCTGGTTGGGTGGCGACATCCCGCTGTACGGGGCGCTCGCTCACCGATCTGGAGCAGCG  
ACACGATGGAAGGAGCTGCACCTGGCCATCCCGGCCAAGATCGCCGGGAGAGCTGGACCAAG  
TGGCGACAGCATGTGACACAGTATGGATCAGCTGTACAGGGGGAAGATGTACTTCCCGGG  
ATTTTCCCAACAGCATGTGCGAAACATCTTCCGGGAGCAGGTGCGACCTCATCCAGAACCCGCATCA  
TCCAAAGGCACTTGGCAGCGAGCTGGGAGGAGGCGAGCTCTCCAGGAGGGACACCGCC  
TAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG  
CTGGGAGTGTTCACCCCGCCCTCCCTGAAAGTTTGCTCATCTACAGCTTGGGGGTCAACCTGG  
GGACCCCTTCTCTCCGGGCCATGGACACATACATAGAAACACAGGCCGCATCGACTGTGACG  
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCTCTGCAACAACATGCACAGCTCGCACCTGAC  
CTCGCTTTGGCTATAACTCGAGTAGGGCTCAGGCATCACACCCCGTCCAGGCCCTTAC  
TGTCTCTGGGGTCCAGGCTCTCTTGGAGGGGGCTCCCGCCTTCACTTGACTGTATCGG  
GTAGGCGGGGCGGTGGGTTACGGGGCGCACACTTCCAAGCGTGTGTCTCCACAGGTTCTCCGG  
CGAAGTGAAGTCAGTGTCTCAGGCGCTCTGAACATCAATAAATCACTGGCACAAAGTAAGTCT  
CTCTCTCAAACCAACACAGCGAGTGTGTGTATGTGACACCTCGTGGGTGAGTATGTGTGGGG  
CACAGGCTGGCTCCCTCAGCTTCCACGCTCTAGAGGGCTCCCGAGGAGTGGAACTCAAC  
CAGCTCTGCGCAGGAGCGGCTGCAGTCTCTTTCTCCTCAAAGTCTCCGACCTCAGCTGG  
AGGCGGGCATCTTTCTCAAAGGGTCCCATAGGGTCTGGTTTCCACCGGATCCAGAGTCTGTGGT  
TCAGACCTTGGGAGGGTTTCCATCAGATGTTAGGGGTGCCCATAGGAGGGCTGACTGCCCA  
CATTGCCTTTTCAGACAGGACACGAGCATGAGGTAAAGCCGCCCTGACCTGGACTTCAGGGGGA  
GGGGGTAAAGGGAGAGGAGGGGGGGCTTAGGGGGTCTCTATAGTCAGTGGGGGCATCGAGCT  
GGGGCTCTCTCTATACCTGGGACACCTGCTGTGATGTCACTTGCACAACCAACCTGATGGTG  
GTTTCATGACAGACCAACGCTCTCTGCTCTTCTTGCCCTTGGGACACAGGACCAACCCCG  
CCTTGTGAGTAGCCACAGGAAGGGAGGCTCCGGAGAAGGGGTGCTCGTAAGCCAACACGAG  
GTGGCGGGCCTGCACACCTTTCGACATCCAGGCACAGGGGTGCTGGTATGTGGCCACAC  
ATGAGACACACAGCTCCAGCTTGGGAGGAGAGGCTGGGGCGCCACAGGAGGAGGAGCGGGGT  
GGGGACATGGAGAGCTGAGGACGCTCTGTTCTCCCGCAGCTGGTATCGCCAGCTTAAGT  
GTCTGGAGCCCCCACTTGTGCGCAACTTGACATCTTGAAGATGTGCTGCTAGTGTCTCAAGAGC  
ACTGACAGCAGCTGGGCCTGCCACCGGCCCAAGCTGGGGGCGAGACTCAGCTGGACGCCCT  
GCCTGTCACTCTGGAGCTGGGCTGCTGTGCTCAGGACCCCTCTCGACCCCGGACAGAGC  
TGAGCTGCGCAGGGCGAGGGCGGGAGGGAGGGAATGGGGGTGGGTCTGTCGAGCATCAG  
CTGCTGGGCGAGTTCGCGACAGCTCGGAGATGTGATTAAGATCTCTGATGTGTTCTC

374/615

**FIGURE 370**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

2025-04-25 10:45:00

**FIGURE 371**

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTGTCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCGGGGGCTTGGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCCTC  
 TCGGCCACGGCTGGGTCTGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG  
 CAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGGCCCCGACCTGAGGCGTTCG  
 CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGACAGCCCCGCGCCGC  
 CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG  
 ATGAGGTGGGCGCACCGGCATAGTGGTTGGAGTTTCTGTAGATGAAAAGAAGTCTGGTCAG  
 AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTAACATGTAAACCAGAGACAGTTATGCGAA  
 TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC  
 TGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCAGAGAAAAGAATATGAAGGTG  
 AAAAGGTTTCTGTCAACAAGATTACTGATTTCCTCATTTAAGTGGAATTCGTCATTATGAAA  
 AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG  
 TTGCATTGAGCAAGAAAAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA  
 CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG  
 AACAAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTCAATTGAATCCCTAAGATTATTTA  
 AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC  
 TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT  
 TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTTACAATAGAG  
 CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAAT  
 TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT  
 ACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAACATGTTTATAAAGTAAAAAA

376/615

## **FIGURE 372**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA  
APAQSPAAPDPEASPLAEPPQEQLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGAPG  
IVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV  
QHYVPEFFEKEYEYGEKVSVTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK  
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF  
KPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

376/615

**FIGURE 373**

GACTACGGGGAGAGAGAGAGGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA  
 GAGCAAAGATGTTTCAAACCTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG  
 CCCAGTTTGGAGGCCTGCCCGTGCCCTGGACCAGACCCCTGCCCTGAATGTGAATCCAGCCCTG  
 CCCTTGAGTCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT  
 GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT  
 ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTGAGTGATTCTTGGCCTGAAC  
 AACATCATTTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCT  
 GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCTG  
 GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG  
 AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG  
 CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCATTCAAGGTCTTCTGGACAGCCTCACA  
 GGGATCTTGAATAAAGTCCCTGCTGAGTTGGTTGAGGGCAACGTGTGCCCTCTGGTCAATGAG  
 GTTCTCAGAGGCTTGGACATCACCCCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA  
 CAGTTTGTGATCAAGGTCTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG  
 TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT  
 GCCCCTCTCCTTCCCACAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAAATGGCT  
 CTTCTTATGCA

378/615

## **FIGURE 374**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533  
><subunit 1 of 1, 256 aa, 1 stop  
><MW: 26713, pI: 5.62, NX(S/T): 0  
MFQTGGLIVFYGLLAQTMAQFGGLFVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL  
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSPVIGLNNIIDIKVTDPLLELGL  
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLGDC  
THSPGSLQISLLDGLGPLPIQGLLDLSLTGIILNKVLPVLVQGNVCPLVNEVLRGLDITLVH  
DIVNMLIHGLQFVIKV

**Important features of the protein:**

**Signal peptide:**

Amino acids      1-19

**Transmembrane domain:**

Amino acids      79-97

**N-myristoylation sites:**

Amino acids      46-52;49-55;58-64;62-68;66-72;80-86;81-87;  
82-88;85-91;86-92;89-95;202-208;233-239

Downloaded from www.nrj.com

**FIGURE 375**

AGTTC TGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT  
 AAATATGTCAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTGTC  
 TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAA  
 TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC  
 AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA  
 TTCTCACAGGCGACCATGGCAGTTTTTGTGTTGGAGACTTGGACTCTATTATGGGACAGA  
 AGCAGCTGTGAGTCCAACGTTTGAATTACCTTCAAACCTCAAACCCCTGACCTATATCCTGT  
 TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC  
 CTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATCCAAAACATCAA  
 ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA  
 GGACAATTGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA  
 AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACCTTTTATGCTACACAACCAAAATTAAT  
 GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA  
 GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC  
 ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCCAGAAC  
 CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG  
 AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT  
 TTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA  
 TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCTTTTACAGTAATGAATGT  
 GGCTCCATAGTCCATAGTGTCTCTGAGGCTCAGGGCTTGGCATTATTCAGCAGCATCATG  
 CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT  
 TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAAACATCCATCACAGATGA  
 CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Discussion**  
 6. **Conclusion**  
 7. **References**  
 8. **Appendix**  
 9. **Index**  
 10. **Table of Contents**  
 11. **Abstract**  
 12. **Keywords**  
 13. **Subject Headings**  
 14. **Summary**  
 15. **Notes**  
 16. **References**  
 17. **Appendix**  
 18. **Index**  
 19. **Table of Contents**  
 20. **Abstract**  
 21. **Keywords**  
 22. **Subject Headings**  
 23. **Summary**  
 24. **Notes**  
 25. **References**  
 26. **Appendix**  
 27. **Index**  
 28. **Table of Contents**  
 29. **Abstract**  
 30. **Keywords**  
 31. **Subject Headings**  
 32. **Summary**  
 33. **Notes**  
 34. **References**  
 35. **Appendix**  
 36. **Index**  
 37. **Table of Contents**  
 38. **Abstract**  
 39. **Keywords**  
 40. **Subject Headings**  
 41. **Summary**  
 42. **Notes**  
 43. **References**  
 44. **Appendix**  
 45. **Index**  
 46. **Table of Contents**  
 47. **Abstract**  
 48. **Keywords**  
 49. **Subject Headings**  
 50. **Summary**  
 51. **Notes**  
 52. **References**  
 53. **Appendix**  
 54. **Index**  
 55. **Table of Contents**  
 56. **Abstract**  
 57. **Keywords**  
 58. **Subject Headings**  
 59. **Summary**  
 60. **Notes**  
 61. **References**  
 62. **Appendix**  
 63. **Index**  
 64. **Table of Contents**  
 65. **Abstract**  
 66. **Keywords**  
 67. **Subject Headings**  
 68. **Summary**  
 69. **Notes**  
 70. **References**  
 71. **Appendix**  
 72. **Index**  
 73. **Table of Contents**  
 74. **Abstract**  
 75. **Keywords**  
 76. **Subject Headings**  
 77. **Summary**  
 78. **Notes**  
 79. **References**  
 80. **Appendix**  
 81. **Index**  
 82. **Table of Contents**  
 83. **Abstract**  
 84. **Keywords**  
 85. **Subject Headings**  
 86. **Summary**  
 87. **Notes**  
 88. **References**  
 89. **Appendix**  
 90. **Index**  
 91. **Table of Contents**  
 92. **Abstract**  
 93. **Keywords**  
 94. **Subject Headings**  
 95. **Summary**  
 96. **Notes**  
 97. **References**  
 98. **Appendix**  
 99. **Index**  
 100. **Table of Contents**  
 101. **Abstract**  
 102. **Keywords**  
 103. **Subject Headings**  
 104. **Summary**  
 105. **Notes**  
 106. **References**  
 107. **Appendix**  
 108. **Index**  
 109. **Table of Contents**  
 110. **Abstract**  
 111. **Keywords**  
 112. **Subject Headings**  
 113. **Summary**  
 114. **Notes**  
 115. **References**  
 116. **Appendix**  
 117. **Index**  
 118. **Table of Contents**  
 119. **Abstract**  
 120. **Keywords**  
 121. **Subject Headings**  
 122. **Summary**  
 123. **Notes**  
 124. **References**  
 125. **Appendix**  
 126. **Index**  
 127. **Table of Contents**  
 128. **Abstract**  
 129. **Keywords**  
 130. **Subject Headings**  
 131. **Summary**  
 132. **Notes**  
 133. **References**  
 134. **Appendix**  
 135. **Index**  
 136. **Table of Contents**  
 137. **Abstract**  
 138. **Keywords**  
 139. **Subject Headings**  
 140. **Summary**  
 141. **Notes**  
 142. **References**  
 143. **Appendix**  
 144. **Index**  
 145. **Table of Contents**  
 146. **Abstract**  
 147. **Keywords**  
 148. **Subject Headings**  
 149. **Summary**  
 150. **Notes**  
 151. **References**  
 152. **Appendix**  
 153. **Index**  
 154. **Table of Contents**  
 155. **Abstract**  
 156. **Keywords**  
 157. **Subject Headings**  
 158. **Summary**  
 159. **Notes**  
 160. **References**  
 161. **Appendix**  
 162. **Index**  
 163. **Table of Contents**  
 164. **Abstract**  
 165. **Keywords**  
 166. **Subject Headings**  
 167. **Summary**  
 168. **Notes**  
 169. **References**  
 170. **Appendix**  
 171. **Index**  
 172. **Table of Contents**  
 173. **Abstract**  
 174. **Keywords**  
 175. **Subject Headings**  
 176. **Summary**  
 177. **Notes**  
 178. **References**  
 179. **Appendix**  
 180. **Index**  
 181. **Table of Contents**  
 182. **Abstract**  
 183. **Keywords**  
 184. **Subject Headings**  
 185. **Summary**  
 186. **Notes**  
 187. **References**  
 188. **Appendix**  
 189. **Index**  
 190. **Table of Contents**  
 191. **Abstract**  
 192. **Keywords**  
 193. **Subject Headings**  
 194. **Summary**  
 195. **Notes**  
 196. **References**  
 197. **Appendix**  
 198. **Index**  
 199. **Table of Contents**  
 200. **Abstract**  
 201. **Keywords**  
 202. **Subject Headings**  
 203. **Summary**  
 204. **Notes**  
 205. **References**  
 206. **Appendix**  
 207. **Index**  
 208. **Table of Contents**  
 209. **Abstract**  
 210. **Keywords**  
 211. **Subject Headings**  
 212. **Summary**  
 213. **Notes**  
 214. **References**  
 215. **Appendix**  
 216. **Index**  
 217. **Table of Contents**  
 218. **Abstract**  
 219. **Keywords**  
 220. **Subject Headings**  
 221. **Summary**  
 222. **Notes**  
 223. **References**  
 224. **Appendix**  
 225. **Index**  
 226. **Table of Contents**  
 227. **Abstract**  
 228. **Keywords**  
 229. **Subject Headings**  
 230. **Summary**  
 231. **Notes**  
 232. **References**  
 233. **Appendix**  
 234. **Index**  
 235. **Table of Contents**  
 236. **Abstract**  
 237. **Keywords**  
 238. **Subject Headings**  
 239. **Summary**  
 240. **Notes**  
 241. **References**  
 242. **Appendix**  
 243. **Index**  
 244. **Table of Contents**  
 245. **Abstract**  
 246. **Keywords**  
 247. **Subject Headings**  
 248. **Summary**  
 249. **Notes**  
 250. **References**  
 251. **Appendix**  
 252. **Index**  
 253. **Table of Contents**  
 254. **Abstract**

FIGURE 376

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
```

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVAA

LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP

APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70



**FIGURE 377**

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGCGGAGAGCGGCCGGGCGTCAGCTCCTCG  
 ACCCCCGTGTGCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCA**AT**GGCCAGGCCCGGC  
 ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCCCTCGGGGGGCATCGGCGCGGCC  
 GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC  
 ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCCCTACAGA  
 TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC  
 GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGCAGC  
 ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA  
 GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAAACATCAATAGCATG  
 TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC  
 ACTGCGCTGACAGAGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG  
 TGCATCTCTCCAGGTGTGGTGGAGACACAATTGCGCTTCAAACCTCCACGACAAGGACCTGAG  
 AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT  
 ATCTACGTCTCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG  
 CAGGTGACCT**Tag**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCCTTCATGGCTTGCCCTCTG  
 CCTCTGGATTTTAGTGTTGATTTCTGGATCAGGGATACCACTTCTCTGTCCACACCCCGACC  
 AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAATG  
 TGAAAATGGGCTGGGAAAGGAGGTGGTGTCCCTAATTGTTTACTTGTAACTTGTCTTGT  
 TGCCCTTGGCACTTGCGCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT  
 GTGGCCAAAATCCCACATCTTCTGACCTCAACGTCTGTGGCTCAGGCTGGGGTGGCAGAGG  
 GAGGCCTTCACCTTATATCTGTGTGTTTATCCAGGGCTCCAGACTTCCCTCTCTGCGCTGCCCC  
 ACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCAGTCTTGCTTCTTGT  
 CCCCTCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCGGGCCTGGC  
 CCAGTGGATTTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAAAAAAAAAAAAA

382/615

**FIGURE 378**

MARPGMERWRDRLALVTGASGGIGA AAVARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT  
LIPYRCDLSNEEDILSMFSAIRS QHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS  
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT  
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ  
MRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

2025 RELEASE UNDER E.O. 14176

**FIGURE 379**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT  
 TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCGAGCTGACGCCCGCTTATTAGC  
 TCTCGCTGCGTCGCCCGCGCTCAGAAAGCTCCGTGGCGGCGGCACCGTGACGAGAAAGCCACG  
 GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACTCCCT  
 CTTCAAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA  
 GAAATATACAATATTGAGGATATTTTTCTTTTCTTTTCAAGTCTTGATTGTGGCTTACCT  
 CAAGTTACCATTTTTAGTCAAGCTGTTTGTGTGCTCTTCAGAAATGTTTTTACAATCTC  
 AAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTGTGCTTGATTTGGACTCATTGGGGATT  
 GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA  
 AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGAACACAGTGGA  
 TGTGAGAACCGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATGTGCTGCTTCT  
 GGATGACATTTTGCAACGATTTGTTGAAGCTGGAGAACAAAGTTGACTATATTTGTTGTGAATGG  
 CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAG  
 AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAATCACCTTGTGCTGCTCCATCCACTG  
 TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC  
 AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCAAGAACTCTAATTTCTGTACATA  
 AAAATTTTAAAGTTATTTGTTTGTCTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCTTTAA  
 AGAGAAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTGTATAAAATCTTTTGT  
 GTTTGAGATCAAGCTGAAATGAAAACTGAAAAACATGGATTCAATTTCTATAACACATTTAT  
 TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAAATGTTTAACTATTCTGTCAATTTGTTCTC  
 AATAGATGTAACGTTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT  
 ATTCCAATTTATGAGCAGAGAAAGGAAATATAATGTTGAAAAATATGTTTGTAAATCATGACCC  
 AAAGAATGTATTGATTGCACTATCCTTCAGAAATAACTGAAGGTTAATTATGTATATTTTAA  
 AAAATTACACTATAAGAGTATAATCTTGAAGTGGGTAGCAGCACTGTCCATTACCTATCGT  
 AAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTTGTAACCTCTAATCTTATACTTATTG  
 AAGAATAAAAGATATTTTATGATGAGAGTAAACAATAAAGTATTCATGATTTTTCACATACAT  
 GAATGTTTCATTTTAAAGTTTAACTCTTTGAGTGTCTATGCTATCAGGAAAGCACATTTATTCC  
 ATATTTGGGTAAATTTTGTCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATTGGAA  
 CTCCTTGAGGACTTTAGCCAGGTGTATATAATAAAGTACTTTTGTGCTGCATTAAATGCTTG  
 GAAAGTGTTAAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA  
 TGCATTAGATATTCATTTTATATAATGGCCACTTAAAAATAAGAACATTAAAAATATAAATCTAT  
 GAAGATTGACTATCTTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAAACCTGAATCTTGGGTA  
 ATTCTAGTATAAAACAAATTATACTTTTATTAAATTTCCCTTGTAGCAAAATCTAATTGCCAC  
 ATGTTGCCCTATATTTTCATAGTATTTATTTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT  
 AGATTTAGACTATAGAAATTAGATATGTATTGTTTCGTCAATTATAATATGCTACCAATGT  
 AGCAATAATTAACAATTTTTATTAAAAATAAATATGTGAATATTTGTTTCATGAAAGACAGATT  
 TCCAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA  
 TTGCCAGGT

384/615

**FIGURE 380**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648  
><subunit 1 of 1, 140 aa, 1 stop  
><MW: 15668, pI: 10.14, NX(S/T): 5  
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
NKNTVDVENGASMAGYADLKRTIAVLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP  
VTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

1052586.03333

AACTTCTACATGGGCCCTCTGCTGCTGGTGCTCTTCTCAGCCTCTCTGGCCGGTGCCCTACACC  
ATCATGTCCCTCCCAACCTCTCTTGACTCGGGCCGCTCAGGTCGACAGTCTCAGTTGCCCAGG  
GAGACACTCCCTCCCGAGGCAGTCTGCTCAGAGGCCCTCGGTCAGCAATTCAGTTCTGGTT  
TCAATGCCAGCCTGTAAAGGCCATGGAATTTGGGTGAATCACCGATGCCATTTAAGAGCGAT  
TTCTGCCAGGATGGAATGTAGTGCTGTCTGTCTGCGCTGTTCAATTCAGTAGCCAGG  
CCACTCTGGCGGCTGAGTGCTGAAATGAGGAATCAGAGAAATTAATTTCTCATGTATTTTT  
CTCATTTATTTATTAATTTAACTGATAGTTGTACATATTTGGGGGTACATGTCATTTATTTGG  
ATACATGTATACATATAATAATGATCAATCAGGGTAACTGGGATATCATCATACATCAAAACAT  
TTATTTTTTATTTCTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTCGAGTGGTGCC  
ATCTCAGCTTACTGCAACCTCTGCCTCCAGGTTCAAGCGATCTCATGCTCCACCTCCCAA  
GTAGCTGGGATCATCAGGCATGCACCAATGCCCAACTAATTTGTATTTTGTAGTAGACG  
GGGTTTTCGCAATGTTGCCAGGCTGGCCTTGAACCTCTGGCCTCAAAACATCACTTGTCCCTCG  
GCCTCCCAAAGTGTTATGATTACAGGCGTGGCGCTGGCCTAAACATTTATCTTTT  
CTTTGTGTGGGAATTTGAAATTAACAATGAATTAATGTTAACTGTCACTCTCCCTGTCTGTG  
CTATGGAAACACTGGGACTCTTCCCTCTATCTAACTGATATTTGTACAGGATTAACCAACCGT  
ACTTCACCCCACTCTCTCTTATCTCTCCCAACTCTGATCACTCTACTCTCTACTCTCTACCT  
CATGAGATCCACTTTTTAGTCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG  
CTGGCTTATTTTCACTTAACATAATGATCTCTGTTCCATCTGGCTGTGCTGCAATGACAGGA  
TTTCGTTCTTAATTTCAATTAATAAACCAACATGCAAAAA

386/615

**FIGURE 382**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQ  
PVKGHGTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

2015-03-27 14:28:11

## FIGURE 383

TTCTTGAGGTAAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG  
CCTTGAGGACATCTTCCTCATCGGGACATAAAATTGGCGTGTTCCCTTCAAGTAGGCCCTCATCAG  
TATAGCTTAAATCTGCTTCCATCTGTGTGTCGTGCGATCGGGTTTATTATTCTGTAATGATC  
GCTTTCTGACATCCATTCCAACAGGAATAACAGAGGATGCTCACACTCTCTACCTTCAGACAAC  
ACCAAATAAATAATGCTGGGGATTCCTTCAGATTGTAAAAACTGCTGAAAGTAGAAGAATAAT  
ACCTATACCACCAAGCTTTAGATGAATTTCCATACCACTCCCAAAGTATGTTAAAGAGTTAT  
ATTTCGAGAAATAACATAAGGACTATCAC'TTATGATTCACTTTCAAAAATTCCCTATCTGG  
AAGAATTACATTTAGATGACAAC'TGTCTCTGCACTAGAGTAGAAGGAGGACATTCGAG  
ACAGCAACTACTCTCCGATGCTTTTCCGTCCCGTAATCACTTAGACAATTCCTCGGGGTT  
TGCCCGAGCATATAGGAAGACTACGCTTGGATGATAATCGCATATCCACTTATTCATCACCAT  
CTCTTCAAGGTC'TCACTAGTCTAAACCGCTGGTTC'TAGATTGAAACCTGTTGAACAACTATG  
GTTTAGGTGACAAAGTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT  
CCCTCGATCTGCTGACAGGATAACTCTCAGGACCAAACTCGAGGAAGCTTATCTTCAAGATA  
ACCATCACTAACCGGGTGCCTCCAAATCGCTTTTCTATCTAAGGCAGCTCATCTCGACTGGATA  
TGTCCTAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGAAATTGGACAATATAACAC  
AACTGATTCTTCGCAAACTCCCTGGTATTGCGGGTGCAGATGAATGGGTACGTGACTGGT  
TACAATCACTACTCTGTAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTT  
GTGGGATGGCTATTAAGGATCTCAATCGAGAACACTGTTTGATTGTGAAGGACAGTGGGATTGTAA  
GCACATTTCAGATAACCTGCAATACCCAACACAGTGATCTCTCGCCAAGGACAGTGGCCAG  
CTCCAGTGACCAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
GGAGTCTCTCAGAAAACCAATTAACAATTCGTGAAGTCTGCACCTCTGATACCTATTCATA  
TCTCTTGGAACCTTGCTCTACCTATGACTGCTTTTGAGACTCAGTGGCTTAACTGGGCCATA  
GCCCGGCATTTGGATCTATAACAGAAACAATTGTAAACGGGGAAACGAGTGAGTATCTTGCT  
CAGCCCTGGAGCTGATTCACCCCTATAAAGATGTCATGGTTCCCATGGAAACCCAGCAACCTCT  
ACCTATTATTGATGAAACTCCTGTTTGTATTTAGACTGAAACTGCACCCCTTCGAATGTACAACC  
CTACAACCAACCTCAATCGAGAGCAAGGAAGAACCTTCAAAAACCCCAATTTAGCTTTGG  
CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTTACATTTGCTCCCTTTGCTTTTGTGTTGGT  
ATGTTTCATAGGAATGGATCGCTCTCTCAAGGAAC'TGTCATATGCAAAAGGAGGAGAAGAA  
AGGATGACTATGCAGAAAGCTGGCATAAGAAAGACAACTCATCTCGAAATCAGGAAAATCT  
CTTTTCAGATGTTACAATAAGCAATGAACCACTCTCGAAGGAGAGTTTGTAAATACACCA  
TATTTCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAGCAGTGAATACCGAA  
GCTACAGAGACAGTGGTATTCAGACTCATGATCACTCACTGTAGTGCTGAGGACTCACAG  
GCAGACTGTGTTTGGGTTT'TTAAACCTAAGGAGGCGATGGT

**FIGURE 384**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRDAGFIYCNDRFLTSIPTGIPEDATTL  
 YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRITITYDSLK  
 IPYLEELHLDNSVSAVSIIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST  
 ISSPSLQGLTSLKRIVLDDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL  
 YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDL NITQLILRNNPWYCGCKMKW  
 VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQTITAIPTNTVYPAQ  
 GQWPAPVTQQPDINKPKLTQDQTTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL  
 KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCIETETAPL  
 RMYNPTTTLNREQEKEPYKNPNPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK  
 GRRRKDDYAEAGTKKDNLSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSES  
 SSNRSYRDSGIPDSHSHS

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44



**FIGURE 385**

CCGTCATCCCCCTGCAGCCACCCTTCCAGAGTCCCTTTGCCAGGCCACCCAGGCTTCTTGG  
 CAGCCCTGCCCGGCCACTTGTCTTCA**ATGT**CTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG  
 GGCGTGAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGCTGCTGAGCGTGTGACCAGCAGTGA  
 GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC  
 GCTGTGGTCTCTCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGACAGACCT  
 GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT  
 GGATGGCATGGTGGGGTCCGAGTGTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC  
 CCAGGAGCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC  
 TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA  
 GCTGACCTCCAGCCCGGGTTTTGGAAGCTCCCATGCTGGATCCACACTGATGCCTCCTT  
 GGTGTACCCACGTTCCGGCCCCAGGACTCATTTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT  
 GCAGCTGCTGGGAACCGGACGAGCAGCAGCGAGCCCTGCGGCTCTCAGACCTCTGCAGGAG  
 CCTCATGACCAAGCCCGGCTGCTCAGGCTACTGCCTGTCCCACCACTGCTCTTCTTCTCTG  
 GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT  
 CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCCTACCCG  
 GGACATCTTCATGGAAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT  
 CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA  
 TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTCGAGGAGAGTGAA  
 GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTGCTCAGGCTGGAGTACAGTGGCGCAA  
 TCTCGGCTCACTGCAACCTTTGCTCCTGGGTTCAAGCAATTCTCTGCTCATCTCTCCGAG  
 TAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAATTTTTATATTTTTTAGTAGAGAC  
 AGGTTTCATCATGTTGCTCATGCTGCTCGAAGTCTGATCTCAAGAGATCCGCCCCACCTC  
 AGGCTCCCAAAGTGTGGGATTAT**TAGG**TGTGAGCCACCGTGTCTGGCTGAAAGCACTTCAA  
 GAGACTGTGTTGAATAAAGGGCCAGGTTCTTGCCACCAGCACTCATGGGGGCTCTCTCCCC  
 TAGATGGCTGCTCCTCCCAACAACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTTATACA  
 TCCTGGCAGAATACCCCCAGCAACAGAGAGCCACACCCATCCACACCGCCACCAAGCA  
 GCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAA CAGACCCCTTTAGTCTCA  
 TCCTTAGATCCTGGAGGACCGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA  
 GCCACCCGACACCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGATAGTGGGGCCGGG  
 AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAA

# **FIGURE 386**

MSARGRWEGGRRACRGSISGLARAQGAERVTSSEQRPMASLGLLLLLLTALPPLWSSSLPG  
 LDTAESKATTIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL  
 SLRVGMLGEKLEAATQRSYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ  
 DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCSLMTKPGCSGYCLSHQLLFFFLWARMRGCTQ  
 GPLQQSQDYINLFCANMMDLNNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS  
 WQKQQEGCFGEPPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP  
 PGFKQFSCLILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPPTSGSQSVGL

## **Important features of the protein:**

### **Signal peptide:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 39-56

### **Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

### **N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

### **Amidation site.**

amino acids 10-14

### **Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

**FIGURE 387**

GGTCTGAGTGCAGAGCTGCTGT**CATG**GCGGCGGCTCTGTGGGGCTTCTTTCCCGTCTGCTGC  
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG  
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG  
TGAAGCCTCAGGACTGGATCTCGGCGGCCGAGTCTGGTAGACGGAGAAGAGCACGTCGGTT  
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG  
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA  
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTGACACTGCCCTATCCTCTCCAAA  
TGAAATCTTCAGGTCACCTTCTTACTTTATTAAAGGGAATCGTGGGGCTGGACAGACTTTC  
TAATGAACCCAAATGGTTATGATGATGGTTCCTCCTTTATTGATATTTGTGCTTCTGCCTAAAG  
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT  
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG  
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGG**TAG**TCAG  
GCCGTCCAGAGCTGGCATTTCACAAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAAA  
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTGTCTGT  
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAAATGCCATTAAATAAA  
TTATATGAACACTACTATACATTATGTATATTAATTAAAAACATCTTAATCCAGAAATCAAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 388**

MAAALWGFFPVLILLLLLSGSDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWIS  
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVS PAYRFDPRVVDITSKGKMRARYVNYI  
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVNTSDPD  
MRREMEQSMNMLNSNHELDPVSEFMTRLFSSKSSGSSSKTGKSGAGKRR

**Important features of the protein:****Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

**FIGURE 389**

GTCTGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCATGCGGTGGAGCCTTGGGAG  
 CTGGCTGGGTGGCTGCTGTCTGGTGTGAGCATTGGGAAATGGTACCACCTCCCGAAAAATGTCAG  
 AATGAATTCTGTAAATTTCAAGAACATTCTACAGTGGGAGTCACTCTCTTTTGCCAAAGGGAA  
 CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC  
 CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAAGGC  
 TGAATTTGCAGATGAGCATTGAGACTGGGTAACATCACCTTCTGTCTGTGGATGACACCAT  
 TATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC  
 CCCTAAAAATTGAGAATGAATACGAAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA  
 TAATGTGAATACTGGAACCAAGTACTGATGAAAAGTTTCAAATTACTCCCAGTATGACTT  
 TGAGGTCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAGGGTTTCTTCC  
 TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAACCAACCCATGACGAAAC  
 GGTCCCTCCTGGATGGTGGCCGTCACTCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT  
 CCTCGGCTGCTTCTCCTTGTGTGGTGCCTTTACAAGAAGCAAAAGTACGCCCTTCTCCCTAG  
 GAATTTCTCTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT  
 TTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAGTGTCAATTGCAGAAGA  
 CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCTGGGCAAGG  
 GCCCAAAGCTAGGCTCTGAGAAGGAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC  
 ACATCTGCCTCAGTGAGGATCAGGGCAGCAACCAAGGGCCAAGACCATCTGAGCCAGCCCCA  
 CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA  
 AAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCATGATGTTTTTCAAGAAGTTGGC  
 CACTGAGAGTGAATTTTCAAGCCTTTTATATCACTAAAATAAGATCATGTTTTTAATTGTGAGA  
 AACAGGGCCGAGCACAGTGGCTCACGCCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG  
 ATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAAATATGGTGAAACCCAGTCTCTACTAA  
 AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCATAATCCAGCTACTCGAGTGCGCTGA  
 GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC  
 ACTGCATCTCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG  
 AGAAACAGAAAACTTAAAAATGAGGAATAAGAATGGAGATGTACATCTGGTAGATGTAACAT  
 TCTACCAGATTATGGATGGACTGATCTGAAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT  
 GCTACACAGAGCAGGACTTTTGGATTCTTTGCAGTACTTTGAATTTTATTTTCTACCTATAT  
 ATGTTTTATATGCTGCTGGTGCTCCATTAAAGTTTTACTCTGTGTTGC

**FIGURE 390**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551  
><subunit 1 of 1, 325 aa, 1 stop  
><MW: 37011, pI: 5.09, NX(S/T): 4  
MAWSLGSWLGGCLLVSA LGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ  
DKCMNTTITLTCDFSSLSKYGDHTLRVRAEFADSHSDWVNITFCPVDDTIIGPPGMQVEVLADS  
LHMRFLAPKIENEYETWTMKNVYNSWYTNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV  
QVRGFLPDRNKAGEWSEPVCEQTTHDETVPSSWMVAVILMASVFMVCLALLGCFSLWCYVYKKT  
KYAFSPRNSLPQHLKEFLGHPHHTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSL  
GTPPGQGPGQS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 222-245

**N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

**N-myristoylation sites.**

amino acids 6-12, 316-322

CTGTGCAGCTCGAGGCTCCAGAGGCCACTCTCAGAGAGAGCCAAGGTTCTGACGCGATGAGGA  
AGCATTCTGAGCTGGTGGTGGCTGGCCACTTGCTGTGATGCTGCTCTCTCAGCCACCTCTCTGCGG  
TCCAGACAGGGGGCATTAAGCACAGAAATAGTGTGAACCGGAAGGCCCTGCCAGCACTGCC  
AGATCACTCGAGGCCGAGGTTGGCTGAGAACCGCCCGGAGGACTTTCATCAAGCAAGGCCGCAAG  
TCGACATTGACTTCGGAGCCGAGGCCAACAGGTACTACGAGGCCAACTACTGGCATTCTCCCG  
ATGGCATCTCACTACAAACGGCTGCTCTGAGGCTTAATGTGACCAAGGAGGCATTGTCAACGGCT  
GCATCAATGCCACCCAGGCGCGAACACAGGGGGAGTTCTCAGAAGCCAGACAAACAGCTCCAC  
ACAGGTTGCTCTGGCGGCTGGTCTCAGGAGCTCTGCTCCCTCAAGCATTCGCAAGTTTGGTTGG  
AGAGGGGCGCAGGACTCTCGGCTCACCATGCACAGCCAGTGTCTCTCTGCGCTTGGCTTTGA  
TCTGGCTCATGTGTAAATAGACTCTGCCAGAGAGGCTGGCAGTACAGAGCGAGCAGCGACGAA  
TCTTGGCAAGTGGACAGCAGCTCTCTCTCCCAAAACCGACGGGTGTTCTGAAGGTGCCAGGAGC  
GGCGATGCACCTGCACATGCAAAATGCCGCTCCACGATATGCGCCCTGGTATGTGCTCTGCTTCT  
GATAGATGGGGGACTGTGGCTTCTCCGCTCATCCATTCTCAGCCCTAGCAGAGGCTGTGGCA  
CACTAGATTAGTAGTAATAAGCTGTAGTGAAGAACAACATCAGGCCTGGCGCACTGCTCTCAC  
AGTACTTCCCAACAACTCTTAGAGGTAGTGTATCTCCGTTTTCAGATAGAAGAAAGCTGAGGC  
CCAGAGAGCTGAAGTACTGCACCCAGTACACAGCTAGAAAGTGGCAGAGCGAGGATTCAAC  
CTGGGCTTGTCTAACCCCAAGGTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT  
TATGTTCTCAGAGGACCCACATCAAAACATGTATCTCTAATGAATTTGTAAGAGCTCCATGTT  
TAGAAATAAATGAAACACCTGA

396/615

## **FIGURE 392**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHKRIKWNRKALPSTAQITEAQVAENRPGAFIKQG  
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK  
LHQVQLWRLVQELCSLKHCEFWLERGAGLRVTMHQFVLLCLLALIWLMMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

2025-10-26 10:55:50



**FIGURE 393**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA  
 TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCCAGCTGCCTCCAGGCAGCCAGCCCT  
 CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA  
 TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG  
ATGAATTTTCAACAGAGGCTGCAAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCTCCCTTTG  
 CTGGCGACAGCCTCTCAAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCCTGCTTCTC  
 TGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG  
 GTTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT  
 AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGCTCTCGGATGCTGAGAGC  
 TGTACCTTGTCCACACCCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAACCCACCACAAT  
 AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC  
 GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGACACACAGG  
 CGTTTTCTGCTATTCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC  
 CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGCTCTGAATGTCTAGA  
 CCAGGACCTCCCTCCCTGGCACTGGTTGTTCCTGTGTCACTTCAAACAGTCTCCCTTCC  
 TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATCTTGGCCACGAGATTATT  
 GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT  
 GAAGAGTCTACAGAGAAGATTCTTGTAATTTATTACAACCTCTATTTAATTAAATGTCAGTATTTT  
 AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC  
 ATGCTTCTTTACCCCTCACAAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT  
 ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAAACAGAGAGGGATG  
 CTTGGATGTAAAACTGAACCTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC  
 AGAGCATTTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAA  
 GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTCAATTTCCCAACCCACACTCGCCAGCTCAC  
 CCAATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT  
 TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC  
 TGTGATGACATTCCTGCTAATAAAAGACAACATAACTCCAAAAA  
 AAAA

**10** **10** **10** **10** **10**

**FIGURE 394**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
>>subunit 1 of 1, 206 aa, 1 stop
>>MW: 23799, pI: 9.12, NX(S/T): 3
MNPQQRRLQSLTLARFPCLPLATASQMQMVVPCLGFTLLLSWSGSAQQGEFHFGPCQVKG
VVPQKLQWAFVAVKDWMTQADQNTISARLLQQEVLVQNSVDABSCLYLVHTLLEFYLKTVFKNHNN
RTVEVRTLKSFSTLANNFVLIVSQLPQSQENEMFSIRDSAHRRLLFRFAQLDVEAALTKA
LGEVDILTWTMOKFYKL
```

Signal sequence:  
amino acids 1-42

N-glycosylation sites.  
amino acids 85-89, 99-103, 126-130

399/615

**FIGURE 395**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT  
TTCTTGATGATTTATAGACTCAAAGAAAAC**CA**AT**GT**TCAGAAGCTCTCTTCTCTTCTGGCCTC  
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA  
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCACTGAGTCTTAGTTTTTATTTTT  
TGAAATTTCAACTTTCAGATT**CAGGGGGTACATGTGAAGTTTGT**TTTATGAGTATATTGCAT  
**GAT**GTCTGAGGTTTGGGGT

10052586.011503

400/615

**FIGURE 396**

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFLQLSDSGGT  
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

105586.01502

**FIGURE 397**

**CATG**CCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG  
 TGTCTCTGGTGGTTTGCCTAAACCTGCAAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
 CCTACAATGGACTCCACGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
 CATATATGGGC AAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
 TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAAGTATTATGCCAAAGTTAAGGCCATTTG  
 GGGAAACAAAGTGTTC AAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT  
 TGGCCACCCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
 AGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT  
 GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCGAGTGTGTGACCAA  
 CCACACGCTGGTGTCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
 CGTCCCGAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
 TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
 GTTTCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
 CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCTCTGTGA  
 AAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
 TATGAGTTTACTGGGAAAAAGCAGTGTATGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAA  
 CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTTGATGGA  
 AATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG  
 CAGAACATACCCCGGATAAAACAGTCATTGAATATGAATATGATGTGAGAACCCTGACAT  
 TTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGAGGAGGAGGTGTCCACACAAGGAACATT  
 ATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCCGCAACGTTACAGTACTCATACCCCC  
 TCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCAACAGACTCGGAGGAGGGGCCGGAGGA  
 AGAGCCATCGACGACCCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCCTTCGCT  
 GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGATGGGCTCGGAGAGGA  
 GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
 CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGA AAAC**TGA**TGCCAACCA  
 CTTCTCTTTGCTTTTGTCTTCTGTGCAACAAGTGAGTCACCCCTTTGATCCCGACCATAA  
 GTACCTGGGATGAAAGAAGTTTTTTCAGTTTGTGAGTGTCTGTGAGAA

1052586.01507

**FIGURE 398**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVITYTVQYF  
 IYGQKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPLETQI  
 GPPEVALTTDEKSIISVVLTAPEKWKRNPELDPVSMQIYISNLKYNVSVLNTKSNRTWSQCVTN  
 HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSKQCARTLKDQSSEFKAKIIFWYVLPISITV  
 FLFSVMGYSIYRIYHVCKEKHPANLILYGNFEFDRFFVPAEKIVINFITLNIISDDSKISHQD  
 MSLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
 RTIPDKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQTLQYSYTP  
 QLQDLDPQAQHTDSEEGPEEESTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE  
 GLLSRLYEPAAPDRPPGENETYLQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
 304-307, 523-526

**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

**FIGURE 399**

CCGCGC**ATGT**CGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG  
 CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA  
 ATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTTACAACATAGTGTGCAACAGGGGAC  
 TATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG  
 GCCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCTGTGTGAGGTGCAAT  
 TACACAGAGGCCTTCCAGACTCAGACACAGCCCTCTGGTGGTAAATGGACATTTTCTACATC  
 GGCTTCCTGTAGAGCTGAACACAGTCTATTTTTCATTGGGGCCCATATATTCTTAATGCAAAAT  
 ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA  
 ATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGT  
 AAGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACAACCTCCCTGGGAAACAGATACATG  
 GCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA  
 CAAACGCGAGCTTCAGTGGTGATTCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAAGCTG  
 ACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC  
 CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAGCAAGCCGGGAGGCTGGCTGCCT  
 CTCCTCCTGTGCTCTCTGTGCTGGTGCCACATGGGTGCTGGTGGCAGGATCTATCTAATGTGG  
 AGGCACGAAAGGATCAAGAAGACTTCCCTTTTCTACCACCACTACTGCCCCCATTAAGGTT  
 CTTGTGGTTTACCCTCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT  
 CAAAACCATTGCAGAAAGTGAGGTGCTCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG  
 GGTCCAGTGCACTGGCTTCCCACTCAAAGAGAGGCAGCAGACAAAGTCGTCTTCTTCTTTCC  
 AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC  
 TCTCAAGACCTCTCCCCCTTGCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCAT  
 CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAGACGATTACAATGCTCTC  
 AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCATGCTTTCTGTGCAGAACTTCTCCAT  
 GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG

**TAG**

**FIGURE 400**

MSLVLLSLAALCRSAVPREPTVQCGSETGSPSEWMLQHDLPDGLRDLRVEFVTTTSVATGDYS  
 ILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF  
 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK  
 NEETVEVNFSTTTPLGNYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPTGDSEGATVQLTP  
 YFPTCGSDCIRHKGTVVLCPOQTGVFPFLDNNKSKPGGWLPLLLSLLVATWVLVAGIYLMWRH  
 ERIKTSFSSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP  
 VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH  
 KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHDGCCSL

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201  
 and 283 - 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452



**FIGURE 401**

GGGAAACAGGGAACTATCAGCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG  
 GGACCTTTTGC GGCGAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTACTTCGGAG  
 CGAACAGCAGGACCAATCCACACTTCCTAGCTCTCTGGGGTCGGCCGCCGAGCCAGCCCG  
 GGGCCCGCCGCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA  
 GATACAGAAATTCATCTCCAAAAAGCGGATCTGCTTTTGCACCTTTCCTGGAAATCAGA  
 TGCACCTGCACTCTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC  
 TTTAGAGCAATTTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTCCGAGATAT  
 TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTCGGGAATTCGGTTTTTTCAT  
 GGTGTTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACCTTAGAAATCACAGC  
 TCTTTGTCCTTAAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA  
 CCAAACTGGTGACATCATTGAGCTGGAATCAAGGATATTTGACAGATACCATGAAAAGCT  
 AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAATTAGGTGT  
 AATTAGCTCTGAAGAGCTTCTCTTTATACTACAGGAGAAGTGTGAGCTAAATAGCAATTC  
 TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCTTTGGGATTGTTAATCCAGGAGTAGT  
 TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCTCTTTAATGAGAGG  
 CCTACAAAGCAAAATTTCTCTGAAGATGATTTTGCTCTGCAATGAGAAAAACAATC  
 CGCATCTTGGGCTTTAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA  
 TGTGGATGCTATGAATGAATACAATAAGCTTTGGAAATAGACAAAACAAACGTTGGAAGC  
 TTTGGTAGCTCGTGGAGCATTTATGTCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA  
 TTTTGGAGCTTGCAATTAGAAAACGTGCCAATCACAGAAATGCAAGAAAATACCTTGCCA  
 GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG  
 TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA  
 GAAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA  
 AGAAAAGCAGAAAACAAGAAAAAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA  
 AGAAGAGAAGAGGCTAAAGAAGAAAAGAAAACCACTTCTCTTCAAGTGTTTCTTC  
 TGCTGATGAATCAGTGTCTTCATCATCATCTCTCTCTCTCTCTGCTCACAAAAGGCATAA  
 GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCAGAGAGGCATTATCTAGGGC  
 ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAAATAC  
 TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG  
 GTTACAGTATGAAAAGACACAGATAAAAGAGAAGATAGATGCCCTCTCTCTTCATCTTC  
 ACTTGAAATACCGGATGATTTTGGAGTGATCTCTATTATTATTAAGAAAGTTAACTATAAA  
 ACAGCCTCAGGCAAGTTCCTTCAGGAGATATTCAGAAGAGGGCATTGTTATCATAGATGA  
 CAGCTCCATTCTAGTTACTGACCTGAAGACCTTCAAGTGGGACAGATATGGAGGTGGA  
 AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCCTAGGTTTATGTGTGTATGTGT  
 CTTAGTTTTTAAACAAAAAATAAAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG  
 AATAAGGATATAAAGAAATATTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA  
 TCACAAAGAGTAAAAAAATTTTACAAATTAATAATGTTTAAAGTTAAAAAGCTCTAGG  
 AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATATTTTTATGAATTTACTGT

**FIGURE 402**

MDRDLRLQSLNCHGSSLLSLRSEQQDNPHFRSLLGSAEPARGPPPPQHPLQGRKEKRV  
 NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLQFMEIPSMRRELFF  
 RDIERGDIVIGRISSIREFGFFMVLI CLGSGIMRDI AHLEITALCPLRDVPSHNSHGDPL  
 SYVYTGDIIRAGIKDIDRYHEKLA VSLYSSSLP PHLSGIKLGVISSEELPLYRRSVELN  
 SNSLESYENVMQSSLG FVNP GVV EFLLEKLG IDESNPPSLMRGLQSKNFSEDDFASALRK  
 KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNV EALVARGALYATKGS LNK  
 IEDFELALENCPTHRNARKYLCQTLVERGGQLEEEEEKFLNAESYYKKALALDETFKDAED  
 ALQKLHKYMQKSLELREKQAEKEEKQTKKIETSAEKLRLKLLKEEKLKKRRKSTSSSS  
 VSSADESVSSSSSSSSSGHKKRHHKHKRNRSESSRRSRHSSRRASSNQIDQNRKDECYVPV  
 ANTSASFLNHKQEV EKL LGKQDRLQYEKTQIKEKDRCPLSSSSLEIPDDPGVYSYLFKKL  
 TIKQPQAGPSGDIPEEGIVIIDSSIHVTD PEDLQVGQDMEVEDSGIDDPDHG

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 138-155

**N-glycosylation sites:**

Amino acids 288-292;508-512;542-546

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 300-304;472-476;473-477;517-521;598-602

**N-myristoylation sites:**

Amino acids 218-224;222-228;271-277;348-354

**Amidation site:**

Amino acids 52-56

**Cell attachment sequence:**

Amino acids 125-128

**FIGURE 403**

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC  
 CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATA  
 GGAAAAATACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCATT  
 ATGACAAACTTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG  
 AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACCCCCC  
 CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA  
 CTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC  
 ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGGCCATTGCCAAGAAGTACA  
 TGTTCAGAAAAAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCCTTCCAGACTTTG  
 ACCCTGTGTGGACAAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCCAACTGCACTG  
 GCTGTGCCCAGAAACACCTGAAGGTGATGCTCTTGGAAAGACGCCCCAAGGAAATTTGAGAGGC  
 TCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTGGAGGAAGAGATTTCAGCATTTTTTGT  
 GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAGTGGTGGCGCTGCT  
 TTCTGTAGCGGTGGTTCCCATTTCTCTTATCCATGGAGGAGACCTCTGAACAGATCACAATGT  
 TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT  
 GCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA  
 TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCAGTGGCCGAAGACATTGTC  
 AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGCACACCCCACTGGAAGG  
 TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTTCATCTGCGATGGAACCGCTTTCTCAGAAC  
 TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACAGGTTGAAAGGGGAA  
 AAATAAAAACAAAACGATGAAACTGCAAAA

408/615

**FIGURE 404**

MDLAANEISIIDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIIVVYK  
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG  
GDEDRPFDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP  
LLEEEIQHFLCQYPEATEGFSEGEFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPVFTHL  
PFPKASLNNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMPIEPGD  
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

2025-09-09 09:00:00

**FIGURE 405**

TGCCGGGCTGGGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGSGCTCCAATCGTCTGCCCTTGGACTCCC  
 GTCTCCTCCTGTCTCCGGCTTCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGGCTCTCGGCGCAGCTTCT  
 CAGCGGAGCGACCTCTCCTGCTCCGGGGCTGAGCCAGTCCCTGGATGTCTGAAACTCTCGAGATCATGGCGGG  
 TTGGCTGCTGCTTCCCGCGGGTGCCTCTGCCAGCGCGCGCTCTGCTGCCCGCTCTCGGCGGATGCTCAG  
 TAGCCCGCTGCCCGGCCCGCGATCCTGTGTCTCGGAAGCGTTTGGCTGCTGCAGATTTGCAGAACTAGTC  
**ATGGT**GCTGTGGGAGTCCCGCGGCGAGTGCAGCAGCTGGACACTTTGGGAGGGCTTTTCTGGGCTGCTGCTGCTG  
 CCCGTGATGCTACTCATCTAGCCCGCGCGGTGAAGCTCGCTCCTTTCCCTACCTCTTAAGTGAAGTCCCAACG  
 CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAATGATCTCTTCTCTGTGACACCAACCTGTAA  
 TTTGATGGGGAATGTTTAAAGAAATTTGGAGACACTGTGACTTGGCTCTGTGAGTCAAGTGCACCAATGACTATGTG  
 CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCCACAGGCTGCATGCAACAGCAGAGT  
 GAGATACTTGTGGTGTGAGAGGATCATGTGCCAGATGAGAGATCAGGATCTGGAGATGGAGTCCATGAAGGC  
 TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAAATGTGACGAAGATGCC  
 GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAAACCACTTCAATCCCTCTCGCTTCTGATGGGAAA  
 TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAGAAATGAAGTCATGCTTTGGGT  
 CGATGTCAAGATAACACAACTACAACTACTAAGTCTGAAGATGGGCATTATGCAAGACAGATATTGACAGAGAA  
 GCTAACAAATTAGAAGAAAGTGCCAGAGAACACACATACCTGTGCCGGAACATTACAATGGCTTCTGCATGCTG  
 GGGAAAGTGTGAGCATTTCTAATCATGAGGAGCCATCTTGACAGTGTGATGCTGGTTTACTGGACAACTGCT  
 GAAAAAAGGACTACAGTGTCTTATACGTTGTTCGGGTCTGTACGATTTCAATGATGCTTAAATCGCAGCTGTG  
 ATTGGAACAATTGAGATTGCTGTCTGCTGTTGGTGGTCTCTGCATCACAAGGAAATGCCCGAGAGCAACAGA  
 ATTCAACAGACAGAGCAAAATACAGGGCACTACAGTTGAGACAATACAAAGAGCGTCCACGAGGTTAATCTAA  
 AGGGAGCATGTTTACAGATGGCTGGACTACGAGAGCTTGACTACACAATACAGTATTATAGACAAAAGATAA  
 GACAAGAGATCTACACATGTTGCCATTGCGTAATCTACACCAATGAAAAATGATGACTACAGCTATATTT  
 GATTATGATGGATATATTGAAATAGTATACATTGCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA  
 TCACACAATATAGTTTTTCTTCCCATGTATTTGTTATATATAATAAATACTCAGCTGATGAG

410/615

**FIGURE 406**

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAPFTSLSDCQTFTGWNC SGY  
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVQCFKCNNDVVPVCSNGESYONECVLRQ  
AACKQOSEILVVSSEGS CATDAGSGSGDGVHIEGSGETSQKETSTCDICQF GAECDEDAED  
VWCVCNIDCSQTNFNPLCASDCKSYDNACQIKEASCQKQEKIEVMSLGRCDNTTTT TK  
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY  
TGQHCEKKDYSVLYVVPGFVRFQYVLI AAVIGTIQIAVICVVVLCITRKCFRSNRIHRQ  
KQNTGHYSSDNTTRASTRLI

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000  
1001  
1002  
1003  
1004  
1005  
1006  
1007  
1008  
1009  
1010  
1011  
1012  
1013  
1014  
1015  
1016  
1017  
1018  
1019  
1020  
1021  
1022  
1023  
1024  
1025  
1026  
1027  
1028  
1029  
1030  
1031  
1032  
1033  
1034  
1035  
1036  
1037  
1038  
1039  
1040  
1041  
1042  
1043  
1044  
1045  
1046  
1047  
1048  
1049  
1050  
1051  
1052  
1053  
1054  
1055  
1056  
1057  
1058  
1059  
1060  
1061  
1062  
1063  
1064  
1065  
1066  
1067  
1068  
1069  
1070  
1071  
1072  
1073  
1074  
1075  
1076  
1077  
1078  
1079  
1080  
1081  
1082  
1083  
1084  
1085  
1086  
1087  
1088  
1089  
1090  
1091  
1092  
1093  
1094  
1095  
1096  
1097  
1098  
1099  
1100  
1101  
1102  
1103  
1104  
1105  
1106  
1107  
1108  
1109  
1110  
1111  
1112  
1113  
1114  
1115  
1116  
1117  
1118  
1119  
1120  
1121  
1122  
1123  
1124  
1125  
1126  
1127  
1128  
1129  
1130  
1131  
1132  
1133  
1134  
1135  
1136  
1137  
1138  
1139  
1140  
1141  
1142  
1143  
1144  
1145  
1146  
1147  
1148  
1149  
1150  
1151  
1152  
1153  
1154  
1155  
1156  
1157  
1158  
1159  
1160  
1161  
1162  
1163  
1164  
1165  
1166  
1167  
1168  
1169  
1170  
1171  
1172  
1173  
1174  
1175  
1176  
1177  
1178  
1179  
1180  
1181  
1182  
1183  
1184  
1185  
1186  
1187  
1188  
1189  
1190  
1191  
1192  
1193  
1194  
1195  
1196  
1197  
1198  
1199  
1200  
1201  
1202  
1203  
1204  
1205  
1206  
1207  
1208  
1209  
1210  
1211  
1212  
1213  
1214  
1215  
1216  
1217  
1218  
1219  
1220  
1221  
1222  
1223  
1224  
1225  
1226  
1227  
1228  
1229  
1230  
1231  
1232  
1233  
1234  
1235  
1236  
1237  
1238  
1239  
1240  
1241  
1242  
1243  
1244  
1245  
1246  
1247  
1248  
1249  
1250  
1251  
1252  
1253  
1254  
1255  
1256  
1257  
1258  
1259  
1260  
1261  
1262  
1263  
1264  
1265  
1266  
1267  
1268  
1269  
1270  
1271  
1272  
1273  
1274  
1275  
1276  
1277  
1278  
1279  
1280  
1281  
1282  
1283  
1284  
1285  
1286  
1287  
1288  
1289  
1290  
1291  
1292  
1293  
1294  
1295  
1296  
1297  
1298  
1299  
1300  
1301  
1302  
1303  
1304  
1305  
1306  
1307  
1308  
1309  
1310  
1311  
1312  
1313  
1314  
1315  
1316  
1317  
1318  
1319  
1320  
1321  
1322  
1323  
1324  
1325  
1326  
1327  
1328  
1329  
1330  
1331  
1332  
1333  
1334  
1335  
1336  
1337  
1338  
1339  
1340  
1341  
1342  
1343  
1344  
1345  
1346  
1347  
1348  
1349  
1350  
1351  
1352  
1353  
1354  
1355  
1356  
1357  
1358  
1359  
1360  
1361  
1362  
1363  
1364  
1365  
1366  
1367  
1368  
1369  
1370  
1371  
1372  
1373  
1374  
1375  
1376  
1377  
1378  
1379  
1380  
1381  
1382  
1383  
1384  
1385  
1386  
1387  
1388  
1389  
1390  
1391  
1392  
1393  
1394  
1395  
1396  
1397  
1398  
1399  
1400  
1401  
1402  
1403  
1404  
1405  
1406  
1407  
1408  
1409  
1410  
1411  
1412  
1413  
1414  
1415  
1416  
1417  
1418  
1419  
1420  
1421  
1422  
1423  
1424  
1425  
1426  
1427  
1428  
1429  
1430  
1431  
1432  
1433  
1434  
1435  
1436  
1437  
1438  
1439  
1440  
1441  
1442  
1443  
1444  
1445  
1446  
1447  
1448  
1449  
1450  
1451  
1452  
1453  
1454  
1455  
1456  
1457  
1458  
1459  
1460  
1461  
1462  
1463  
1464  
1465  
1466  
1467  
1468  
1469  
1470  
1471  
1472  
1473  
1474  
1475  
1476  
1477  
1478  
1479  
1480  
1481  
1482  
1483  
1484  
1485  
1486  
1487  
1488  
1489  
1490  
1491  
1492  
1493  
1494  
1495  
1496  
1497  
1498  
1499  
1500  
1501  
1502  
1503  
1504  
1505  
1506  
1507  
1508  
1509  
1510  
1511  
1512  
1513  
1514  
1515  
1516  
1517  
1518  
1519  
1520  
1521  
1522  
1523  
1524  
1525  
1526  
1527  
1528  
1529  
1530  
1531  
1532  
1533  
1534  
1535  
1536  
1537  
1538  
1539  
1540  
1541  
1542  
1543  
1544  
1545  
1546  
1547  
1548  
1549  
1550  
1551  
1552  
1553  
1554  
1555  
1556  
1557  
1558  
1559  
1560  
1561  
1562  
1563  
1564  
1565  
1566  
1567  
1568  
1569  
1570  
1571  
1572  
1573  
1574  
1575  
1576  
1577  
1578  
1579  
1580  
1581  
1582  
1583  
1584  
1585  
1586  
1587  
1588  
1589  
1590  
1591  
1592  
1593  
1594  
1595  
1596  
1597  
1598  
1599  
1600  
1601  
1602  
1603  
1604  
1605  
1606  
1607  
1608  
1609  
1610  
1611  
1612  
1613  
1614  
1615  
1616  
1617  
1618  
1619  
1620  
1621  
1622  
1623  
1624  
1625  
1626  
1627  
1628  
1629  
1630  
1631  
1632  
1633  
1634  
1635  
1636  
1637  
1638  
1639  
1640  
1641  
1642  
1643  
1644  
1645  
1646  
1647  
1648  
1649  
1650  
1651  
1652  
1653  
1654  
1655  
1656  
1657  
1658  
1659  
1660  
1661  
1662  
1663  
1664  
1665  
1666  
1667  
1668  
1669  
1670  
1671  
1672  
1673  
1674  
1675  
1676  
1677  
1678  
1679  
1680  
1681  
1682  
1683  
1684  
1685  
1686  
1687  
1688  
1689  
1690  
1691  
1692  
1693  
1694  
1695  
1696  
1697  
1698  
1699  
1700  
1701  
1702  
1703  
1704  
1705  
1706  
1707  
1708  
1709  
1710  
1711  
1712  
1713  
1714  
1715  
1716  
1717  
1718  
1719  
1720  
1721  
1722  
1723  
1724  
1725  
1726  
1727  
1728  
1729  
1730  
1731  
1732  
1733  
1734  
1735  
1736  
1737  
1738  
1739  
1740  
1741  
1742  
1743  
1744  
1745  
1746  
1747  
1748  
1749  
1750  
1751  
1752  
1753  
1754  
1755  
1756  
1757  
1758  
1759  
1760  
1761  
1762  
1763  
1764  
1765  
1766  
1767  
1768  
1769  
1770  
1771  
1772  
1773  
1774  
1775  
1776  
1777  
1778  
1779  
1780  
1781  
1782  
1783  
1784  
1785  
1786  
1787  
1788  
1789  
1790  
1791  
1792  
1793  
1794  
1795  
1796  
1797  
1798  
1799  
1800  
1801  
1802  
1803  
1804  
1805  
1806  
1807  
1808  
1809  
1810  
1811  
1812  
1813  
1814  
1815  
1816  
1817  
1818  
1819  
1820  
1821  
1822  
1823  
1824  
1825  
1826  
1827  
1828  
1829  
1830  
1831  
1832  
1833  
1834  
1835  
1836  
1837  
1838  
1839  
1840  
1841  
1842  
1843  
1844  
1845  
1846  
1847  
1848  
1849  
1850  
1851  
1852  
1853  
1854  
1855  
1856  
1857  
1858  
1859  
1860  
1861  
1862  
1863  
1864  
1865  
1866  
1867  
1868  
1869  
1870  
1871  
1872  
1873  
1874  
1875  
1876  
1877  
1878  
1879  
1880  
1881  
1882  
1883  
1884  
1885  
1886  
1887  
1888  
1889  
1890  
1891  
1892  
1893  
1894  
1895  
1896  
1897  
1898  
1899  
1900  
1901  
1902  
1903  
1904  
1905  
1906  
1907  
1908  
1909  
1910  
1911  
1912  
1913  
1914  
1915  
1916  
1917  
1918  
1919  
1920  
1921  
1922  
1923  
1924  
1925  
1926  
1927  
1928  
1929  
1930  
1931  
1932  
1933  
1934  
1935  
1936  
1937  
1938  
1939  
1940  
1941  
1942  
1943  
1944  
1945  
1946  
1947  
1948  
1949  
1950  
1951  
1952  
1953  
1954  
1955  
1956  
1957  
1958  
1959  
1960  
1961  
1962  
1963  
1964  
1965  
1966  
1967  
1968  
1969  
1970  
1971  
1972  
1973  
1974  
1975  
1976  
1977  
1978  
1979  
1980  
1981  
1982  
1983  
1984  
1985  
1986  
1987  
1988  
1989  
1990  
1991  
1992  
1993  
1994  
1995  
1996  
1997  
1998  
1999  
2000  
2001  
2002  
2003  
2004  
2005  
2006  
2007  
2008  
2009  
2010  
2011  
2012  
2013  
2014  
2015  
2016  
2017  
2018  
2019  
2020  
2021  
2022  
2023  
2024  
2025  
2026  
2027  
2028  
2029  
2030  
2031  
2032  
2033  
2034  
2035  
2036  
2037  
2038  
2039  
2040  
2041  
2042  
2043  
2044  
2045  
2046  
2047  
2048  
2049  
2050  
2051  
2052  
2053  
2054  
2055  
2056  
2057  
2058  
2059  
2060  
2061  
2062  
2063  
2064  
2065  
2066  
2067  
2068  
2069  
2070  
2071  
2072  
2073  
2074  
2075  
2076  
2077  
2078  
2079  
2080  
2081  
2082  
2083  
2084  
2085  
2086  
2087  
2088  
2089  
2090  
2091  
2092  
2093  
2094  
2095  
2096  
2097  
2098  
2099  
2100  
2101  
2102  
2103  
2104  
2105  
2106  
2107  
2108  
2109  
2110  
2111  
2112  
2113  
2114  
2115  
2116  
2117  
2118  
2119  
2120  
2121  
2122  
2123  
2124  
2125  
2126  
2127  
2128  
2129  
2130  
2131  
2132  
2133  
2134  
2135  
2136  
2137  
2138  
2139  
2140  
2141  
2142  
2143  
2144  
2145  
2146  
2147  
2148  
2149  
2150  
2151  
2152  
2153  
2154  
2155  
2156  
2157  
2158  
2159  
2160  
2161  
2162  
2163  
2164  
2165  
2166  
2167  
2168  
2169  
2170  
2171  
2172  
2173  
2174  
2175  
2176  
2177  
2178  
2179  
2180  
2181  
2182  
2183  
2184  
2185  
2186  
2187  
2188

**FIGURE 407**

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG  
 ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCCGCTGTAATCTGAACCACTGTT  
 GTCAGACTGAGGCCCATTTGCAATTGTTTAACTACTAGAAAATGAAGTGTTCATTTTAA  
 CATTCTCTCTCAAAATGGTTTAAATGCTGAATTAAGTGAAGGGCTAAGCAAAACAGGTGCTT  
 GCGCTGAGGGCTCTGTCAGTGGCTGGGAGGACCCCGCGCTCTCCCGTGTCTCTCCACGACT  
 CGCTCGGCCCTCTGGAAATAAAACACCCGCGAGCCCCGAGGGCCAGAGGAGGCCGACGTGCC  
 CGAGCTCTCTCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCTCTCTCGCGCG  
 TCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA  
 GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT  
 GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCCTGCCGAGGAGACATGATGTGTGTTA  
 ACCAAATGGCGGGTATTTATGCATTCCCGGACAAACCTGTGTATCGAGGGCCCTACTCGA  
 ACCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCCTCTCAGCTCCAA  
 ACTATCCACGATCTCCAGGCCCTTATATGCGCCTTTGGATACCAGATGGATGAAAGCAACC  
 AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACAGTGCAACCCACCCAGATCTGCA  
 TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCGAT  
 GCTTAGACATTGATGAATGTGCGTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTGTGAT  
 CCTATTCTGTACATGCAACCCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAAGATG  
 TGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAACCTGCGTCAACACCTACGGCTCTCTCA  
 TCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTTCATTGCGATGATATGGACG  
 AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACAGCCCGGCACATACCTTCT  
 GTCCTGCCCTCCAGGCTACATCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT  
 GTGAGCACAGGAACACACGCTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA  
 AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT  
 GTCCTGTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCCTTTGTACCCGGACATGGACG  
 TGGTGTGAGGAGCCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCCTG  
 GGGCCTATTACATTTTCCAGATCAAACTCTGGGAATGAGGGCAGAGAAATTTACATGCGGCAAA  
 CGGGCCCATCAGTGCCACCCTGGTGATGACACGCCCATCAAAGGGCCCGGGGAAATCCAGC  
 TGGACTTGGAAATGATCACTGTCAACACTGTCACTCAACTTCAGAGGCAGCTCCGTGATCCGAC  
 TGGCGATATATGTGTCGAGTACCACTTCGAGCCCTCGGGCTGGAGCCTCCGACGCTGCCTCT  
 CATTTGGACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAAATGAGAGCGCACAGACGT  
 TAGGCATTTCTGCTGAAAGTTCCTCCGAAAGAGTCAAGCCCGACTTCTGACTCTCACCTGTA  
 CTATTGAGACCTGTCAACCTGCAGGACTTGCCACCCCGAGTTCCTATGACACAGTTATCAAA  
 AAGTATTATCATTGCTCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT  
 TCCACTATTTTCAAAGAAAATAGATTAGGTTTGGCGGGGCTGAGTCTATGTTCAAAGACTGT  
 GAACAGCTTGCTGTCACTTCTCACCTCTCCACTCCTCTCACGTGTGTACTGCTTTGCA  
 AAGACCCGGGAGCTGGCGGGGAAACCTGGGAGTAGCTAGTTTGTCTTTTGGGTACACAGAGAA  
 GGCTATGTAAACAAACACAGCAGGATGCAAGGGTTTTAGAGAATGTGTTCAAACCATGC  
 CTGGTATTTTCAACCATAAAAGAGTTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATCT  
 GTCTTGTTCATTTTGTAGTATTTTAAAAAATATGTCGTAGAATTTCTTCGAAAGGCCCTTCAGA  
 CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCTCTCTCATTTTCCAGTGTGTTTCTTT  
 GAGGACCCCTTAATCTGTCTTTCTTTAGAAATTTTACCACATTTGGATTTGGAATGCAGAGGTCT  
 CCAAACTGATTAAATATTTGAAGAGA

412/615

## **FIGURE 408**

MPGIKRIILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSILICRCDPGYELEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation sites.**

amino acids 283-287, 296-300

#### **N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

#### **Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

#### **Cell attachment sequence.**

amino acids 54-57

#### **Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

2025 RELEASE UNDER E.O. 14176



**FIGURE 409**

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTCA  
 GGGAGGAGCACCGACTGCGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT  
 TCGCTGGTCCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT  
 TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGCTGGG  
 AAGATCCAAAAGGAAGAGAATTGAGTTTGGTGGGCCCTTCCCGAGGACTGAACATGAAGAGT  
 TATGCCGGCTTCCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA  
 GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCCTCTGGCTACAGGGTGGGCCGGGAGGTTCA  
 TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAAGTAACATGACCTTGCCT  
 GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA  
 GGCTTCAGTTTTACTGTATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT  
 TTTATACAGTGCACTAATTCAGTTTTTCCAGATATTTCTGAAATATAAAAAATAATGACTTTTAT  
 GTCACTGGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC  
 AACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT  
 CCCGAATCAATTATAGGGGGCTATGCAGAAATTCCTGTACCAAAATTGGCTTGTGGATGAGAAG  
 CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACAATCAGGAAGCAGAACTGG  
 TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC  
 TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT  
 CAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAAGCCATCCACGTGGGGAAAT  
 CAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAGAAGATACAGTACAGTCAGTT  
 AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTCAATGCGCAACTGGAC  
 ATCATCGTGGCAGCTGCCTGCAGAGCGCTCCTTGATGGGCATGGACTGGAAGGATCCCAG  
 GAATACAAGAAGGCAGAAAAAAGTTTGGAAAGTCTTTAAATCTGCAGTGAAGTGGCTGGT  
 TACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC  
 TATGACCAGCCTCTGAGAGCTTTGACATGATTAATCGATTCAATTTATGGAAGAAGGATGGGAT  
 CCTTATGTTGGATAAACTACCTTCCCAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA  
 AATCGTAAAAACAGAAAATGTATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT  
 TTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTTGGGGGGAGATGTTTACT  
 ACAAATTAACATGAGTACATGAGTAAGAAATTACATTATTTAACTTAAAGGATGAAAGGTATG  
 ATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTAA  
 ATTTCTCTAAGAGTAAGTGAAAAGTGCACTGTGAACAAACAAAGCTGTAACATCTTTTTCTCG  
 CCAATAACAGAAGTTTGGCATGCGGTGAAGGTGTTTGGAAAATATTATGGATAAGAAATAGCTC  
 AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAAATGTATAA  
 AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAAAGAA

# **FIGURE 410**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKGRELSLV  
 GPFPGGLNMKSYAGFLT VNKT YNSNLF FWF FPAQIQPEDAPVVVLWLQGGPGGSSMFGLFVEHGP  
 YVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F F Q I  
 F P E Y K N N D F Y V T G E S Y A G K Y V P A I A H L I H S L N P V R E V K I N L N G I A I G D G Y S D P E S I I G G Y A E F  
 L Y Q I G L L D E K Q K K Y F Q K Q C H E C I E H I R K Q N W F E A F E I L D K L L D G D L T S D P S Y F Q N V T G C S N Y Y  
 N F L R C T E P E D Q L Y Y V K F L S L P E V R Q A I H V G N Q T F N D G T I V E K Y L R E D T V Q S V K P W L T E I M N Y  
 K V L I Y N G Q L D I I V A A A L T E R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q A G D F H Q V  
 I I R G G H I L P Y D Q P L R A F D M I N R F I Y G K G W D P Y V G

## **Signal sequence:**

amino acids 1-22

## **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

## **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352, 353-357, 424-428

## **Tyrosine kinase phosphorylation site.**

amino acids 423-432

## **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

## **Serine carboxypeptidases, serine active site.**

amino acids 200-208

## **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

**FIGURE 411**

GCAAGCCAAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGGACCCATGTGGAGGAGGGGACATTGTGTACCGCT  
 CTACATGCGGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA  
 CATCAAGTTGGACGTGGACTGCACCGTGGACATGTGAGAGCCTGACGGGCTACCGCAGCTTACCGTGTGCCACCC  
 CTTGGCCACACTCTTCAAGATCTCTGGCGTCTTCTCATCAGCCTAGTCACTCTTACCGGCTCATCTGCATGTA  
 CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGGTGAGGAGAGCAGCTACAG  
 CGACATCCCGCGAGCTCAAGAACGACTTCGCTTCATGCTGCACCTCATTTAGCAACATGACCCGCTCACTCCAA  
 GCGCTTCGCGCTCTTCTGTGCGAGGCTGAGTGAAGAACAGCTGCGCGAGCTGAACCTCAACACGAGTGGACGCT  
 GGACAAGCTCCGCGAGCGGCTCACCAAGAACCGCGCAGGACAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
 CCCTGACACTGTGTTTGACCTGTGTGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCGCAGGTGACCATCCGCGC  
 CAGCATTTGCCAGCTCAGGGGCTCAAGGAGCTGTGGCTTACACACAGCGGCAAGATTGAAGCGCTGCGCT  
 GGCCTTCTGTGCGGAGAACCTGCGGGGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
 TAGCTGAAGACATCTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGGGAGAACACCGCTCATCTGTCATCGA  
 CGGGCTGCGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCA  
 AGATGTGGCGGTGCACCTGCAAGAGCTGTCATCAACAATGAGGGCAACAGCTCATCGTCTCAACAGCCTCAA  
 GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
 CCACACGCTGCAGGAGTTTACCTCAAGGACAAACAACTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT  
 GCACCGCTCAGCTGCTTAAAGTGTGGTACAAACCATCGCTCATCCCCATCCAGATCGGCAACCTCACCAA  
 CTTGAGCGCTCTACCTGAACCGCAACAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCGCCAGCTGGG  
 CTACCTGGACCTCAGCCACAAACCTGACCTTCTCCTCCTGCGACATCGGCTCTGTGAGAACCTCCAGAACCT  
 AGCCATCACGGCCAAACCGGATCGAGAGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCTTCACCT  
 GGGCAACACAGTGTGTCAGTCACTGCCCTCCAGGTTGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGG  
 CAACCGCTGGAGTGCTGCTGCTGTGGAGCTGGGCGAGTGCCCATGCTCAAGCGCAGCGGCTTGTGTGGAGGA  
 GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGCTGACAAAGGAGCAGGCTTGAAGGAG  
 GCGGCTCAGCAGCAGCAGCAGGACCGCTGCCAGTCTCAGGCGCGGAGGGGAGGCTAGCTTCTCCAG  
 AACTCCCGGACAGCCAGGACAGCTCGCGCTGGGCGAGGAGCTGGGCGGCTTGTGAGTCAGGCGAGGCGAGA  
 GGACAGTATCTGTGGGGCTGGCCCTTTTCTCCTCTGAGACTCACTGCCCCAGGGCAAGTGTCTGTGGAGGAG  
 AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCTGGAGCGACCTGCTGCCCGAGGGCTGAG  
 CTGCCACAGAGGTCCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTCTCCTCATCTCCACCTCCTTATCCT  
 AGATAACTTATACATTTCCCAAGAAAGTTCAGCCAGATGGAAGGTTTCAGGGAAGGTGGGCTGCCCTTTTCCCC  
 TTGTCTTATTTAGCGATGCGCGCGGCACTTAAACCCACCTGGACTTCAGCAGAGTGGTCCGGGCGAACAG  
 CCATGGGACGCTCAGCCAGCTGCGGGCTGGGCTTCCGGTGCAGTCCAGGAGAGCAGGCTCAGCTGGA  
 AAGCGAGGCTCGGAGCTTGCTCTTCAGTCTTTGTGGCAGTTTGTGTTTTTGTTTTTTTTATTAATCAAA  
 AAACAATTTTTTAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAACATTAAAAA  
 AAAGACACTAACCGGACGCTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAACAGCAGCAGCT  
 TGAATGTGTTTCTTCTTCCCTGGGCGCAGGGTGCAGGTGTCTTCCGATCTGGTGTGACTTGGTCCAGAGTT  
 CTAATTGTCTCTGGGAGGAGGTTTTTTTGTGTTTTTGGGTTTTTGTGTCTGTGTTTCTTCTCTCTC  
 ATGTGTTCTGGCAGGCACTATTCTGTGGCTGTGCGCGCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAG  
 ACTCGGCTGGCTAATCCCGGATGAACGGTGTCTCATTCGACCTCCCTCTCGCTGCTGCTGCTGCTCTTCA  
 CGCACAGTGTTAAGGAGGCAAGGAGGCACTTCGCGCAGACTTTGTTTCCCAACCTCTCGGCGCATGGGTGTG  
 CAGTGGACCGCTCGGCTCTCGCTGCTTCCATCAGCCTGTGCGCACCTGTGCTTCATGAAGAGCAGACCTTA  
 GAGGCTGTGCGGGAATGGGAGGCTCGCCCTGGGAGGGCAGGCGTGGTCTCAAGCCGGTTCCGCTGTGGCG  
 CTGGAGTGACACAGCCAGCTCGGCACCTGGTGGCTGGAAGCAACCTGCTTTAGATCACTCGGTTCCCACTT  
 AGAAGGGTCCCGCTTATGATCAATCAGTGACACTAAGGCACGTTTATAGATCTCTTGTCTTAATGATTATG  
 CCATCGGTCTGTGCGGTCAATTTGTGTTTTCTGCGCTGTGTCATTGGATATGCAAGAAATGTCACACTAG  
 CCTTGACACCATGAAGCAAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAATAAAA  
 ATCTATAACAGAAAAAATAAAAAA

**FIGURE 412**

MRQTIKVIKIFILICYTVYYVHNKIFDVDCTVDIESLTGYRTRYCAHPLATLFPKILASFYIS  
 LVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF  
 AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHFLMMSGIPDVTVFDLVELEVLL  
 ELIPDVTIPPSTIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWIYSLK  
 TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG  
 KLIVLNSLKMANLLELIRCDLERIPHSIFSLHNLQIDLDKNNLKTIEEIIISFQHLHRLT  
 CLKLWYNHAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG  
 LLQNLQNLAITANRIETLPPLEFQCCKLRALHLGNNVLQSLPSRVGELTNLTQIELRGNRLC  
 LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
 398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

**FIGURE 413**

GAATCATCCACGCACCTGCGAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC  
 TTCATCATTATATGAGGAAATAAAGTGGTAAAAATCCTTGGAATACAAATGAGACTCATCAGAA  
 ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGGTGATGCTCCAGAGCTGCCAGAAG  
 AAAGGGAGATGACCAACTGCTCCAAACATGTCTCTAAGAAAGGTTCCCCGAGACTTGACCC  
 CAGCCCAACAGTACCTGGATTTATCTCTATAACCTCTCTTTTCAACTCCAGAGTTTCAGATTTTTC  
 ATTCTGTCTCCAACTGAGAGTTTGTATTCATGCCATAACAGAAATCAACAGCTGGATCTCA  
 AAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG  
 TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTTTGACACCA  
 TGCCATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAAATCCTAGGTTTGAGTGGGGCAA  
 AAAATACAAAAATCAGATTTCCAGAAAAATGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT  
 TCAGAACTCTTCTCATTATGAAGAAAGGTAGCCTGCCCATCTTAAACACAAACAAATCGCAC  
 TTGTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGTGTATGGAATCAAGACTTCAAAAA  
 TATTAGAAATGACAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAAATGCCAACGAAATC  
 TTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG  
 ACCTTTCTCTTATCTTCAAAATTTGTTTGGCATACATCAGTGGAAACACTTTTCAGATCCGAAATG  
 TGACTTTTGGTGGTAAAGGCTTATCTTGACCAACAATTCATTTGACTACTCAAACTACTGTAATGA  
 GAACATAAAAAATGGAGCATGTACATTTTCAGAGTGTTTTACATTCACAGGATAAAATCTATT  
 TGCTTTTGACCAAAATGAGCATAGAAAACTTGACAAATTCAAATGCCAAATGCCCAAGACTGC  
 TTTTCCGAAATTTCTCAGAAATTTCCAAATTTTAAATTTTGCCAATAATCTTAAACAGAGC  
 AGTTGTTTAAAAAGAACTATCCAACTGCTCCTTGTAAAACTCTCATTTTGAATGGCAATAAAC  
 TGGAGACACTTTCTTTAGTAGAGTTGCTTTTGCTAAACAAACACCTCTTGGAAACACTTGGATCTGA  
 GTCAAAATCTATTAACACATAAAAAATGATGAAAAATTGCTCATGGCCAGAAACTGTGGTCAAT  
 TGAATCTGTCTATACATAAATTTGTCTGATCTGTCTTCAGGTGCTTGGCCAAAGATTTCAAA  
 TACTTGACCTAAATATAACAAATCCAAACTGTACCTAAAGAGCATTTTTCATCTGATGGCTC  
 TACGAGAACTAAATATTGCATTTAAATTTCTAACGTATCTCCGTGGATGCGAGTATTTTCAGTA  
 GACTTTTCAGTTCTGAACATTGAAATGAACCTTCATTTCTCAGCCCATCTCTGGATTTTGTTCAGA  
 GCTGCCAGGAAGTTAAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGTACTGTGAAATTA  
 AAAATTTTCATTTCAGCTTGAAACATATTCAGAGGTGATGATGGTTGGATGGTCAGATTCATACA  
 CTTGTGAATACCTCTTAAACCTAAGGGGAACTAGGTTTAAAGAGCTTCATCTCCACGAATTTAT  
 CTTGCAACACAGCTCTGTTGATTGTCACTTGTGGTTATTTATGCTAGTTCTGGGGTTGGCTG  
 TGGCTTCTGTCTGTCTCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC  
 AAACATGGCAAGGTTAGCAAAACAAACCAAGAGAACCTCAGAGAAATGTCCGATTCACACG  
 CATTTATTTCATACAGTGAACATGATTTCTCTGTGGGTGAAGATGATTTGATTCGCCAATCTAG  
 AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAGCTACTTTGACCTCGGCAAAAGCA  
 TTAAGTGAATAATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCACTTTGTTTGTCTCCCA  
 ACTTTGTCCAGATGAGTGGTGCATTATGAATTTCTACTTTGCCACCAACATCTCTTCCAT  
 AAAATTTGATCATATAATTTCTATCTTACTGGAACCCATTCCTATTCTTATGCTATCCCAACA  
 GGTATCATAAATGAAAGCTCTCTCGAAAAAAGCACTATTTGGAATGGCCAAAGGATAGGC  
 GTAATATGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTATGTTTAAATGATTATGACCAACA  
 GAGAAATGTAATGAATCGACACTTCACAGAGTTAAATGAAGAGTCTCAGGTTCTCAACTCT  
 CTCTGATGAGAACAGATGTTCTATAAAATCCACAGTCTCTGGGAAGTTGGGGACACATACA  
 CTGTGGGATGACATTGATGATAACCTTTATGATGGCAATTTGACAAATTTATTAAGAAATAA  
 AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAAATGTAATCTTATAGAAACA  
 CCTTCAAGATTTTAAAGGCTTTATGAAAAAGGTTTCAATCCAGGATTTGTTTATATCATG  
 AAAAATGTGGCCAGGTGCGAGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCCAGGTTG  
 TGACCCACAGAGTCAAGAGATGGAGACCATCTCGGCCAACTAGGTGAAACCTGTCTCACT  
 AAAAATACAAAAATTAGCTGGGCTGTATGGTGCAAGCTGTAGTCTCCAGTACTTTGGGAGGCT  
 GAGGCAGAGATTCGCTTGAACCCGGGAGGTGGCACTGAGCTGAGATCGAGCTGACACATG  
 CATCTCCAGCTTGGTGACAGAGCAGACTTCCATCTCAAAAAAAGAAAAAAGAAAAA  
 ATGGAACACATCCTCATGGCCACAAAAATAAGGTCTAATTCATTAATAATATAGTCAATTAATGT  
 AATATAATATTTACATGCCACTAAAAAGAAATAAGGTAGCTGTATTTCTTCGGTATGGAATAAAA  
 CATATTAATATGTTATAAATAATAGTTAGTTGGTGCAAAACTAATTTGGGTTTTTGGCATTTGAAA  
 TGGCATTGAAATAAAAGTTAAAGAAATCTATACAGATGTAGTAACAGTGGTTTGGGTCTGG  
 GAGGTTGGATTCAGGGAGCAATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTTGTT  
 TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 414**

MRLIRNIYIFCSIVMTAEGDAPELPEEREELMTNCSNMSLRKVPADLTPTATTTLDLSYNLLFQL  
 QSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF  
 NDFDTPMICEBAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN  
 TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV  
 DLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ  
 QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFAANNILTDELFKRTIQLPHLKTLL  
 LNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENCSWPETVVNMNLSYNKLSDSVFRCL  
 PKSIIQLDLNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFRLSVLNIEMNFILSPS  
 LDFVQSCQEVKTLNAGRNPFRCCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLKDV  
 HLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQQLKR  
 NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKISENIVSFIEKSYKSI  
 FVLSPNFVQNEWCHYEFYFAHHNLFHENS DHII LILLEPIPFYCIPTRYHKLKALLEKKAYLE  
 WPKDRRKCGLFWANLRAAINNVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

[illegible]

420/615

## **FIGURE 416**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQLPLISLCEAPSPQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDIFYGVFSSPGYTHLASVSHPOQCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG
PGPPSSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCDREKCVYETWVCDGQPDCAADGSDWDSCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRLSLQLLRQDMTPGGGPGARRRQGRRLMRLVRLRLRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPPLPSLPLEPSLLSGVVQALRGRLPLSLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVVWVAEAEDEPLLT
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domain:**

amino acids 442-462

#### **LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393



**FIGURE 417**

GTGCTTCTCTTGTCTCTCGCGCCGAGTCTCTCTCTCTGTTCTCTCAGCCGCTGTGCGAGGAGAGCACCCCGGA  
 GACGCGGGCTGCAAGTCTGCGCGGCTTCTCTCCGCTTGGGCGGCTCTCGCCCTGGGCGAGTGCTGAGCGCCCTAG  
 AGCCCTCTCTTGGCGCTCCCTCTCTGCCCAGCGCAGCAGTGACATGGGGTGTGTGAGGTAGATGGGGCTCCG  
 GCGCGGAGGCGCGCGTGTGATGCGGCGCTGGGCAAGAACGCGCCGATTCCAGCTCTGCCCGCGCGCCCGGGCG  
 CCCCCTGCGAGTCCCGGGTTTCAGCTGGGGAACCTCTCCGAGCAGCAGCAGCCGCTCGCCTCTGTGCAAGCGCATC  
 GCCCGCGAGCCACAGCCACGATGATCGCGGGCTCTCTCTCTGCTTGGATTCTCTTAGCACCCACAGCTCAG  
 CCAGAACAGAAAGGCTCGAATTCTCATTTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTTGTAACCAACAAGCCCTGCGCGTCTGCAAGCAGTTGCCCT  
 GTGGGGACCTTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCCATG  
 ATTGAGAAATTTACCTTTGTCTGCCCTTACTGACCGAGAAATGCACTTGCCCACTGGCATGTTCAGCTGTAAACGCT  
 ACCTGTGCCCCCATACCGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
 TGAAGCAGTGTGTCTCGGGTACCTTCTCAGATGTGCCCTTCTAGTGTGATGAAATGCAAAAGCATACACAGACTGT  
 CTGAGTCAGAACCTGGTGGTGATCAAGCGGGGACCAAGGAGACAGACAACCGCTGTGTGGCACCTCCCGTCTCT  
 TCCAGCTCCACCTTCACTTCCCTGGCACAGCCATCTTTCCAGCCCTGAGCACATGAAAACCCATGAAGTCCCT  
 TCTTCCACTTATGTTCCCAAAGGCATGAATCAACAGAATCCAATCTTCTGCTCTGTGTAGACCAAGGATCTG  
 AGTAGACTTCAGGAAGGGACAGTCCCTGACAACAAGACTCAGCAAGGGGGGAAGGACGTGAACAAGACCTC  
 CCAAACCTTCAGGTAGTCAACACCAAGGCCCCACCAACAGACACATCTGAAGCTGCTGCGGTCATGGAG  
 GGCATCTGGGGGCGAGAAGTCCAGCAGCCCATCAAGGGCCCCAAGAGGGGACATCTAGACAGAACTTACAAAG  
 CATTTTGACATCAATAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGTCTGTGGTGTGTTGTGGTG  
 TGCAGTTTCGGAAGAACTCTGAGGACTCTGAAAAGGGGGCCCCGCGAGGATCCAGTGGCATTTGTGAAAAGCA  
 GGGCTGAAGAAAATCCATGACTCCAACCCAGAAACCGGGAAGAAATGGATCTACTACTGCAATGGCCATGGTATGCT  
 ATCTCTGAAGCTGTAGACAGCCAAAGTGGGAAGCCAGTGGAAAGATATCTACTAGTTCTTTGCAATGCCAGTGA  
 AGGAGGTTGCTGCTCTTCCCAATGGGTACACAGCCGACACAGGCGGCTCAGCTGCTCTGACAGCTGACAGTGGAC  
 ATCCGGCGCCCGAGCCGCTGCCAGCTTAATTAGCGCCCTGCGCGCAGCCAGGAGAAACGATGTTGTGGAG  
 AAGATTCTGCGGCTGATGGAAGACACCCACAGCTGGAAACTGCAAACTAGCTCTCCGATGAGCCACCGCCG  
 CTTAGCCCGAGCCCATCCCCACCCCAACCGCAAACTTGAATTTCTGCTCTCTGACCGGTGAGGCTTCTCCCA  
 CAGGACAAGAAACAGGGCTCTTCTGGTGGTGGTGGAGCCCTTCTCGCTGTGACTCTACATCCAGGCGCTC  
 TCCGCGCTAGCAGGAACGGTTCTTTATTAACAAGAAAAGAGGACACAGTGTTCGCGAGGTACGCTGAG  
 CCCTGTGACTTGCAGCCTTACTTGTGATGACATGCTCCACTTTCTAAATCTGAGGAGCTCGGGTGTATTGAAGAG  
 ATTCCCGAGGCTGAGGACAACTAGACCGCTATTTCGAAATATTGGAGTCAAGAGCCAGGAAGCCAGCCAGCC  
 CTCTGAGCTCTGTTTATAGCATCTTCTGACCTGCTGTAGAACATAGGGATCTGCAATCTGGAATTTACTCA  
 ATTTAGTGGCAGGGTGGTTTTTAATTTCTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTGT  
 GTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAAATATGGCCAGTGCTTGAATTTCTTCTCTCTCT  
 TCTCTCTCTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCCTTTCAGGTTGAATCTGTGAA  
 ATACCCACCACTAAAGTTTTTTAAAGTTCCATATTTCTCCACTTTTGCTCTTATGTATTTTCAAGATTTACTGT  
 TGCACTTTAAATTTACTTAACTTACATAAATGCAAGTGACTTTTCCACACACTGAGATTGTGAGGCTTTAACT  
 TTCTTTAAAGTATTAATGGCACTTTGTGAATCTTAAAGCAGTCTTTATGCTCTTAAACTTCAACCACTTTT  
 AAAACAAATATTATTACTATTTTATTATTGTTTCTCCTTTATAAAATTTTAAAGATTAAAGAAATTTAAGA  
 CCCCATTGAGTTACTGTATGCAATTTCACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTCAATTTCAATG  
 CTGAACTTGACACACATTTGCTGATTTGTATGGTTTCACTGGACACCGTGTAGAATGCTGTTATCTTTGTAC  
 TCTTCTTATGCTTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
 GACAACTGGCCACCAAGAACTTGAACCTTCACTTTTAGGATTGAGCTGTTCTGGAACACATTTGCTGCACTTT  
 GAAAAGTCAAAATCAAGTGCAGTGGCGCCCTTTCCATAGAGAAATTTGCGCAGCTTTGCTTTAAAGAGTGTCTGT  
 TTTTATATACACATATCAATAGGCTCCAATCTGCTCTCAAGGCTTGGCTCTGTTGGGATTCCTTCAAAAT  
 ACTTTAATTAAGAGTGGCTGCACTGTGAAGACCTTGTCTGATATATTGCAACTGTGCTCCCATTTCAAAAT  
 TACCTTTAATGCTCAGTTGCGAGGTTTCCAAATGCAAGGTTGGCGGACTCCCTTGTGTGGGGTGGGTTTGG  
 GTAGTGGTGAAGGACGATATCAGAAAATGCTTCAAGTGTACTAATTTATTAAATACATTAGTGTGTTGTTA  
 AAAAAAAA

422/615

# **FIGURE 418**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pi: 8.22, NX(S/T): 8  
MGTSPPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHHVDRATGQ  
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCAAL  
TDRECTCPPGMFQSNATCAPHTVCPVGVGVRKKGTETEDVRCKQCARGTFSDVPSSVMKCKAY  
TDCLSQLNVVVKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSSTYVPKGMN  
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPS  
MEATGGEKSSSPIKGPKRGHPRQNLHKHFDINEHLPWMI VLFLLLVLVVIVVCSIRKSSRTLK  
KGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS  
EREVAAFSNGYTADHERAYAALQHW TIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQL  
ETDKLALPMSPLSPSPSPIPSPNAKLENSALLTVEPSPQDNKGFFVDESEPLLRC DSTSSGS  
SALSRRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE  
IIGVKSQEASQTLSDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

U  
S  
E  
R  
S  
E  
Q  
U  
E  
N  
C  
E

**FIGURE 419**

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
 ATCACC CGCTGGCCGACTCTCACC<sup>A</sup>TGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCGAG  
 AAGGGGACAAGACAGCTGTAGGCTCACGCAGCAGCTGGAGCTGCTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
 GCACCTGCTCTTGGGCTGCCCTGTGGCCCTAGGGGTCCAGTACCACAGAGACCATCCACAGCACCCTGCCTTACA  
 GAGGCTCTGCATTGCAGTGGCTGGAAAAATCTTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
 CAGTTCTCCTGTGGGGGTGGATTCTGGAGGAACCCCTGCGCGAGTGGGCGTCTCGCTGGAAACACCTTCAACAGC  
 CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGA AAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
 CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTTGAGGAGCTGGGAGCCCGCCACTTGAGA  
 GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAG  
 GCAGTAGCAGGGACCTACAGGGCCACCCCATCTTCAACGCTCATACATCAGTGCAGCTCTAAGAGTTCCAAACAGC  
 AATGTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
 AAAGTGCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGTGGGCGGCCACCTCCACGAGG  
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAATCAGAGTGCCCGAGGACCAGCGGCGCGAC  
 GAGGAGAAGATCTACCAAGAATGAGCATTTCCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT  
 CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTCAG  
 CAGGTGTGAGAGCTCATCAACCGCACGGAAACCAAGCATCTGAACAAATTACCTGATCTGGAACCTGGTGCAAAAG  
 ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG  
 TCCTGTGTGCGAGGTGGCAGACCTGCATCTCCAACACGAGTGAGCGCCTTGGCTTTGCTTTGGGGTCACTCTTC  
 GTGAAGGCCAGCTTTGACCGGCAAGCAAGAAATTGACAGGGGGATGATCAGCGAAATCCGGACCGCATTTTGAG  
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGACAGCAAGGAGAAGCAGATGCCATCTAT  
 GATATGATTGGTTTCCAGACTTTTATCCTGGAGCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
 GAAGATCTCTTTCTCCAACCATGTTGAATTTGTACAACCTCTCTGCGAAGGTTATGGCTGACACAGCTCCGCAAG  
 CTTCCCAACCGAGACCTGGAGCATGACGCCCCAGACAGTGAATGCCACTACTCTTCCAACCTAAGATGAGATC  
 GTCTTCCCGCTGGCATCTGACAGGCCCTCTTATGCCCGCAACACCCCAAGGCCCTGAACTTCGGTGGCATC  
 GTGTGGTCTATGGCCATGAGTTGACGATGCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTCTG  
 CGGCCCTGTGGCAGAAATGAGTCCCTGGCAGCTTCCGAAACCAACGSCCTGCATGGAGGAACAGTACAATCAA  
 TACCAGGTCAATGGGAGAGGCTCAACGGCCCGCCAGACGCTGGGGGAGAACAATTACTGACAACGGGGGCTGAAG  
 GCTGCCACAAATGCTTACAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCAACTGCCACCGCTGSGGCTCACC  
 AACCCAGAGCTCTCTCTCGTGGGATTGCGCAGGTGTGCTGCTGCGTCCGCACACCCAGAGAGCTCTCAGAGGGG  
 CTGGTGACCGACCCCAAGCCCTGCCCCCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTCTCGG  
 CACTTCCGCTGCCCTGTGCGCTCCCCCATGAACCCAGGCGAGCTGTGTGAGGTGTGGT<sup>A</sup>GACCTGGATCAGGGGA  
 GAAATGGCCAGCTGTACCAGACCTGGGGCAGCTCTCCTGACAAGCTGTTTGCCTTGGGTTGGGAGGAAGCAA  
 ATGCAAGCTGGGCTGGGCTAGTCCCTCCCCCACAGGTGACATGAGTACAGACCTCTCAATCACCACATTTG  
 TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCACCATTCACCTGTGACATCTTCCCTGTGACCCCT  
 GCCTGGAAGAGGTCTGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

MNVALQELGAGSNVGFQKGTROLLGSRQTQLEVLVLGASLLLAALLGLCLVAGVQYHRDPSSH  
 TCLTEACIRVAGKI LESLDRQVSPCEDFYQVSGCWTNRNLPDGRSWNTFNSLWDQNOQAI  
 KHLLENTTFNSSSEAEQKTRFYLSQLQVERIEELGACQPLRDLBKIGGWNITGPWDQNFME  
 VLKAVAGTYRATPFFTYYISADSKSSNSNVIQVDQSGFLPSRDYYLNRATANEKVLTAYLDYM  
 EELGMMLGGRPTSTREQMQLVLEILQANITVPDQRDEBEK YHKMSI SEIQLALAPSMDWL  
 EFLSPLLSELESDSEPVVVYGMXYLQVQSELNRTBPSILNNYLIWNVLQTSLSLDRFES  
 AQEKLELTLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKIEAEGMI SEIRTA  
 FEALQVLVMMDKEPTQAAKEKADATYMI GFDPFLPEKLDELVDVYDGBIE SEDSFQNMNLN  
 NFSAKQMVDLKRKPPSRDQWMTPTVTYNMGLPTKNEI VFPAGILQAPFYARNHKKALNFGGI  
 GVVMGHETHAFDDQGREYDKEGNLRPWQNESLAARFNHTACMEEQYNQYQVNGERLNGRQT  
 LGENTIDNGGLKAAANYNAWRLKHGEEQLPAVLGLTNHQLFVFGFAQVCSVTRPESSEHGL  
 VTDHSPARFVLGTLSNDRFLRHGCPVGSGPMNPGLCEVM

Type II Transmembrane domain:  
amino acids 32-57

**FIGURE 421**

GGCGCCGCTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC  
 GCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG  
 GTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGCGCCCTG  
 CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCCG  
 GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCTGCCCCCAGAGCCGCC  
 CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGGCAGTGCTGGTGCCCTT  
 CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA  
 GAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC  
 GCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT  
 TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGGCCCTTCCACGT  
 GGCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGCATCCTGCTGCT  
 CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA  
 GGACGACGAGTTCTACCGCGGCATTAAAGGGAGCTGGGCTCCAGCTTTTCCGCCCTCGGGAAT  
 CACAACCTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACAGAA  
 GCGCATCGCAGCTCAAAAAAGGAGCAGTTCAAGGTGGCAGGGAGGGAGGCCTGAACACTGT  
 GAAGTACCATGTGGCTTCCGCACTGCCCTGTCTGTGGGCGGGCCCCCTGCATGTCTCTCAA  
 CATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGACATTAGCTGAGCTGGATGGAC  
 AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG  
 GCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA  
 CCCGCCCGCAAGGCAGGCTTGGGCTGGGCCAGGACAGTGGGGTGCTGGGACGCTGCTTGC  
 CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGCTCTGTCCGGGACCCCCCTGCCTTCTGTC  
 TCACCTTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA  
 CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGGTAGTGGGGAGGG  
 CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAA

105256.0150  
 2014.09.25

**FIGURE 422**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL SLGFFSLLWLQLSCSGDVARAVRG  
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFPVPHMRRFLSRKKIRH  
HIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGFFHVASPE  
LHPLYHYKTYVGGIILLSSKQHYRLCNGMSNRFWGWGREDDFYRRIKAGLQLFRPSGITTY  
KTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD  
CDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

CCATCCCTGAGATCTTTTATAAAAAACCAGCTCTTTGCTGACCAGACAAGCATACCAGATC  
TCACCCAGAGATCGCAGACATATGCTGCTCCATCGGCCCTGCCAGGTGTCTGTGATGCT  
GCTTTCTGCTGCTTACTCTGTGTGTCAGGTTCAAGGTGAAGAAACCAGAAGCAATGCCCT  
TCCACGGATCAGCTGTCCAAAGGCTCCAAGGCTTATGGCTCCCCTGCTATGCTTGTTTT  
GTCAACAATAATCTGGATGGATGCAGATCTGGCTTGGCAGAAGCGGCCCTTGGAAAACTGGT  
GCTGTGCTGTCAGTGGGGCTGAGGATCTTCTGTGCTCTCCTGGTGAGAGACATTAGTAACAG  
CTACTCATATACATCTGGATTGGGCTCCATGTACCCCAACACAGGGCTCTGAGCGCTGATGAGATGG  
ATGGGAGTGGAGTACGACTGATGTGATGAATCTTTGCTGGGAGAAAAATCCCTCCACCAT  
CTTAAACCTTGGCCACTGTGGGAGGCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAGATTA  
TAACCTGTGATGCAAAAGTACCTATGCTGCAAGTTCAAGGACTAGGCGAGGTGGCAAGCTCAG  
CAGCCTCAGCTTGGCGTGCAGCTCATCATGAGACATGAGACAGTGTGAAGACTGCACTGGAA  
GAGAATATTCTCCCAAACTGCCCTACCTGGACTACCTTGTGATGATCCTCCTTCTTTTCTCT  
TTTCTTCACTCTTATTTCAGGCTTTTCTGTCTTCATGCTCTTGAGATCTCAGAGATAATA  
ATAAAATGTTACTTTATAAAAAAATAAAAAAATAAAAAA

428/615

**FIGURE 424**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965  
<subunit 1 of 1, 175 aa, 1 stop  
<MW: 19330, pI: 7.25, NX(S/T): 1  
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD  
ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIWGLHDPTQGSEPDGDGWEWSSTD  
VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

1005236.01502



**FIGURE 425**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTGG  
 CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC  
 AACATCCGGGGCAAAC**TGGT**GTGCTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT  
 GTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC  
 CTGGGCCCCCACCAC**TTA**ACGTGCTCGCC**TTCC**CCTGCAACCAGTTTGGCCAACAGGAGCC**T**  
 GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCCATGTTT  
 AGCAAGATTGCAGTCA**CCG**GTACTGGTGC**CC**ATCCTGCCTTCAAGTACCTGGCC**C**AGACTTCT  
 GGAAGGAGCCACCTGGA**ACTTCT**GGAAGTACCTAGTAGCC**CC**AGATGGAAGGTGGTAGGG  
 GCTTGGGACCCAACTGTGT**CAGT**GGAGGAGGTCAGACCCAGATCACAGCGCTCGTGAGGAAG  
 CTCATCCTACTGAAGCGAGAAGACTT**TATA**CCACCGCGTCTCCTCCTCCACCACCTCATCCCG  
 CCCACCTGTGTGGGGCTGACCAATGCAA**ACTCAA**ATGGTGTCTTCAAAGGGAGAGACCCACTGA  
 CTCCTCCTCCTTTACTCTTATGCCATTGGTCCCATATTCTTGTGGGGGAAAA**ATTCT**AGTAT  
 TTTGATTATTTGAATCTTACAGCAACAAATAGGA**ACTCCT**GGCCAATGAGAGCTCTTGACCAG  
 TGAATCACCAGCCGATACGAACGTCTTGCCAA**CAAAAA**ATGTGTGGCAAATAGAAGTATATCAA  
 GCAATAATCTCCACCCAAAGGCTTCTGTAA**ACTGGG**ACCAATGATTACCTCATAGGGCTGTTG  
 TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC  
 AATGAACATTTTTTG**CATATA**AAACCAAAAA**ATAA**CTTGTATCAATAAAAA**ACTTG**CATCCAAC  
 ATGAATTTCCAGCCGATGATAATCCAGG**CCAA**AGGTTT**AGTT**GTGTGTTATTTCTCTGTATTA  
 TTTCTTCATTACAAAAGAAATGCAAGTT**CATT**GTAA**CAAT**CCAA**ACAAT**ACCTCACGATATA  
 AAATAAAATGAAAGTATCCTCCTCA**AAAA**

429/615-01450

430/615

**FIGURE 426**

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQH  
YRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH  
PAFKYLAQTSGKEPTWNFWKYLVPDGGKVGAWDPTVSVEEVRPQTALVRKLI LLKREDL

2025-01-10 10:55:01

**FIGURE 427**

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGCC  
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCCT  
CTCCAGCCAGTTCCTCAACTCAGGAGACAGGTCCCAGGCCATGGGAGATCTCTCCTGTGGCTTT  
GCCGGCCACTCA**TGAG**AGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT  
GATTTAATAACCATCCTTTGCGAAGTTTATGAGGCTTTAGGGGAATGTCAACCCCTCAAATTT  
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT  
AAGTTTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATCTTCACTA  
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG  
GGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAATGTTATTCT  
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG  
AGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

100  
90  
80  
70  
60  
50  
40  
30  
20  
10  
0

432/615

**FIGURE 428**

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPVTQETGPKAMGDLSCGFAGHS

2025-03-03 10:00:00

**FIGURE 429**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG  
 CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT  
 GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT  
 GTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA  
 TCATGCTCTTCTACCACAATTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC  
 CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA  
 TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATACACCTGGGTCAAG  
 TACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG  
 AAACCTCTGCAAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT  
 GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT  
 CATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTCAAAGAAATACATCCTTGGTTTACAC  
 TCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTCAGTCAGAAAATA  
 TAAATGCTGTATTTATA

434/615

## **FIGURE 430**

><ss.DNA57834  
><subunit 1 of 1, 176 aa, 1 stop  
><MW: 19616, pI: 7.11, NX(S/T): 0  
MVLTI FGIQSHGYEVFNII SPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH  
GYIASRVLSRRACFILKMDHQNI PPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK  
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

### **Important features:**

#### **Signal peptide:**

Amino acids 1-26

#### **N-myristoylation sites:**

Amino acids 48-54;153-159;156-162;167-173

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 431**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA  
 CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA  
 GAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAAACATTGCTCTTTTGGGAGAACAGATTATTT  
 TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT  
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTTGATGGAGA  
 GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCAAATAAA  
 GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG  
 CAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC  
 CAGTGCCTTAGGGTTGTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA  
 GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG  
 AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

2022-09-29 10:25:00  
 105555-0-1-100

436/615

**FIGURE 432**

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILTE  
QLEAEREKMLLAKGSQKS

2025-09-25 10:55:00



**FIGURE 433**

GAATTCTGTCTTCGGCACTCACTCCCGGCCCGCCGGACAGGGAGCTTTTCGCTGGCGCGCTTGGCCGGCGACAGGA  
 CAGGTTTCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTTACAGATCCGCAAGCCCGGGATGGGGCCGCGCC  
 CGCTCGCGCTGCTGCTGGGCTCTTCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGCGCAAGGGAGAGAGCCA  
 AGCCTTTACCCGCTATTTCGCGGACCTTTTCAGGGAGCCTGCAAACTGCACACACCGCTGTTATCCCTTCTCTC  
 AGCCAGTGGGTACAGCCTGCCCTGTGATGTTTTCACCAACCCAGCCTGGAAGACACATACAGGAAACGTAGCCATT  
 CCCCAGGTGACCTCTGTGCAATCAAAGCCCTACCGCCTCTTGCTTCAAACACACAGTTGGACACATAATACTT  
 TCTGAAACATAAAGGTGTCAAATTTAAATTTGCTCAATCAATGTACCTAAATATATACAGGACACACAATTTCTTGG  
 TGGAAAGATGGGAAGGAATTTGCTTGGGGGACATCATCGAATTACACAGTTTATCCAGATGATGAAGTTACAGCA  
 ATAATCGCTTCTTTCAGCATAACAGTTGTCAGCGTTTTCAGCAATGGGTGCTATATCTGTGAAGATGAAAATAAAC  
 AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTCAAGGACTTCTCTCACTTTTACAGCAGCCTGAGAGC  
 ATGAATGTCAACAGAAACACAGCCTTCAACCTCACTGTGAGGCTTGGGGCCCGCTGAGCCCGTCAACATTTTC  
 TGGGTTCAAACAGTAGCCGTGTTAAACAGACAGCCTGAAAAATCCCCGGCGTGTAACTGTTCAGGCTGACG  
 GAGATGGCGGTCTTCAGTTGTGAGGCCCCAATGACAAAGGGCTGACCGTGTCCCAGGGAGTGCAGATCAACATC  
 AAAGCAATTCCTCCCCACCACTGAAATGAGCTGAGCATCCGTAAACAGACTGCACACAGCATTTCTGATCTCTGGGTT  
 CTGTGTTTGTATGGATACTCCCGCTTCAGGAATTCAGCATTGAGCTCAAGGAGCTGATCCGCTGGGTAAATGGC  
 TCAGTCATGATTTTAAACCTCTGCCCTTACACATCTGTACCAAAATCAAGCAGCTGCAAGCCCTGGCTAAATAC  
 AGCATTTGTGTTTCTCTGCAATGAATGAAATAGGCTGGTCTGAGTGAAGCCCTTGGATTCTAGCAAGCAGCACTGAA  
 GAGCCCATCATGAGCACTTTAAATGTCACTGTCTGATGAATCTAGTGATAATGTGGACATAGCATGAGTGG  
 ATGAAGCCTCGACTAAGCAGCAGGATGGAGAACTGGTGGGCTACCGGATATCCCAAGTGTGGCAGAGTGCAGGG  
 ATTTTCAAAGAGCTCTTGGAGGAAGTTGGCCAGAAATGGCAGCCGAGCTCGGATCTCTGTCAAGTCCACAATGTCT  
 CCGTGCACTGTGAGGATTCAGCCCGTCAACAGAGGGGGAGTTGGGCCCTCTCACTGATCCAGTGAATAATTTATC  
 CACTGACACAGGTTGGGTAGATTGTGCCCTCTTCACTCCGGCCCTGGCAACGACAGATCTGTGCTCATCATC  
 TTTGCTGCTTTTGGGTGATTTATTTAGTGGGTTGATTTATACATCTCTTGGCCATCAGAAAGAGTCCAG  
 GAGACAAAGTTTGGAGATGCATTTACAGAGGAGGATTCGAATTAGTGGTGAATTTATAGCAAGAAATCCTCT  
 TGTGGCGCAGGAACTGAACTTACCTTACATAGCTTGGGATCAGTGAGGAATTAACAAATAACTAGAAGATGTT  
 GTGATTGACAGGAATCTTCAATCTTGGAAATAATCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAT  
 CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTGGACCACTCTCATCTGGGAG  
 ATCGAGGAGTTTCTCAGTGAGGCGAGCTGCATGAAGAACTTCAGCCACCAAAATGTCAATTCAGCTTTAGGTGTG  
 TGTATAGAATGAGCTCTCAAGGCATCCCAAGCCCATGGTAATTTTACCCTTCATGAATAACGGGACCTGCAT  
 ACTTACTTATTTGATTTCCGATTTGGAGACAGGACCAAGCATATTCCTCTGCAGACACTTTGAAGTTCTATGGTG  
 GATATTGCTCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTCATCGAGATTAGCTGCTCGAACTCGCAT  
 TTGCGAGATGACATGATCTGTCTGTGCGGACTTCGCGCTCTCAAGAAATTTACAGTGGCGATTTATACCG  
 CAAGCCGCATTTGCTAAGATGCTGTTAAATGGATCGCCATAGAAAGTCTTGCGACCGAGTCTACACAGTAA  
 ATGATGTTGTGGGCTTTGGCGTGACCATGTGGGAAATACTGACGCGGGGAATGACTCCCTATCTGGGTCCGAG  
 AACCATGAGATGATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCGGAAGCTGCTCGATGAATCTGAT  
 GAAATTAATGTACTTTGCTGGAGAAACCGATCCCTTAGACCGCCCACTTTTTCAGTATTTGAGGCTGCGCATGAA  
 AAATCTTTAGAAAGTTTGGCTGACGTTTGGGAACCAAGCAGAGCTTATTAGCTACATACACAGTTGCTGAGAGC  
 TCTGAGGCGCTGGCCCGAGGGCCACCCCTTGCTCTCACTGAGCTTGAACATCGACCTGACTCTAATTTGGCTCC  
 TGCACTCCCGCGCTGCCATCAGTGTGTTGACAGCAGAAAGTTTCATGACAGCAAGTTCATGAAGAGCGGTACATC  
 CTGAATGGGGCGAGTGAAGAAATGGGAAGATTCGACTTCTGCCCCCTCTGCTGAGTGCAGCTGAAAGAGCAAGT  
 GTTTTACCGGGGAGAGACTTGTAGGAATGGGGTCTCCGTGGTCCCATTCGAGCATGTGCTGCTTTGGGAGGCTCA  
 TTGCCGATGAATTTTGTGTTGCTGACGACTCTCAGAAAGGCTCAGAAGTCTGATGTGAAGAGAGTGGCGGGA  
 GACATTCAAAAATCAAGCCAATCTTCTGCTGAGGAGAAATCAATGTACCTGATGTTTGGTATTTGCTCT  
 CCTTACCAAGTGAATTCATGGCCCCAAGACCCAGATGAATGTTGTTAAGGAAGCTGTCTTAAAAATACATAA  
 TATATATTTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATTTTAAATAAAACATTGATCTA  
 TTTCAATTTCACTTATCTGCATATCTTAAAAATAGGCTTCAGCTGCTCCTTGATTTAAACCTTTGTACAGAGTGG  
 AAGTTGTTTCTTCACTTCTTTCTTTTCACTACTATTAATGTAAAAATATTTGAAAAATGAATGGCCATATT  
 TGACTTGGCTCTGGTCTTGATGATTTGTATAGAAATGATTAATTTTCTGATATGGCTCCATATATAAATTTGAA  
 ATAGGA

**FIGURE 434**

MGPAPLPLLLGLFLPALWRRRAITEAREEAKPYPLFPGPFGSLQTDHTPLLSLPHASGYQPALMFSPTQGRPHT  
 GNVAIPOVTSVESKPLPPPLAFKHTVGHILSEHKGVKFNCSINVNPITYQDTTISWWKDGKELLGGHHRITQFYPD  
 DEVTALIASFSITSVQSRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTTKQPESMNVTRNTAFNLTCQAVGPPE  
 PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCEAHNDKGLTVSQGVQINIKAI P SPPT EVSIRNSTAHSI  
 LISWVPGFDGYSPPFRNCISIQVKEADPLGNQSVMI FNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL  
 ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQDGLVGVYRISHVQAGISKELLEVEVGQNGSRARISV  
 QVHNATCTVRIAIVTRGGVGPFPDVKIFIPAHGWDVYAPSSTPAGPNADPVLIIFGCFGCFILIGLILYISLAI  
 RKRVOETKFGNAFTEDSELVVNYIAKKSFCRRRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS  
 VMEGNLKQEDGTSCLKVAVKTMKLDNSSHREIERFLSEAACMKDFSHPNVRILRLGVCIERMSSQGIPKPMVILPFMK  
 YGDLHTYLLYSRLTGPKEHPLQTLTKFMVDIALGMEYLSNRNFLHRDLAARNCMRLRDDMTVCVADFGLSKKIYS  
 GDYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFVGTWWEIRTRGMTYPYGVQNHMYDYLLHGHRLKQPEDC  
 LDELYEIMYSCWRTDPLDRPTFSVLRRLQLEKLLSLPDVRNQADVIVYNTQLLESSEGLAQGPTLAPLDLNDP  
 SIIASCTPRAAISVVTAEVHDSKPHEGRYILNGGSEEWEDLTSAPSAVTAEKNSVLPGERLVRNGVSWSHSSML  
 PLGSSLPDELLFADDSSEGSEVLN

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

**FIGURE 435**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGATG  
 TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGGAT  
 CCAAGC**ATG**GAAATGCTGCCGTGCGGCAACTCTGGCACACTGTCTCTTTCTGGCTTTCCTG  
 CTCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGCACGGCCTATGGGATGCCTGGGGC  
 CCATGGAGTGAATGCTACGCACCTCGCGGGGAGGGGCCCTCCTACTCTCTGAGGCGCTGCCTG  
 AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA  
 CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATATATGATGTCAAGCACCATGGC  
 CAGTTTTATGAATGGCTTCTGTGTCTAATGACCTTGACAACCCATGTTCACTCAAGTGCCAA  
 GCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT  
 ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG  
 GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG  
 GTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCCGATGTATCTGTGGTTGCACCT  
 CCGTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCCTGATCACTTATATCTGGAAACC  
 AAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTCTTGTGGAC  
 AATTCTAGTGTGGACTTCCAGAATTTCCAGACAAGAGATACTGAGAATGGCTGGACCACTC  
 ACAGCAGATTTTCATTGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC  
 TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCTTGTCTCAGCAACCTGT  
 GGAGGAGTTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT  
 GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAACCCAAGCTTCAGGAGTGCAAC  
 TTGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC  
 CTTCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCTCTCTCGTGTGGGGGGGCATCCAG  
 AGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAAAGAGTGG  
 AAATGCTGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTGACTGCCCTAAA  
 TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG  
 GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCAAAAACAAAGCCCCAC  
 ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAAACTTCCAGTCGAG  
 GCCAAGTTGCCATGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGAGAGGAG  
 CCCTCG**TAA**AGTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTGTTTAAAGAAAGCA  
 GTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGAACTAAGTGTAAATCATCTCACCAAAGCTTT  
 TTGGCTCTCAAATTAAGATTGATTAGTTTCAAAAAAAAAA

440/615

## **FIGURE 436**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847  
<subunit 1 of 1, 525 aa, 1 stop  
<MW: 58416, pI: 6.62, NX(S/T): 1  
MECCRRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECSTCGGGASYSRLRCLSS  
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPSCLKCQAK  
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR  
GQYKSQLSATKSDDTVVALPYGSRHRLVLKGPDLHLYLETKTLQGTKEGNSLSSTGTFLVDNS  
SVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCSATCGG  
GYQLTSAEYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMFYDLYHPLP  
RWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL  
AQEWSPTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKECIVPTPCYKPKKLPVEAK  
LPWFKQAQEEGAASVEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

2025-09-25 10:00:00

441/615

# FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCCAGATGTTGGTTACCCCTTGGTCTCCTGT  
CTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC  
AGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAACAGGACAACCTATGTTA  
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC  
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATGAGATG  
GCACAGGTGACCACGCAGAAGCCACAGAATCTTGCTGCTGCTTATTCTCCTCCCAAGTCTGT  
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG  
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT  
CCCTGTCAGCCAGTATTAACATGTCCCCCTCCCCCTGCCCGCCGTAGATTCAGGACATTCGC  
CCCTGTGTGCCACCAACAGGACTTTCCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC  
CCAGCAAGACGTCTGTGTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC  
CATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAATGGG  
GCCATGTGAATGCAGCTGCTCTGTCTCCCTACCCTGAGGAAAAACCAAGGGGAAGCAACAGG  
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCTGTCAGATGCTGTTGAAGGGGCAC  
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT  
GGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGGAAGTCACTCAGCTCC  
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAAACCAAGGAAACAAACA  
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA  
AAACAAAATTCTCTAACACTGAAA

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

**FIGURE 439**

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAATGAGGAACCTCAGCGGACCGGGAGCGAGCAGCTT  
 GAGGGAAGGATCTCTGAGGAGGCTGCGAGGCGGAGGCTGACGAGGTGGCCGAGGTGTCTGAGGGCGCTGG  
 GGCAGGTGAAAGACTTTTCAGAAAGCTTCTCTGGACCCATGACCCATGAAGTCTTGTGCACATTTATACCGT  
 CTGAGGGTAGCAGCTCGAAACTAGAGAAGTGAGGTGTTCCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC  
 GGCCATATGGGACGCTTGGCTCTCAGACCTTTGTGATACCCATGCTGCGCTGGGACGATGACGGCGTGGAGAGGAAT  
 AGGCTCTGAGGTCACATCTGCTCTGCTCTCTCTCTAGGCCACAGCAGGCTGCTTTGCTGATTTGAACAGAGTCCCTCAG  
 GTCAACCGTCCAGCCTGCGTCCACCCTCCAGAAAGCCCGGAGGCACTGTGATCTTTGGGCTCGGTGTGGAAACCTTCA  
 AGGATGAATGTAACCTTGGCGCTGTAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCAAC  
 CACGGGACCCCTCGTATCATCTGCCCTTAAACAACACACCTGTGGGACGGTACCAAGTGTGTGGCCGGATGCGTGGG  
 GGGGCTGTGGCCAGCGTGGCCAGCCACTGTGACACTAGGCAATCTCCAGGAACTCAAGTTAGATGTGAGCAGCAGTG  
 ATTGAAGTAGGTAGGGGAACACAGCAGCTCATTGCTGCCACCTGCCGTGAGAGCCAACCCAAAGCCAGGTCCGG  
 TACAGGCTCAAAACAAGAGTGGCTGGAGGCCCTCCAGAGGTAACTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGAGCCTACAACCCAGTACCCAGGAAGCTGAAACCT  
 TCCGGCTCCAGCGCAGGCTACGTTGTGGCGGCTCCACCGCTGAGGCTGCGCGCATCATCAACCCCGCAGGCGC  
 CAAACCATCATGCTCAACAAAGGCGCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCCAACCCCGCAGGCTC  
 ACTGGGCGCAAGGATGGGTGCTCAGTGCTCACCGGCTTACAAACAAGACGGGCTTCTGCTGAGCAACCTCTCATGAGC  
 ACCACCCAGCGAGGAGCACTCAGGCACTTACCGTGCATGGCCGCAAACTGGGTTGGGACCCCGGGCAGCGCTC  
 ATCCTCTCAATGTCCAGCTTTTGAACCCCTGAGCTCAGCATCCAGGCTATCCAGCATCTCCCTCTGGGCG  
 CAGAGTGCACAGCTTACTCTGTAAGGTGGTGGAACCCCGCCCTCTCGTGTGTGGCTGAGGAATGCTGTGCCCT  
 CTCTACTCCAGCGCAGCGCTCTCCGCTCTCCCGCAGGGCCCTGCGGCTGCTCAGCATGGGGCTGAGGACGAAGGG  
 GTCTACAGGTCATGGTCCGAGAAAGAGGTTGGGAGCGCCATGCGGTAGTCAGCTGGGAGCTCTCAGGCCAAGC  
 ATAAACCCCAAGGCTATGGGAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATACCTCTTCAAACTCGGCAAC  
 CTTGAGCAGATGCTGAGGGGGCTGCGCGCTCCCGACACCCCAAGTCAAGTGGGGCTGCTTCCCGAAGTGT  
 CCAGGAGAGAAGGGGCGAGGGGCTCCCGCGAGGGCTCCATCATCTCAGTCTCCCTCCGACCTCTCAAGACAGAG  
 TCCATATGAATGTTGGCGGCTCTCGCATGAGGGCAGTGGCGGGCGCAATGCTCTACTATGTGGTGAACAC  
 CGCAGCAGAGGTCAAAATTCCTCTGACGATGGAGCACTCTCTGGATCTCCAGCBAACAGCAGCCGCTGACCTCTC  
 ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGCTGTGGGGAGAGGGCCAGACAGCC  
 ATGCTCACTCTTCGAATCTGGACGGCGGCCCAACCCGAGATTCATGGCCAGCAAGAGCAGCAGATTCAGACAGAGC  
 GACCTCGGAGCCAGTCCCGAGAGCAGCAGCAGCCAGACCAACGGCCGCTCTCCCGCCAGGAAGCTCCCGACAGG  
 CCCACCATCTCCAGCGGCTCCGAGAGCTCAGTGTACGCTGACCTTGAATCCCCCGTGGGAATGTGTGGTTCCTCAATC  
 CAGTCTCTCCGTGTGAGTACAGAAAGCTAAAGAAGTGGGAGACTGGAATCTCTGGCACAGCCCATCTCCCGCTC  
 TCGCGCTGCTCTGAGAGTACAAGGCTTAGAGAAAGGACCTCTCAACAGCTCGGGCTCTGAACTG  
 CTGGGGAGAGCGAGCCAGCCGCCCTCTCTCGGCCCTACGTGGTGTCTGGGCTACAGCGGCTCGCGTGTGACAGAGG  
 CCGTGTGGAGCTCTTATATCACTCACTTCCAGGATGCGGTCAATGAGACCACTATGCTCAAGTGGATGTGATCTC  
 CCAGCAAGTAACAACAACACCCCAATCCATGCTCTTTATATCTATTCAGCCACACAGCAGTGAACATGATAGT  
 GACTACAGGAAGGATATGGTGGAGGGGGAACAGTACTGGCACTTCCATCAGCCTCAGCAGCAGAGACTCTCTAC  
 GACATTTAAGATGCACTGCTTCAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGAGCAAGCT  
 CGGAAGTCTCTTGCCAGCTGGTCTGACTGCCACCCCACTCTGGCCGCTGCTGAGGCGCCCTCTCTGAAACCT  
 ATAGAGCGCCGCTGGGACCTGGGGCATGGTGGCTGCTCCAGCGACCTGCCCTATCTGATTTGTGGGCTCGTCT  
 CTGGGCTCCATCTTCTCATCATGCTCACTCTCATCCGCTCTGCTTTGTGGAGGGCTCGGCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCTCTCTGCCGATATACATGATGGTCCATGGGAGGACCTC  
 CCAGGCGCCAGCGGCTGGACAGCCCTACCTCAGTGGCATGAGGAGCGGCGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCGCTCTCGCTCAGTGGGCTACCCGGGCAATGAAGCCCGCAGCAGCTGCCCGGCGAGCTTCAG  
 CAGCAGGTGACACAGCAGCTGCTGAGGACAGCCCATCTGGCAATGGAATGACCCCAAGCTCACCAGATC  
 ACAGGGGGTCCCAAGTGTATGCGCGAGGCGCTCTTTTATACATGCTGCGGACCTGCGGACACTCCACACAGCT  
 CTGCGGCCCTCTGAGTCTGCGCAAGCGCAGGAGCAGCTCTGCTGTGGGCACTCAGGGTGTGAGAGAGCC  
 CCGCAGACTCTGTGCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGCCCCCACTGCTGCTTGGGCGTGTG  
 CAGTGTGAAGAGGTGACAGCTGCTGACTCTCTGCAAGTGAAGTGGAGGAGCACTGGTGTGCCACAGCCCGTAGGG  
 GCTCTAGTGAAGACAGAAAGCTTGAATGAGTCACTCTCTCCCGGGCCACTGGTGGCGTGTGCTTTTGAACACCACTC  
 CTCACAATTTAGGAGAGAGCTGATATCCCAAGAAAGCATATATTTTTTTTTTTTAAAAAAGAAAGAAAAA  
 AGAGACAGAGAAAATTTGTTATTTATTTTCTATTTATAGCATATTTATATTTATGCACTTTGTAATATAATGTA  
 TATGTTTATATTTTGTGAGAGACATAGGAGTCTACCCGTTGAGGTTGGAGAGGAAAAAAGAAAGCTGCCA  
 CTTAACAGGAGTCAACCGAGAAAGCACGCACAGGCTGGCGGGGACAGACTCTTAACCTGGGCGCTCTGCACTG  
 CAGGCGAGGCTGTGAGGAGGCCACAGATAAGCTGGGAGAGGAAGGATCCAGGACATGTGTTTCATCAGCAGCA  
 TGAAGGAAACACGAAGGGGACAGGATCACAGCTGGAGACACCAACACAGATGGCTGGATCCGGTGTACGGGAA  
 ACATTTTCCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCAATTAAGAAAGCTTCCAGAT  
 CAATATCTCCGTCACACATCTTCTGTAAAAACAAACACTGTAACTTTCAATATAATGTTTATGCTTCCCTGTAAAA

**FIGURE 440**

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPPR  
 MNVTWRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN  
 LQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN  
 ASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIITYPPEAQTIIVTKGQSLILEC  
 VASGIPPPRVTWAKDGSSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVVGQPGAIVILY  
 NVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV  
 LSMGPEDEGVYQCMANEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM  
 LRQQPALPRPPTSVGPASPKCPGEGQGAPAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP  
 ILYYVVKHRKQVTNSSDDWTISGIPANQHRLLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR  
 TGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTVIPR  
 GNGGFPIQSFVRVEYKLLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRVRALNMLGESEP  
 SAPSRPYVVS GSGRVERPVAGPYITFTDAVNETT IMLKMMYIPASNNNTPIHGFYIYYRPT  
 DSDNDSYDKDMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNVMICETKARKSSSQP  
 GRLPPTLAPPQPLPETIERPVGTGAMVARSSDLPLYLIVGVVLGSI VLIIVTFIPFCLWRAW  
 SKQKHTTDLGFFRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCP SAA  
 VGYPGMKQQHCPCGELQQQSDTSSLLRQTHLGNQYDPOSHQITRGPKSSPDEGSFLYTLPDSS  
 THQLLQPHHDCCQRQEQPAAVVGSGSVRRAPDSPVLEAVWDPPFHS GPPCCCLGLVPVEEVDSPD  
 SCQVSGGDWCPQHVPAGAYVQEPGMQLSPGLVVRVSFETPPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



**FIGURE 441**

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC  
 TCTGGCAGGCTCCTGGCAGC**ATGG**CAGTGAAGCTTGGGACCCCTCCTGCTGGCCCTTGCCCTGG  
 GCCTGGCCAGCCAGCCTCTGCCGCGGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTCGCT  
 CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG  
 GAGTAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC  
 TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACCCCA  
 CCAACAAGTCCCTTTGACATTGGCGTCAACAAGACAGCCTAATGCCTCTCTGGTGGAAATGGAT  
 CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGTCTACATGTACTACTGGCCAG  
 GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCAA  
 CGGATATCAATTTTGC CAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCGG  
 ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC  
 CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCTTGAAGTACATGACCAAGTGGATCC  
 AGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCACGGAATGACCGACA  
 TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG  
 TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCTTGGGAAACACTCTGAGATATATA  
 ACAAACTGAGCA CAGTGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT  
 ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA  
 CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCCGCGAGGCGGGAAGGTTGGCAGC  
 GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTCTCTGGCCTTCGGAC  
 CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTCAATGTGATGT  
 GCAATGTGGTGGGCATCACCCGCTGCCCAACAACGGATCCTGGTCAGGSGTGATGTGCATGC  
 TGAAGGGCGCGCCGGCACTGCCCGCCTGTCTGGCCAGCCACTGTGCCCTGGCACTGATTTC  
 TTCTCTTCTGCTTGCA**TAA**CTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG  
 TGGGCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA  
 AGACCATGCACATTGTAATAACATTATTTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT  
 TAAA

446/615

## **FIGURE 442**

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDYL  
TPDFPSLSYPNYITLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMPLWNGSEPLWVT  
LTKAKRKVYMYWPGCEVEILGVRPTVCLEYKNVPTDINFANAVSDALDSFKSGRADLAAIYH  
ERIDVEGHHYGPASQQRKDALKAVDTVLKYMTKWIQERGLQDRINVIIFSDHGMTDIFWMDKV  
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF  
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWGHYDNE LMDMRGIFLAFGPDFKSNF  
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCLKGAGTAPPVWPSHCALALILLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

446/615

447/615

**FIGURE 443**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC  
ACCAAGTGTGTGAGGGGAGCAGGCAGCGGTCTTAGCCAGTTCCTTGATCCTGCCAGACCA  
GCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT  
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAAGGAGCCACAGGAGGAGGTGGTTCC  
TGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG  
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC  
AACATCTCCCGAAGAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT  
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCTTCATCC  
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA  
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG  
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTTTTCCCTGTCC  
CAATCCCCAGGTGCGCACGCTCCTGTTACCCCTTTCTCTTCCCTGTTCTTGTAAACATTCTTGTG  
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC  
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGTCTACATTAAAAAT  
ATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

2025-01-15 10:00:00

**FIGURE 444**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA  
LSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS  
LGTEEQRPIL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

# 1326

TGGACTTCTCTGGACCACAGT/CCTCTGCCAGACCCCTGCCAGACCCAGTCCACCATGATCATCTGGGTACAT  
CCTCTCTCTGCTTTGTCTCCAGTGGCTGCAGCTGCAGACGACTCCAGGAGAGAGATCATCATCTCGCTGCTTTA  
CTCTGGCACTTCAGGCTCTGTCTCCGAGTGGTGCCTCTCTCTGGCGCTCTGGCAGGCTTCGGTGGCTGTA  
TGCGGTGGCATCGTGCTCATCTGTGGGGGGCGTGTCTCTGTGGCGCAGCCCAAGCCGACCCCGCAAGATGG  
CAAGATCTACATCAACATCCGAGCGAGGGGGTGAACCTCTTGCAGCTTGGACCTTGAGCTTGCACCTCTCATC  
CTGGATGTGTGTGGTGGCAGCAAGAACCCCGCCCACTTTTGATTGTAAATAAACAATTTGAACAACA

450/615

**FIGURE 446**

MIHLGHILFLLLLPVAAQTTPGERSSLPAFYPGTSGSCSGCGLSLFLLAGLVAADAVASLLIVGAVFLCARPR  
RSPAQDQGVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 447**

GCCAGGTGTGCAGGCCGCTCCAAGCCAGCCTGCCCCGTGCGGCCACCATGACGCTCCTCCC  
 CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCACCATGACCCCTCCCTCAGGGG  
 GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGC  
 CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCTGTAGCCCTGGTGTCT  
 CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC  
 GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACAGCGCTCCATCTCACCCCTGGAG  
 ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCCTGT  
 CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT  
 CCAGAGCCTGCTGGTGCTGCGCCGCCGCCCTGCTCCCCGCGACGGCTCGGGGCTCCCCACACC  
 TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGGCTGCACCTGCGTGCTGCC  
 CCGTTCAGTGTGACCCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG  
 CACCCCTATTTATGTGTATTTATGTATTATTTATATGCCTCCCCAACACTACCCCTTGGGGTC  
 TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT  
 TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTACACGG  
 CTGCTGTACCTTGGCTCCTGTCTGCTCCCGGCTTCCCTTACCCCTATCACTGGCCTCAGGC  
 CCCGCAGGCTGCCTCTTCCCAACCTCCTTGAAGTACCCTGTTTCTTAAACAATTATTTAAG  
 TGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

20211010 14:50:01  
 105235.0150

452/615

## **FIGURE 448**

MTLLPGLLFLTWLHTCLAHHDP SLRGHPHSHGTPHCYSAEELPLGQAPP HLLARGAKWGQALP  
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKLAF  
AECLCRGCIDARTGRETAALNSVRL LQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHV P VGC  
TCVLP RSV

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 112-121

**N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

**Leucine zipper pattern.**

amino acids 3-25

**Homologous region to IL-17.**

amino acids 99-195

10055356.01353



**FIGURE 449**

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT  
 GTGGCTGTTGCTGTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA  
 AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT  
 TGGGAAAGATGTGAAGATAGACCTGTTTGAAGAGAAGAGGTCGGGGGCGCCTGGCTACCAT  
 GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCATCCATCCTTTAAATCTGCACAT  
 GAAACGTTTTGTCAAAGACCTGGGTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT  
 ATATAATGGAGAGACTCTGGTATTGAGGAGAGCACTGGTTCATAATTAACTGATTAATTA  
 AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA  
 GTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTGAAAAAATTACT  
 TCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTGAAACCTTGCA  
 AAAGGCCGGCTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA  
 TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG  
 CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGTCTCAGGGCTTCTGCAGGCATCCAAAG  
 CAATCTTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA  
 TCCAAACAAAGATGTATGAAGTGGTCTACCAATTTGGAACGAGACTCGTTTCAGACTTCTATGA  
 CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA  
 TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA  
 ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCCTTAATACAGTTTTAAC  
 CACTGATAATTTCAGATTGTTTCATTAAACAGTATTGGGATTTGTGCCCTCTGTGAGAGAAAAAGGA  
 AGATCCTGAGCCATCAACAGATGGAACATATGTTTGAAGATCTTTTCCCAAGAACTCTTAC  
 TAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC  
 ATATCCTCACTATAAGCCCCCGGAGAAATGCCCTCTATCATTCCTCCATGATCGACTTTATTA  
 CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGAGCCACACACGC  
 TGCACCTCTTGCTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA  
 TGAGAAACTTAAACTGAACCTATGAAGTGACACACTCCTTTTTTCCCCTCCTAGTTTCCAAATGA  
 CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCATATTTTGGCCAT  
 TATCATTGTTTAAATAAAAGTAATCCCTGCTGGTCATAGGAAAAA

1052536.011502  
 20110.032501

454/615

## **FIGURE 450**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880  
<subunit 1 of 1, 505 aa, 1 stop  
<MW: 56640, pI: 6.10, NX(S/T): 4  
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPD KIA IIGAGIGGTSAAAYYLRQKFGKDVKI  
DLFEREEVGGRLATMMVQGGQEYEAAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL  
VFEE SNWFIINVIKLVWRYGFQSLRMHMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD  
DFLGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG  
GNKLVCSG LLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDIVLVAT  
PLNRKMSNITFLNFDPP IEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT TDNSDL  
FINSIGIVPSVREKEDPEPSTDGT YVWKI FSQETLT KAQILKFLSYDYAVKKPWLAYPHYKP  
PEKCP SIILHDLRLYYLNGI ECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEK LKTEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 196-200, 323-327, 353-357

#### **Tyrosine kinase phosphorylation site.**

amino acids 291-298

#### **N-myristoylation sites.**

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,  
119-125, 260-266, 384-390, 459-465

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

2025-10-27 14:58:50

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAAATGG  
CATCTTACCTTTATGGATGACTCTTTGGCTTTGGCCCTCTGTCCTCAATCTACTGTGTGTCC  
CGCCCAATGCCCCGATACATACCCGCCCTTTCTTCCACAAGAGACCCCTGCTCTACAGG  
TGTATTTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGTTTGGAGACCCCGA  
GTACAGAACTACTTCTTCTCCCTCTGGATGTGTCTCCACTTCCCTGGCCATGCTCTCCCTGGG  
CCCATCTAGTCAACAGGCCAGATTTCTCAGGGCTGGGCTTCAACCTACACACACACAG  
AGTCTGCCATCCACCAGGGCTTCCAGCACTTGTTTCACTGACTGTTCAGCTGTTCCAGCAAGACCT  
TGACCTTGAAGATGGGAAGTGCCTTCTTCGTCAAGAAGGAGCTGAGCTGCAGGCAAAATTTCT  
TGGGCAATGTCAAGAGCGTGTATGAAGCAAGATCTTTTCTACAGATTTTCCAACCCCTCCA  
TTGGCCAGGCGCAGGATCAACAGCCATGTGAAAGAAAGACCCAGGGGAGGTTGTAGACATAA  
TCCAAGGCTTGTACTCTGACGGCCATGGTTCTGTGTGAATCACATTTTCTTAAAGCCAAGT  
GGGAGAAGCCCTTTCACTTGTAATATCAAGAAAGAACTTCCATTCTTGGTGGGCGAGCAGG  
TCACTGTGTCAAGTCCCATGATGACCCAGAAAGAGAGCTTGCCTTTTGGGGTGGATACAGAGC  
TGAACCTGTTTGTGCTGCAGATGGATTAACAGGGAGATGCTGCTGGCTCTTTGTCTCTCCTA  
GCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACACTGATAAAGTGGAGCC  
ATCTCACTCAGAAAGAAAGTGATAGAGTGTTCATCCCGAGATTTTCCATTTCTGCTCCTTACA  
ATCTGGAACACTCTCCGAGATGGGCATCCAAATGCTTTGACAAAATGTGATTTT  
CTGGAATTGCAAGAGAGACTCCTTGCAGGTTTCTAAAGCAACCCACAGAGTGTGCTGGATG  
TCAGTGAGAGGCTCATGAGTGCACAGAGCTACCCACCAAGTTCTAGATGTCGATCGAAG  
ATGTTCCCTTCAATGCTTCTCTTCTTAATGAGACTTCTGATGATGATTACAATAAAG  
CCACAGATGATATTCTCTTTCTAGGGAAGTGGAATAACCACTAAATCCTAGGTGGGAAATG  
GCCTGTAACTGTGGCACATTGCTAATGCACAAGAAATAACCAACCACTCCTCTTATG  
TCTGAGGGTGCATTTGACCCAGTGGAGCTGATGCTGTGCAGGAGTGCCTTCAAGGCT  
CAATCACCACCAACCATCAACAGGGGACCCAGTCAACAGCCAACACCCATTACCCCATGCTAGT  
CCCTTTTCCCAAAATCTCCAGGTAACTAGCTTCTATGGGATGTTGTGGGTTTACCATTTTCT  
CATTCCTTGGAGCTCCCAAGATGGAATACGCCAACCCAGGTTAGGCACCTCTATTGCAGAA  
TTACAATAACACATTCAATAAACTAAATAATGAATTCAAAAAATAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

456/615

## **FIGURE 452**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET  
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESA IHQGFQHLVHSLTVPSK  
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVSTDFSNPSIAQARINSHVKKKTQGKVVD  
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT  
ELNCFVLQMDYKGDVAFFVLPSKGGMRQLEQALSARTLIKWSHSLQKRWIEVFI PRFSISAS  
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS  
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

TCCGGGCTCCCAAGGGGCTCTCGCGGGCGGGCTGGCAAGAGGGGACGATTCAGTGGACATCTCAGSAAAGACGGCG  
 CGCGCGGGGGGAGTACCGTGGCTGACCTGATCACTCACTCACTCGCGGGCGGGGGCCCCGGAGGGGCACTCG  
 GGGGGCGGACCTCGCGGGGCGAGCTCGCCCGCTGAGTTCGCGCGCAGGCCACTTCAGCCGCGAGCGCGGGACACCGTCT  
 GCTCTCTCTCCGAATCTCTGCGCACCGGATGGCGCTGAGAGACTGGCTCGCGGCCCTAGGGGCGCGCTGCGCG  
 CCTCGGACACCGCTCTGCTGCTCTGCTCTGCTCTGCTCTGCGACCGCGCGCTCGACACTGGGCGCTCGAGC  
 CCGCGATTCAGCTTGCTTGGGCTCTGAGAAAGGGCGCATTCCTCAGATTCTGAAGTGTGACAACTATCCAATCA  
 ACAGCGCTTCTCTGCTGAGCAGGATGGCAGGCCACTGTGATCGTGGTGCTCGAGAGGCCCTCTTGAATCACTAGTAGC  
 AAGCTCAGCTTCTCTCGCAGCGGGGAGTACAGGAGCTGCTTTTGGGTTGCGAGCGACAGCAAGAAAGAAACAGCACTG  
 AGCTTCAAGGGCAAGGACCTCAGACCGGCACTGTCAAACATCATCAAGATCTCTCTCGGCTCGACCGGCACTCAT  
 CTGTTCACTCTGGCAGCAGCACTCTCAGCCCGATGTGTACCTATCAACATGAGAACTTCACTTCCGCGAAG  
 CAGCAAGAGCGGAATGTCTCTTGGAAATGTGCAAGGGCGGTTGCTCCCTTCGACCAGCAATCTCAAGTCCACTGCTCC  
 TGGTGTGTATGCGAGACTCATCACTGGAACAGTCAACAGCTCAGAGCTTCGCAAGGAATACCCGCGCATCTCGCGAGC  
 TAAAGCCTTCGCGCCACCGAGACCGAGACTCTCCTCAACTCTGCTCGCAAGCCAGCTTTTGTGTGGCTCAGCCTTAC  
 ATTTCTTGAGAGCGCTGGGACGCTTGCAAGGCGATGATGACAAGATCATCACTTTTCTTCAGCAGCACTTGCCACAGAA  
 TTTGAGTCTTTTGAGAAACCACTTGTGTCCGCAATGCGCCGATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCTGCTTCGCAAGGCCAGGTGCTGTGCTGCTGCGCGCGACAGTGTATGCTTCCCTTCACT  
 GTGTGTCAGGATGTCTTACGCTCGGCGCCAGCCGAGACTGGGCTGACACCTTTATGTGGGTTCTCACT  
 TCCAGTGGCAGCGGGAATCAGAGAGGCTCGCGGCTGTGTGCTTCTCAATGAAGGATGTGCGAGAGATCTTC  
 AGCGGCTCTTCAAGGAGGATGAAACCTGAGACACAGAGGTGATCAACGTCGACCAACCCGCTGGCCACACCCCGC  
 CTGTGAGCGTGCATCAACAACTGCCCAGGGAAGGAAGATCAACTCATCTCTCGACTCCCGACAGCCGCTGTGCTG  
 AACTTCTCTCAAGGACCACTTCTGATGAGCGGCGAGCTCCGAAGCGCATGCTGCTGCTGCGACGCCAGCTTCGCT  
 GAGCAGCGCTGCGAGTACACCGGCTCTGGCTGGGTGACCAACTTACATGATGTCTCTTCTGGGCACTGGTGAAG  
 TCCCGGCTTCCAGGCTCAGGCTCAGGCTGGGGCCCCGGGTCACATCATGTAGGAGTCTGAGATCTTCTCATCGGGA  
 CAGCCGCTGTCAGAAATCTGCTCTGCGACAGCCAGGGGGCTGCTGTATCGGCGCTCACTCTCGGGCGTAGTGCAG  
 GTGCCATGGCCCACTGCAGCCTGTATCCGAGGTGTGGGAGTGCCCTCTCGCCGGCGGACCCCTACGTGCTGTGCT  
 GCGCGCTCCAGCTGCAGACGACTCGAGCTCTACACCGCTCACTGGTGCAGCTCAGGCGCCAGGCGGTGATACAGGAACTGAG  
 GGAGCCAGCGCCGAAGAGCTTTGACGCGGCTCTTGGTTGTGTCGCCGTTTGTATCAACAAGGGGGAAGAGCA  
 TGTGAGCAAGTGCAGTTTCAGCGCCCGCAACAGTGACATCTTGCGGCTGCCCTCTGCTCTCCAACCTGGGACCCGGA  
 CTCTGCTGTACGCAACGGGGCCCGGTAAGTCTGGCTCTGCGCACTGCTACCCACTGGGGAACCTGCTGTGCTG  
 GTGGGCAACCAACAGCTGGGGAGTTTCAGTGTGTGTCATGAGAGAGGCTTCCAGCACTGTGTGAGAGGCTATC  
 TGCCCAAGGTGTGTGAGAGCAGGGGTGGCAGACCAACAGATGAGGGTGGCAGTATCCGCTCATTTATCAGCACTA  
 TCGGCTGTGTAGTGCAACCTGCTGGTGCAAGGCGACTGGGGTGCAGACAGTTCCTATGGAAGGAGTTCTGTTGGT  
 ATGTGCACTCTTTTGTCTGGCGCGTGTCTCCAGATTTTATTTGTCTCTACCGGACCGGAACAGGATCTGATGAA  
 GTCTTCTCGAGCAGGGGGAATGTGCGACGTGCAACCGCAAGACTGCGCTTCTGCTCTGCTCTGCCCTTGAGACCGCG  
 CCATCTCAACGGCTATAGGGCCCTAGCACCGCGCTGATACCGAGGGGTACAGCTGGTCTGCTCAGACAGCCCCCG  
 GGGGCGCGAGTCTTCACTGATCAGAGAGAGAGGCACTCAGCATCCAGAGCACTTGTGAGGAGTTATCCGCGAGT  
 TGTCCCGCGCCCGGGCTGCTGCGCTTGGCTCGGAGATCCGTCAGTCTGTGGTGTGAGCAGTCACTTCAGAGAGCG  
 TGCCCTTGCTCTCAGGGGCTGTGAATCTGCGAGGGGTCAACTGGACCTCTCCCTCGGCTCTGCTCTCTGTTGGAAC  
 ACAGCGCTGGTGCGCGGCTCTGGAGGCTTGGAGAGCTGGCGCTGCTGCTCTCAGTTCAGTATGAGCAAGCTCTC  
 TACCTCCCTCAGATCCAAACAGCGCTGGCCCGAGAGGTCCTGGCCAAATATGGGGCGGCTGCTGAGTGTGTGGA  
 CAGTGCTCTTATGTAACTGAGCCCTTTGTTTTAAAAAAGTTCCAAATGTGGAATAGAACTAGAGGGGAAGAG  
 ATAGCATGCGATCAGCAGCAACCGGCTGCTCCAGTTTCATGGCTTCCAGTCCAGGGGTGCTGGGAGTGATCTCAAAGTGG  
 TGTGTCGAGAGAGATTTGAAACCTCTCAACACTGGGCTCTTCACTTCCAAATTATCCGCTGCGCCACCGGCTGC  
 CTTGCTCTCACTGCAGATTCAGGACACGCTTGGGCTGCGTGCGTTTCTGCTCTGCAAGCTCAGCCGAGGATGTGATGTT  
 TGTGTCGCTGTCCCAACACTCAGGAGCAGAGGGGTAGTTTGGCATTCGCGGCTCATACAGGCTCTGGGCTCT  
 GGACCCCAACTCTGGACCTTTCCAGCGTGATACAGGCTGTGGCCACAGAGAGGACGCGAGCTCAGGAGAGA  
 TTTTGGTGCAGATGTACGCTCTTCTCAGAAATCAGGGAAGAGACTGTGCGCTCGCTTCTCGGTTGTGTGCTGA  
 GAACCCGTTGTCGCCCTTCCCAACATTCACCTCTGCTTCATCTTTGAACTCAAAACAGGAGAACTAACTGCACCC  
 CTGGTCTCTCCCGAGTCCCAAGTTTCACTCCATCTCTCACTTCTGCACTTGAAGGATATCAACACTGCCCGCC  
 AGCAACAGGGGCGCTGAATTTATGTGTTTATATCATTTTATTAAGATGCACCTTATGTCACTTTTATTAATAA  
 GCTCTGAAGAATTATGTTTAAAAAATAAAAA

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
>>subunit 1 of 1, 837 aa, 1 stop
<<MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSLWLAAPGALPPRPPLLLLLLLLQLLPPTTAPRISLPLGSEERPFPLRFE
AEHISNITYALLSRDGTIVLVGAREALPSSNNLSFLPGGBYQELLWGADAEEKKQCSFKGKD
PQRDCQNYIKILLPLSGSHSLCTGCTAAFPSCMTYINMENPTLDEKGNVLLEDGKRCRCPFD
NFKSTALVVDGELTYGTGVSSFCQNDPAISRSQSLRPTKTBSLNLQWDPAFVASAYIPESLGS
LQGDDDKIYFFPSETGQFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRDD
GFPFNVLQDVFTLSPSPQDWRDLTFLVGYFTSQWHRGTGSAVCFMTKDVQVRFSGLYKEVN
RETQQWYTVTHPVPTPRGACITNSARERKINSLLQDPDLVNFVKDFHLMQDQVRSRMILLQ
PQARYQVAVHRVPLGHMLTYDVLFLGTGDGRHLKAVSPYKRWIIIETQLFSSGGQPQNLLLD
THRGLLYVAHSHSGVQPMANCLSYRSCGDCLLARDGPCVMSGSCSHVSLYQPLATRPWIQ
DIEGASAKDLCSSAVVSPSFVPTGPKCSBQVQFQPNVTNLCAFLLSNLATRLWLNGGAPVN
ASACHVLPDLGLLLVGTQQLGEPQKCEVQFQQLVASCEPVEDGNADQTDTEGRSVPV I
STSRVSAPAGGKASWADGRSYWKEFLVMCTFLVLA VLLPVLFLLYRHRNSMKVFLKGECASV
HPKTCPPVLPPTLRPLNDGLPSPSTPLDHRGYQSLSDSPPGARVPTSEKRPLLSIQDSFVEVSP
VCPRPVPLRSLGSLRISGVV
```

**Transmembrane domains:**  
amino acids 23-46 (type II), 718-738

**FIGURE 455**

TAAGATGAGGGCATCCCTCACGTTACACCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC  
AAGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG  
AAACAGAAATTTCAACGGGAAGCTGGTTTGCCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT  
ATTTGGGTTTAGGGACTGATCCCTTGCACTTTACTTCTGGATCACCATGAATGGCCAAGATGG  
TGGCAGAACACGCTCTGGACCCCTGAGTTAGAGACAATGCAAAATGTTGGATTGGGTGTAATTCT  
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG  
GGAACCGTGTAAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA  
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT  
CCCACCATGGCTGCCACTTTTTTATCTATTGGAGAAAAGACCTTGATATAAATTCGAGGCC  
GAGTGACTAACGCTCTGTCTCACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC  
CACTTTTTCAGTACACTTCTCACTCAGCTGCACCTTACACTTCTCACTCAGGTGCACCCCT  
TCTGTCTCCTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGTATTGGCCACACTGGGTGC  
CAGCTCAGCAGCCCCCACCTCTCTTTATTTCTCTCCAAAGCTGGTCTTTCTGACTATCATTTGT  
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAAGAGACACACGGGGTGAC  
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC  
GAGGCCATGGCACTCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC  
GTCCTGCAGCGAAGTCTCTGTCTGAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT  
ACCGGGGTGGTGGTGTCTGGCTTGCACTCTGGCCAGTTTCAGAGAAAAGTTGCAGAGATCAGGG  
GCCAAGGATGTATAGCCCCAGGTGTCTCCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG  
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCTAGTTCCCTCACTCCA  
GCGGGCTCCCTCACTGCACAGAACCACCCCTTCTGTGTGGGCACCTGCTGACCACACAGATG  
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG  
GTTCAAGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCCCTA  
TCTCACCGTTACTTCAGTTACCTTGCAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC  
CAGGGTTTAAAGCCGGCCATGCCCTCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC  
CCCAAACTGAAGGAAGGAGATCCTTCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA  
AAGCTTGAGAAGATGGACCCCTTGGCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGGTGTG  
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC  
TTGGGCTGCGCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT  
GTCCTAACAGCAGCCTGGAGCTACCCCAATCCCTACAGCCTGACCCTCTCATTCATCA  
GATCTCGTGCCG

460/615

**FIGURE 456**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPORTGSRANWVFATLGASSAAPH  
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSSLATTRHPRPW  
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 64-78

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 103-107

**N-myristoylation sites:**

Amino acids 53-59;94-100

1005336.01501



**FIGURE 457**

CCGCGCGCCCCCTGGCACTCAATCCCCCGCC**ATG**TGGGGGCTCCTGCTCGCCCTGGCGCGCTTC  
 GCGCCGGCCGTCGGCCCGGCTCTGGGGGGCCCAAGAACTCGGTGCTGGGGCTCGCGCAGCCC  
 GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGCG  
 GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCAGTTCATCAAGAAGAAAAGGTC  
 ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTCCCGGGCCC  
 CTTGTGACCCCCACTCCAGCAGGGACCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTCT  
 CCTTTGGGCTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC  
 TTTGGTCTTGACCACACCGAGGACGGCTCAACATTCATTCAGGCCCTGGAGGACGGCGATCTA  
 TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG  
 CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTGTCTGGAGGTATGACTGG  
 GTCACATCATACAAGGTCAGTTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCA  
 AGCAGTGGGATGGACGAGTATTCTGCCCAATTTCAGACCCAGAAACTCCAGTGCTGAACCTC  
 CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCAGACTGGCTCCAGGGAGGC  
 GCGCCTTGCCCTCGGGCAGAGATCCTGGCCTGCCCCAGTCTCAGACCCCAATGACCTATTCTCT  
 GAGGCCCTGCGTCGGGATCCTCTGACCCCTAGACTTTTCAGCATCACAATTACAAGGCCATG  
 AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAATCAGCCGCATCTACAGCATTGGG  
 AAGAGCTACACGGGCTGAAGCTGATGTGATGGAATGTCCGACAGCCCTGGGGAGCATGAG  
 CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGTCATGGGAACAGAGCCCTGGGGCGGGAG  
 TTGCTTCTGCTCCTGATGCAAGTTCTCTGTGCCATGAGTTCTGCGAGGGAACCCACGGGTGACC  
 CGGCTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCCTGATGGCTATGAGATC  
 GCCTACCACCGGGTTTCAGAGCTGGTGGGCTGGGGCCAGGGCCGCTGGAAACAACAGAGCATC  
 GATCTTAACCATAAATTTTCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG  
 GTGCCCCACATCGTCCCCAACCATCACTGCCATTGCCCCACTTACTACACCTGCCCAATGCC  
 ACCGTGGCTCCTGAACCGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCCTTTGTGCTAAGT  
 GCCAACTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTTCAGATGACTCGCACCCCGTGG  
 GCTGCCCGGAGCTCACGCCCCACACAGATGATGCTGTGTTTCTGCTGGCTCAGCACTGTCTAT  
 GCTGGCAGTAATCTGGCCATGACAGGACACAGCGCCCGACCCCTGCCACAGCCAGGACTTCTCC  
 GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC  
 AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCCTCAC  
 GAGAATGAATTGCCCGAGGTGGGAGAACAACAAGACGCCTCTCACTACCTCGGAGCAG  
 GTGCGCATGGGCTATGCAAGGATGGTGAGGGACAAGGACAGCGAGCTTGGGATTTGCTGACGCT  
 GTCATTTGCCGTGGATGGGATTAACCATGACGTGACACACGGCGTGGGGCGGGGATTATTGGCGT  
 CTGCTGACCCAGGGACTACATGGTGACTGCCAGTGCCAGTGGCAGGGCTACCATTCAGTGACACGG  
 AACTGTGCGGTCACTTTGAAGAGGGCCCCCTTCCCTGCAATTTCTGCTCACCAGACTCCC  
 AAACAGAGGCTGCGCGAGCTGTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCGAGGCGC  
 CTGAGCGGGCTAAGGGGACAGAAGGAT**TGA**TACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG  
 ACCTGTCAAGACGGGAGGGGAAGAGTAGAGAGGGAGGGACAAGTGAAGAAAAGGTGCTCAT  
 TAAAGCTACCGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

462/615

## **FIGURE 458**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60, NX(S/T): 6
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVMRYDWVTSYKVFQFSNDSRTWWSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRVYAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAVHRGSELVG
WAEGRWNNQSIDLNNFADLNTPLWEAQDDGKVPVHIVPNHHLPLPTYTTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGEVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHVDVTTAWGGDY
WRLLTPGDYMVMTASAEGYHSVTRNCRVTFEEGPFPFCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

[illegible]

## FIGURE 459

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCCTACAAACAGCGTCAGAGAGAA  
AGAACTGACTGAAGACCTTTGAGATGAGCAAGAAAGTCTCCCTCTGATCAGACGCCATCTTGGCAG  
GGCTGTTGGTTTCCCACTCTCTCAGAACCGAGAACGAGAAAAAAGAGTATCAGTGAACAGCA  
TGAATTAGCTTCAGGGTTTTTGTGTTCCCTTACCCATATCCATTTCGCCACTTCCACCAAT  
TCCATTTCCCAAGATTTCATGTTTATAGACGTAAATTTCCCTATCCAAATCACTGAACTGCCCC  
TCAACTCCCCCTTCTGACGAAAGTAAACAGAAAGGATAAGTCAGATAAACCTGGTCACT  
GAAATTGAAATTGAGCCACTTCTTGAAGAATCAAATTCCTGTTAATAAAAGAAAAACAAAT  
GTAATTGAAATAGCACAGACATCTCTGATCAATATCTTTAGTGATCTTCTTAATAAACAT  
GAAGCAAGAAATTTTGGTTTCTTAATTTCCCA

464/615

## **FIGURE 460**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290  
><subunit 1 of 1, 85 aa, 1 stop  
><MW: 9700, pI: 9.55, NX(S/T): 0  
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPFRPLPPIPFPRFPW  
FRRNFPPIPIPESAPTTPLPSEK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Homologous region to B3-hordein:**

amino acids 47-85

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-20

**N-glycosylation sites:**

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 80-84

**N-myristoylation sites:**

Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;  
538-544;560-566;637-643

**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

**Zinc carboxypeptidases:**

Amino acids 391-411

AGCAGGAGCAGGAGAGGGGACA**ATG**GAAAGCTGCCCGTCCAGGTTTCATGTTCCCTCTTATTTCTC  
TCTCAGCTTGAGCTGGCTGCGAAGATTGCTGCGAAGTTGAGAAATCTCAGATGGTCTGGT  
GCTGCCAGAGAACCCACGCTGGCTCAGATAGTCCAGCTGCCATGGAAATCATTCGTGCCACT  
GAGGTGGCTGTATAGGCTTCTTCCAGGATTTAGAAATACACAGAGCTGCCATCTCATATGC  
ATTGTTGCAAAAAATCCGAGGCGTGCAATTGGGATCAGCAGTGATTCTGAGGTTCTGACAAC  
ACAACAATCATCTGGGAAGACCATCTGCCTCTTTTCGCTGGTAGACAATGAACAACATGAATTTA  
GAGGACAGAAAGCATTAAGAAAGCATTGATGCGACCAAAATGAGCGCGTTTCATTGAGATCAACAGC  
CTCCAATGGTGACAGATACAACCCGTGACGTGATGGGTTATTACCAAGCGTAATTTACG  
ATTTCATCTCCTCCTGATAATGAACAAGGCGCTCCCCAGAGTATGAAGAAGACATGCACAGATAC  
CAGAAGGCAAGCAAGCTCTTCCAGGGGGAAGATTTCTTTAATCTGGTGAGCAGGTGGTATGAAA  
GAAATGGGAAGGTGATATCATTTTTCACAACTAAAGAGATCTCAACTGCCAGCTTTGGCAATT  
TACCAGACTTCTAGATGACGAGTGGGATACACTGCCACAGAGAAGTTTCCGTAGAGCATGTG  
AAAAAATCTTGTGATGGATCTCTTAAGTGGAAAAATTTGTAAGAAAAAATCTGTAATCAGAAGGA  
AAGACTCAAAGGCTGAACCT**TGA**CTTCTCTTGGAACTACATATGGCCAGGATATCTACTTTA  
TGCAAAGTAAAAAGGCACAATCAAAATCTCAGAGACATAAAACAAGGATACACTAGGCCCTGC  
CAACCAACACACACAGCAGCTGCACACACGCGACGCGTGACACACACAGCGCACACAC  
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTCTCTCTCTTTTAA  
TTTCAATCTCTCATCCCTATCCAATTTCTCTTATCGTGACATCATATCTGTAGAGCCCAT  
CTGTAAACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCTCTATGAAGAAGGCA  
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGTTTGTATATGACATGACTT  
ACACACAATGTTCTCTGCTCTTTTAAAGTTACCTAAGGTTGAAATCTACCTCTTTTCAT  
AAGCATATGTCGCTCTCTGACTCAGGATCAAAAACAAGGATGGTTTTAAACAACCTTTGTGA  
AATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC  
ATGTGAAAACCTCATCTGTTGGTAGATCTCCAACCTCCCTATGTAATCAACAACCTGCAATA  
TAAATAAAGGAAGCAATCATGTTTATA

466/615

## **FIGURE 462**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDPVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSFGISDSEVLTHYNITGNTICLFRILVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSCMKENGKVISFFKLKESQLPALAIYQTLDDWDWTLPTAEVSVVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

467/615

**FIGURE 463**

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAGG  
GTGCCCCGCACAAACCAGACGCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCC  
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC  
CCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG  
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG  
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATACATCACA  
AAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC  
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCCTACCCAGCCAAGAGGGGCAG  
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG  
AATATCCACTAGAGGAGCCGACCACCTGAGCCACCAGTTAATCTCACATACTCAGCAAACTCA  
CCCGTGGGTGCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC  
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT  
GCAGAAAA

205110.9852501

468/615

## **FIGURE 464**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLLTALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

**Signal peptide:**

amino acids 1-22

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615



[illegible]

470/615

## FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788  
><subunit 1 of 1, 813 aa, 1 stop  
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRRARGTPLL LLLLLLLLWVPVPGAGVLQGHIPGQPVTPHWVLDGQPVWRTVSL EEPVSKPDMGLVALEAEGQ  
ELLLELEKNHRL LAPGYIETHYGPDGQPVVLA FNHTDHCYQGRVGRGFPDSWVVLCTCSGMSGLITLSRNA SYLL  
RPWP PRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT  
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEVWTERDRSRVTQDANATLWAF LQWRERGLWAQRPHDSAQL  
LTGRAFGQATVGLAPVEGMCR AESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA  
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECD CGPGQCECRDLCCFAHNCS  
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPDPVYLLDGS PCARGSGYCWDGACPTLEQQ  
CQQLWGPQSHPAPEACFQVNSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCGGKPSLLAPHMV PVDSTVHLD  
GQEVTCRGALALPSAQLDLLGLGLVEPGTCCGPRMVCQSRRCRKNAFQELQRCLTACHSHGVCSNHNHNCAPGW  
APPFCDKPGFGGSMDSGPVQAENHDTFLLAML LSVLLP LPGAAGLAWCCYRLPGAHLQRCSWGCRDPACSGPKD  
GPHRDHPLGGVHPMELGPTATGQWPPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSCLW

### Important features of the protein:

#### Signal peptide:

Amino acids 1-27

#### Transmembrane domain:

Amino acids 702-720

#### N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

#### Tyrosine kinase phosphorylation site:

Amino acids 236-244

#### N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;  
400-406;402-408;454-460;504-510;510-516;517-523;580-586;  
601-607;661-667;687-693;717-723;719-725

#### Amidation site:

Amino acids 200-204

#### Neutral zinc metalloproteases, zinc-binding region signature:

Amino acids 342-352

Downloaded from www.nrj.com

**FIGURE 467**

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAACA**ATG**CAGCTCGGCACTGGGCTCCTGC  
 TGGCCGCCGTCTTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAAGTGCACGG  
 GCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCACTG  
 CCACCCGGGTCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATAGGCT  
 GCCCCGATATCCCCAGCCTGGGGCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGACCAGCC  
 TCTGCAACCATGACT**G**ACGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCCACAGCCCC  
 CACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCACCTCTCCCG  
 GCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTAGGGAAGTCTGCGTGGAGTCTTGCTCTCA  
 ATCTGCTGCCGTCCAAAGCCTGGGGCCCATCGTGCCTGCCGCCCTTCAGGTCCCACCTCCCC  
 ACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

472/615

## FIGURE 468

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLA AVL SLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVT TATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYVSIACCQTS LCNHD
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 469**

**C**ATGGAGCCTCTTGCACTTACCCGCTAAAAATGTTCCGGGCCAGAGCAAAGGTATTTGCAGT  
 TTTGCTGTCTATAGTTCCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC  
 TAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTCTCTGGA  
 AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG  
 AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTGGC  
 TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC  
 AAGAAAAAACTACGGAGTAACTTTCCTCATCTTCCACAAGATTAAAGATTCTAGGATCTGAAGG  
 AGAACCTGCATTAGATTCTTGTGTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA  
 GTATCTTGTCAACCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTTGAAGT  
 CATCAGGCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG  
 AAGATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA  
 AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCCTT  
 CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTTAAATGTGGCAATGAAGGATTTTT  
 TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCAGGATGAGGATGTTACCCAAAG  
 CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACTCTTCTCTGACCATACT  
 AAAGAATTCAAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT  
 CTAGGACTGTACTTGATGAAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT  
 GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACAAATGTT  
 GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC  
 AGGATTTTGTTTTTCTTTTTAAGTACAGGTTCCCTAGTGTTTTACTATAACTGTCACTATGTA  
 TGTAACTGACATATATAAATAGTCATTATAAATGACCGTATTATAACATTGAAAAAGTCTT  
 CATCAAAAAAAAAAAAAA

474/615

## FIGURE 470

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTFLFLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGVSLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFIHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEPIEV
IRPDIAALVRQVIIKKEDL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

2025-03-26 10:00:00

## FIGURE 471

GCCCTAACCTTCCACGGGCTCAGCTCTTTGGAGCTGCCATTCTCTCCGGCTGCAGAAAGGACGCGCGCCCTGCCG  
 TCGGGCGAAGAAAGAAAGCAAATCTTGTCGGGAGGGTTTCGTCTCACTCAACCTCTCTCCCGCAAACCTTAACCTCTCT  
 GCCCGGGCCATCCCTAGACAGAGGAAAGTTCTCTGCAGAGCCGACACGCCCTAGTGAGTCTGGGGCAGGCGAGCGGC  
 GCTGTGCTGTGSAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCAACCGTCCGCGGGC  
 ACCGGGTTCGGCTGCGGAGGTGGAACCGACAGTTTTCGAGGCTCGGCTGCAAGTGGCTCTCTCTCCCGCGGTT  
 TTGTGTTAGTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAGAGAGCCCTCAGAGGTCCGAAGAGCGCTGCG  
 CTCTACTCGCGTTTCGTCTTCTCTCTTCTCGGTTCCCTACTGTGAATTCGACAGCGACATTTACAAAGGCGCTCCG  
 GGTCTCAACGAGACCGATCCGACAGCGTTTGGCCCGTTCGTGCTATTGCATCGGGAGCCCCGAGCACCGCGGAA  
 GGACTGGCGGGTGGGTAGGGAGGTGGCGCGCGCGCATGCGAGGTTCCCGAAGGCCGACCTTGGCGCTGCAGG  
 AGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTTCAGTTTCGCCGATGGGAAACCCGAGACCAAATCCTTGA  
 TTGGCAGTATGGAGTTACTCAGGCGCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTCAACGCGTACAGCCA  
 CAGGTGGAAAAGAACTTGGACTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTGGGCCAAGACTCTCTGA  
 GCCAGAGACCTTCAACAGCTTGTCTGTGATGATGGGCAGGACAAACACTCAGATCGAGGAGGATACAGACCA  
 CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCGGGATTATGGGTGAACATAGACCAAAT  
 GGAAAAGATAAAGTGAAGATTATGGAATATTGTCCAATCTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT  
 CGATTTTCCATTTTATGGCCACTTCTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT  
 CGTACATCGAATGCTAAACGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCAGTGTATCCAGAAA  
 TTCAACTGTGCAGATATTTGTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA  
 TAACCTGGGAAGCTTCAATTCCAGGCAACCGTGTCTCATGGATGGAAGAAATCATCTTTGGATACAAAGAAATTC  
 TGTCTTTGGTACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGAGTCTCCGATGCAATTTGTCTGTGTTCCA  
 CAGGATCCAAACAAATTCCTCAATTTGCAAGAAGAACAAATTTATGAATACCAACGAGTACAGCTACAAATGTCAAA  
 AATTACCAACTTTTCGGCTGTGGAGATGACCCCAATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCTGTGT  
 ATCTTCTCAGATTGGCTTCACTGCAGTTGGTGTAGTAACTTCAAGATGTTCCAGTGGATTTGATCGTCTCG  
 GCGAGGACTGGGTGACAGTGGATGCGCTGAAGAGTCAAAAGAGAAGATGTTGTGAGAAATACAGAACCAAGTGAAC  
 TTCTTCTCGAACCACCACAACCGTAGGAGCGCAACACCACCAAGTTTCAGGTCCTTAATACCAACAGAGAGCAGT  
 GACTTCTCAGTTTCCCAACAGCCTTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAGATATATGGAGC  
 TTTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGCCTCATCATTTGGAACTCTCATCTCT  
 GGTCTCATTTAGCCACAGCCATTCTTTGACAGTCTATATGTATCACCAACCAACATCAGCAGCCAGCATCTT  
 CTTTATTGAGAGCGCCCAAGCAGATGGCTGCGATGAAGTTTAGAAGAGGCTTCGACATCTTCCCTATGCTGA  
 AGTTGAACAGTTGGAGAGAAAGAGGCTTTATTGTATCAGAGCAGTGCTAAAAATTTCTAGGACAGAACACACC  
 AGTACTGTTTACAGGTGTTAAGACTAAATTTTGCTATACCTTTAAGACAAACAAACAAACACACACAAAC  
 AAGCTCTAAGCTGCTGTAGCTTGAAGAGACAAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA  
 AAAAATAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCTAGTGGAAATGTCTATCTATAGTTCACT  
 CGGACATCTCCCGTGGACTTATCTGAAGTATGACAAGATATAATGCTTTTGGCTTAGGTGACGGGTGCAAGG  
 GGATCAGAAAAAAAATCATATAAGGCTTTAGTTCATGAGG

**FIGURE 472**

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTVQAFPHTEEEVEVD SHAYSH  
 RWKRNLDFLKAVDNTRASVGQDSPEPRSFDTLLLDGQDNNTQIEEDTDHNYISRIYGPSDS  
 ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFFFYGHFLREITVATGGFIYTGEVV  
 HRMLTATQYIAPLMANFDPBSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD  
 GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQIPNVRRTIYEHYHVELQMSKIT  
 NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHRQDWDVDSGCPEESKEK  
 MCENTBPVETSSRTTTTVGATTTQFRVLTTTTRAVTSQFPFTSLPTEDDTKIALHLKDNASTD  
 DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAAISFFIERRPSRWPAMKFRR  
 GSGHPAYAEVEPVGEKEGFIVSEQC

**Important features of the protein:****Transmembrane domain:**

amino acids 454-478

**N-glycosylation sites.**

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 297-301, 492-496, 503-507

**N-myristoylation sites.**

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,  
 455-461



**FIGURE 473**

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCATGCAACCCCG  
CGCCCTGCGCCCTTAACAGGAGCTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT  
GCAGCCTCCAGGTGGCTGGGAAGAACTCTCCAACAATAATACATTGTATAAGAAAGATGGC  
TTTAAAGTGCTACTAGAACAAGAAAAACGTTTTTCACTCTTTTATTAGTACTAGGCATTTT  
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTACAGGATCGGTCTGG  
AAACTGTGTTCCCTGCAACCAGTGTGGGCGAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC  
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC  
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGTGAACCGCTTTTCAAGAGGCAAAATTGTTC  
GCCACCACTGATGCCATCTCGCGGGACTGCTTGGCCAGGATTTTATAGGAAGACGAAACTTGT  
GGCTTTTCAAGACATGGAGTGTGTGCTTGTGGAGACCTCCTCCTCCTTACGAACCGCATGT  
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCTCCAGCCACGGGACACGGCGCTG  
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTGCATC  
TATTGTAAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTAG  
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC  
TGCTGCCAGTGCAGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCGCTTGCTCCCATCATG  
TGCTGTGAGGAGGCTGCGAGCCCAACCCGGCGACTCTTGGTTGTGGGTGCATCTCTGACGC  
AGTCTTCAAGCAAGAAACGCAAGCCAGCCGGGAGATGGTGGCAGTTTCTTCGGATCCCTC  
ACGCACTGCATCTGTGGCGAGTTTTTACAGTGCCTGGCTCTGATGCAAGATCCCATGGGTGGT  
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAAT  
CCGAACCTTGAAGCTCAAGCTCTTTGGATTCAAATAGCAGTCAAGATTGGTTGGTGGGGCT  
GTTCCAGTCCAGTCTCATTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAAC  
ACATCGGTAGAAATCAGCATCAACTCAGGATGCATTAACATAGAGAAGCCAGCTAGATCAGGAG  
AGTGGCGCTGTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC  
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTAGGCTTATGGACTGA  
GCAGTCTGGACCTTGATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG  
AAGCCTTTAGCCAGTGTGCTTCTGAGCCAGACCCAGCTGAAGCTGAAACCTCAATGAATAACA  
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCATACATGAGAAGCTTCTCTGCCAC  
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCATGAGATTGTGGACATATAACAA  
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA  
GAGTATACCTTTTCTTTCCAGAATAATTTTCATACCGCCTATGAAATATCAGATAAATTACCT  
TAGCTTTTATGTAGATGGGTTCAAAGTGAGTGTGTTCTATTTGAGAAGGACACTTTTTCATC  
ATCTAAACTGATTGCGATAGGTGGTTAGAAATGGCCCTCATATTGCTTGCCTTAACTCTGGGTT  
TATTAGTAGAAGTTTACTAGATCAGAGGAATCAGACAGGAGAGTAGCTTTTCCAGATCC  
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA  
GGGATGTGGTGCAGAAAGGGCAGCCCATTTGCCAGAAATTAACACATATTGTAGAGACTTTGTA  
TGCAAGGTTGGCATATTTATATAGAAATTAGTTGCTATAGAAAACATTGTTGTCATCTGCTCC  
TCTGCTGAGCTTAGAAGGTTATAGAAAAGGGTATTTATAACATATAATGACCTTTTACTTG  
CATGTATCTTATACATAAAGGCTTTAGAAAATTACAACATATCAGGTTTCCCTACTACTGAAGT  
AGCCTTCGTGAGAACACACACATGTTAGGACTAGAGAAGAAATGCACAAATTTGATGGGTTT  
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACACGAGCAATTTGCTGCTCCTTCCAAT  
TGTGTAAGATTAGTACCATATCTCCTACTTTAGCCATCCGGTGTGGATTGTAGAGGAC  
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCTACCATCTACACATTAGCATTTGCTCTAGAG  
CTAAGACAGAAATTAACCCGTTTCAGTCACAAAGCAGGGAATGGTTCACTTTACTCTTAATCTT  
TATGCCCTGGAGAAGACCTACTTGAACAGGACATATTTTATAGCTCTGAACATCAGTATGT  
TCGAGGGTACTATGATATTTTGGTTTGAAGTTGCCCTGCCCAAGTCACTGTCTTTAACTTTT  
AAACTGAATATTAAATGTATCTGTCTTCTCT

478/615

## **FIGURE 474**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210  
><subunit 1 of 1, 417 aa, 1 stop  
><MW: 45305, pI: 5.12, NX(S/T): 6  
MALKVLLQEKTFFFTLLVLLGYLSCKVTCESGDCRQQEFDRDRSGNCVPCNQCGPGMELSK  
ECGFGYGEDAQCVTCLRHFRFKEDWGFQKCKPCLDCAVVNRFOKANCATSDAICGDCLPG  
FYRKTCLVGFQDMECVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT  
VLLALLILCVIYCKRQFMKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD  
SVQTCGPVRLLPSCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI  
CGEFSDAWPLMQNPMGGDNI SFCDSPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV  
PVQSHSENFTAATDLSTRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-25

#### **Transmembrane domain:**

Amino acids 169-192

#### **N-glycosylation sites:**

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 200-204;238-242

#### **Tyrosine kinase phosphorylation site:**

Amino acids 207-214

#### **N-myristoylation sites:**

Amino acids 55-61;215-221;270-276

#### **Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 259-270

#### **TNFR/NGFR family cysteine-rich region proteins:**

Amino acids 89-96

105556.01502

**FIGURE 475**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCAGGTGGCCAGCTCAGCA**ATG**GCAATG  
 GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA  
 GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATGAAG  
 CTGCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT  
 CGCGCGCCGGTGACCTGGTGCGGAAGGGCTGCTGGACCGGGCTCCTGCGGGCCAGACGCAA  
 TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC  
 AACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCGGACG  
 CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG  
 TCCCGACGAGTCCAGTGTACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA  
 GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACACCCGAG  
 GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC  
 AACAGGAAATCCATGACCAGCCCTTACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA  
 CAGGTCTGGCCCTGCTCCTCCAGTCTCCTGCTGGTGGGGCTCTCAGCA**TAG**ACCGCCCCCT  
 CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCTATCACATAGC  
 TCACTGGAAATGATGTTAAAGTAAGAATTGCAAAA

480/615

## FIGURE 476

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAPHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-19

#### Transmembrane domain:

amino acids 233-251

#### N-glycosylation sites.

amino acids 120-124, 174-178

#### N-myristoylation sites.

amino acids 15-21, 84-90

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

CCACCGCTGTCGGGACAGCTAACTTAAAGAGAGAGCTTTAGCTGCACAAAGATTGGGAAAGGGAAAGACAAAAA  
AGACCCCTGGCTGACACGGCGTGTAGCTGAGCGGTTTCTACTGCTGTTCTTTATGCTGGGAGCTGTGGCTGTAA  
CAATAGGAATAAAGCTGTACAGCAGCTATGGCGTGTACAGAGATTTGTCTTCCCAAGACAAAGCGAAGTCTGT  
TCTTTTCTTTTGTGGGAGTGTCTTGGCAGGATTCGGGTTTGGACGTTATTCCGTGTACTAGGAAACAGAGAA  
AGATCTCTTTGTGTCAATCTGSCAAAGATTCTGGGACTACAGAGAGGGAGCTGCGTGCAGAGGGAAACAGGGT  
GGTTTCCGATGATGACCAACATACTGCTCTCTGGATTCACATACCGGGAAATTTGTCGACAAATAGGAAATCTGGA  
CCGAGAGAAAGCTGTGTGGCCCTTAAAGAGCCCTGTATGCTGTATTTCAAATTTTAATGGATATCCCTTCAGAT  
TACCGGCGTGTAGCTGAGAGTCAGGGATATAAATGATACCGCGCGGATATTTCAGGACAAAGAAAGATCTTCAAT  
AATACAGAAATACAGAGCTGAAGGACAGCATTTAGATAGGAAGAGACAGGATCCAGATGGAGGAGCTTAAACGG  
TATCCAAAATACACAGTACGCCCAACCTCTTTTTCATATACGAAATATGTGGCGGTGATGAAGCATGATATA  
TCCAGAGCTAGTGTGTGGAACAAGACGTGATCGGGAGAGACAGGAGAGCTCAGCTTAACCCCTCAGACGCTGGA  
GTGTGGGTTCTCCATCCAGTCTGGGACCTCTACTGTACAGCATGTGTGTCTTGGAGCTCAATGCAATCCGCCCA  
GTTTCCCGAGGCTGTGTAGAGACCCAGGCTCCAGAAACACGCCCACTGGGTTCTTATTTATAGGATATGGCG  
AGAGATGTAGACTGTGGAGTCAACCGCGGAAGTATCTTATTCATTTTATGATGCTCAGAAATATTAATCGAACAC  
CTTTCAATCAATCCTTTTCTGGGGAATCTTCTCAGAGAAATGCTGTGATTATAGCTGTATAAATCTTCAACAA  
ATAAATATACAGCAATGACGCTGTGGAGTCGTTCTCAGAGATGTAGGGTTTAASTGGAAGTATTGGACACGAA  
TGACAACTCCCTCAGCACTGATGTATCATTTTCCAATCTGTGTGAGAAATTTCTGTAGACGCGCTCGTCCG  
TGTTTTTAAGATTATGACAGAGACTCTGGAGAAATGGAAGAGATGTGTTGCTCATCATTCAAGAGATCTGCCATT  
CTACTAAACCTTCTGTGGAGAAATTTTACATCTTAATACAGAGAGGCGCTGGACAGAGATCAGACGCGGA  
GTACAACATCACTATCACGCTCAGCTGACTGTGGGAGCCACAGGCTGAAACACGAGACAAACATAACGGTCTGT  
CTCGAGCATATGACAAAGCCGCCCGCTTACCACAACTCTCTCAACCTGTTCGTCCGAGAGAAACAGCCGC  
CGCCCTGCACATCCGCGAGCTCAGCGCCACAGACAGAGACTGGGCAACAGCCGCAAGCTCACTACTGCTGCT  
CCGCGCCAGACGCCGAGCTGCCCTGCCCTCGTGTCTCATCAACGCGGACAGCGCACCTTGTGCCCT  
CAGGTGCTGACATCAGGAGCCCTGAGGCTTCTCAGTTCCGCTGGGCGCCACAGACCCGCGCTCCCCGCGCT  
CAGGACAGAGGCGCTGTGCGCGCTGTGTGCTGAGCGCCACAGCAACTCGCTCTGTGCTGATCCGCTGCA  
GAAAGCTCTCGCGCTCTGACAGAGCTGTGTCCCGGCGCGGACGCGGCTACTGTGTTGACAAAGTGTGTGG  
GTTGACAGCGCATCTCGGCAGAAAGCCTGTGTGTGTGTCACAGCTCTCAAGCGTCCAGGAGCCCGGCTGTCTGT  
TGTGTGGGCGCAATGGGGAGGAGCGCTCAGCCAGCGGCTGTGAGCGAGTCGAGCGACAGCAAGCAGGCTGTCTGT  
GGTGTCTGTCAAGGACAAATGGCGAGCTCTCTGCTCGGCCACGCGCAAGCTGCACTGTCTGTGTTGACAGCGCT  
CTCCAGCGCTTACCTGCTCCCTCGGAGGCGGCGCGGCGCAGGCGCAGGCGAGGCGGCTTGTCTACCGCTCTA  
CAGTGTGTGGGCTGTGGCTCGGTGTCTCTGCTCTTCTGCTCTGGTGTCTCTGTTCTGTGGCGGTGCGGCTGTG  
CAGAGGAGAGGCGGCGCTCGGTGGTGTGCTGCTGCTGCGGCGAGGCTCTTCTTCCAGGCACTCTGTGTGAGCT  
GAGGGCGCTCGAGACCTGTCCAGGAGCTACAGGATAGAGGTTGTCTCAGCGGAGGCCCGGGGACAGTGAGTT  
CAAGTTCTTGAACCCAGTATTTCCGATATCAGGACAGGGGCTCGGAGAGAGGGTTGAAGAAATTTCCACTCT  
CGAAATAGTTTGGATTTAATATTTCAGTAAAGTGTGTTTTAGTTTTCATATATTTGTGTGTGTTATAGTACA  
TGTTTCTATATGTTTACTTTTAAATCTCAAATTAAGTATTATGAACTCAAGCACTATTTTCAAGTATATA  
CCCTCGTGGTGTTTACAAGTGTTCATCATTTTGTGATATATACAACTGGGTTTAAATTAATGAGTATTTTTTT  
CTAAATGATAGTGTTAAGGTTTAAATCTTTCACATGCCCAAGAAATTTGATCATATTATATCTCATTCACAGAA  
ATCAGAGTGTGATTCATTTCCAGGCTGTGATCTCATGATCTAATCACTCTGTCTAAGTGTGATCTGCTCAT  
TTTAGAGAGGATCATCTCAATTCACAACTCATTCATCATCTATATATGTGTTTGAAGTCACTGTCAATTA  
TTTCTACATCTGATTTTAAAAGAAATATTTCTCTACTACTGTCTCATGACAAATGAAACAAAGCATATGT  
GAGCAACTCTGAACATCAATAACCTTAGTTTATATCATTTATTTATCTTTAAGTACTGCTATCTTTACT  
GGCAATATTTCTATGTTTAACTTTGCTGATGTATAAACAGCATGTGCTCTATATTTGAATATAAATTTATAA  
TCTGCTTGAAATTTGATTAATAAATAAATTTTGAATTTGAAATAAATAAATAAATAAATAAATAAATAAATAA

**FIGURE 478**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFVLFVWVSLAGSGFGGRYSVTEETKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLSHTGNLLTNEKLDREKLCGPKCEPCLYFQILMDDPPFIYRAELRVRI
NDHAPVFDKQETVLKISSENTAEGTAFRLERAQDDPDGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGEISLTTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVMADVDVSGVNAEVSYSFFDASENIRTFQINPFSGEIFLRELLDYELVNSY
KINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPEPPLAVFKINDRDSENG
GKMCYCIQENLPFLPKPSVENFYILITEGALDREIRAENITITVTDLGTPRLKTEHNITVLV
SDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHLPLASLV
SINADNGHLFALRSLDYEALQAFEFVRVGATDRGSPALSRREALVRVLVDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA TE PGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSPGFNIQ

```

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 687-711

**N-glycosylation sites.**

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

**Glycosaminoglycan attachment site.**

amino acids 28-32

**Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

**N-myristoylation sites.**amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

**Aminoacyl-transfer RNA synthetases class-II signature 1.**

amino acids 117-138

**Cadherins extracellular repeated domain signature.**

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

**FIGURE 479**

CTCGGCTGGATTAAAGGTGCGGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCCC  
 GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**ATG**GGACCTGTGCGGTTGG  
 GAATATTGCTTTTCCTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG  
 ACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC  
 AGGCGGAACTGAGTCGACCCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA  
 CAGGCAAGAGGAAGAGACCGTGCTTACAGCGTTTACAGAGACAAGGCTGGAAGAGGCCTTAG  
 AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT  
 ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCCTAGTGCAGAAGGGGGTGAAGG  
 TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCACGCGTGGAGGTCACATACCTCAAGA  
 AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC  
 AGGAGCAGCCCCACAAAATTTTCTCTGTGAAGGTCATGTGCTCCAGCTGCTGAAACTGCAT  
 GTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG  
 AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG  
 GAAGCCACCCAAACTTGACCGAGAAGATCTTT**TGA**CCCTTGCCCTTTGAGCCCCCAGGAGGGGA  
 AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGGTGTGTT  
 TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG  
 TGAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG  
 AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT  
 AACTGATCCCACCCCAACCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC  
 ACTTAGCTCCTTAAGTCTGTTTTTAGACCCCTTCCAAGGAAGGCCAGAACCGGACATTTCTCT  
 GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG  
 GACACTGGGTGATGGCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA  
 GCTCAATGTAACCCAGAGGCCACCATATAGTTTTATAGGTGCTCAACTTTCTATATCGCTATT  
 AAACCTTTTTTCTTTTTTCTA

**FIGURE 480**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCCKLLSTELQAELSR TGRSREVL E
LGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQT MATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLLKKQCETMLEEFEDIVGDWYFHHQE QPLQNFLCEGHVL
PAAETACLQETWTGKEITDGEKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

**N-myristoylation site.**

amino acids 115-121

**Amidation site.**

amino acids 70-74



**FIGURE 481**

GCGCTGTGCAAGGCGGGGTCCGGCCCCGCGCAGGTCGGGTAAGCGCGTCTAGGCGCGCTGCGCGG  
 CGCAGCGAAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCTGCTTTGTGCCTCTGA  
 CCTGCTGCTGCTGCTGCTACTGCTACCAACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCCG  
 GACGCCGACGAGTCTACCCCACTCCCCGGAAGAAGAAGAAGGATATTGCGGATTACAATGA  
 TGCAGACATGGCGGCTTCTTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT  
 TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA  
 AAGCATATTGAAAAATGACGAAAAAAGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG  
 CCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA  
 CTATGACGTCAGAGGTTTATTGTGGGATCAGACCGTGTCTATCTTCATGCTTCGCGATGGGAG  
 CTACGCCCTGGGAGATCAAGGACTTTTGGTGGTCAAGACAGGTGTGCTGATGTAACTCTGGA  
 GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA  
 GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAATCGAGCTGG  
 GAATAAAGAGAAGACCTGTGAATGGGGCAGCAGTGACGCGCTGTGGGGGACAGGTGGACGTG  
 GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT  
 TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGGTCAAAGAATTACTGCTTAA  
 TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT  
 ACTATAAAATCTCCTTACATGGAATGTGACTGTGTGCTTTTCCCATTACACTTGGTGAG  
 TCACTCAACTCTACTGAGATTCCTCTCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT  
 GATCAGATAGCAAATTCATGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT  
 TCAATGCCATATACATCATTTTCTATTATGTTAAAGGTAATAATGCTTTGTGAACCTCAGATGTC  
 TGTAGCCAGGAAGCCAGGGTGTGTAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA  
 TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG  
 AGAACTCTTGGTGTCTGTCAAGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTCC  
 TTAATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT  
 AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT  
 TTGTTTTCTAAACATTTTCTTTGATAAAGTGCTAAATCTGTGCTTTGCTATAGAGTAACATG  
 ATGTGCTACTGTTGATGTCTGATTTTGCCTTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG  
 AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCCTTTGGGAAAAACCTCAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

486/615

## **FIGURE 482**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLPPPGSCAEGSPGTPDESTPPPRKKKKDIRDYN
ADMARLLEQWEKDDDIIEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGS LFNANYDVQRFIVGSDRAIFMLRDGSYAW EIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKENKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-32

#### **N-glycosylation site:**

Amino acids 201-205

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 85-89

#### **Tyrosine kinase phosphorylation site:**

Amino acids 50-59

#### **N-myristoylation sites:**

Amino acids 30-36;138-144;153-159;176-182

#### **Amidation site:**

Amino acids 207-211

## FIGURE 483

GTTGCTCCGGCGGGCGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCCTAGGGCCCGGGCCACCATGG  
 CGTTCGCTCCAGGCCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAGCT  
 CAGGTTGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGGCACTTCGGG  
 AGAATGAACGCCACGCCTTCACTGCCC GGTTGGCAGGGGGGCTTGGCACC CCAGATTGGCCT  
 GGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGGGGAGG  
 CCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCCATCGGGCCAGCATGAGCTCAACT  
 GCTCTCTGCAGGACCCAGAAAGTGGCCGATCAGCCAACGCCCTGTGTATCTTAAATGTGCAAT  
 TCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCAGGCCCTCTGG  
 TTGTCCTGTTTGGCCCTGGTGCGTGCCAAACCGCCGGCCAATGTCACTTGGATCGACCAGGATG  
 GGCCAGTGACTGTCAACACCTCTGACTTCCTGGTGTGGATGCGCAGAACTACCCCTGGCTCA  
 CCAACCACACGTTGCAGCTGCAGCTCCGACGCTGGCACACAACCTCTCGTGGTGGGCCACCA  
 ATGACGTGGGTGTCAACAGTGCCTCGCTTCCAGCCCCAGGCCCTCCCGGCACCCATCTCTGA  
 TATCAAGTGACTCCAACAACCTAAAACTCAACAACGTGCGCCTGCCACGGGAGAACATGTCCC  
 TCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGTGAAACCAGCAGACC  
 GGCAGATGGCTCAGAACCAACAGCCGGCCAGAGCTTCTGGACCCGGAGCCCGCGGCCCTCTCA  
 CCAGCCAAAGTTTCATCCGCTCCAGTGCTGGGCTATATCTATCGAGTGTCAGCGTGAGCA  
 GTGATGAGATCTGGCTCTGAGCCGAGGGCGAGACAGGAGTATTCTCTTGGCCTCTGGACACCC  
 TCCCATTCCTCAAGGCATCTCTACCTAGCTAGGTCAACCAAGTGAGGAAGTTATGCCACTG  
 CCCTTTTGTCTGGCCTCTCTGGCTGGGGTGCCCTCCATGTCACTGACGTGATGCATTTCACTG  
 GGCTGTAAACCGCAGGGGACAGGTATCTTTGGCAAGGCTACAGTGGGACGTAAAGCCCTCA  
 TGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTTCCAGAGGGAGCTCTTTGGCCA  
 GGGGTGTTTCAGATGTCATCCAGCATCCAAGTGTGGCATGGCCCTGTGTATACCCACCCCAAGT  
 ACTCCACAGCACCTTGTACAGTAGGCATGGGGCGTGCCTGTGTGGGGGACAGGGAGGGCCCT  
 GCATGGATTTTCTCTCTCTATGCTATGTAGCCTTGTTCCTCAGGTAAATTTAGGACCCCT  
 GCTAGCTGTGCAGAACCCAAATTGCCCTTTGACACAGAAACCAACCCCTGACCCAGCGGTACCGG  
 CCAAGCACAAACGTCCTTTTGTGTCACACGTCCTTGCCCTCACTTCTTCTCTGTGCCCC  
 ACCCTCTCTGGGAATTTCTAGGTTACACGTTGGACCTTCTCTACTACTTCACTGGGCACTAGA  
 CTTTCTATTGGCCTGTGCCATCGCCAGTATTAGCACAAAGTTAGGGAGGAAGGCGAGGCCGA  
 TGAGTCTAGTAGCACCCAGGACGGCTTGTAGCTATGCATCATTTTCTACGGCGTTAGCACTT  
 TAAGCACATCCCCTAGGGGAGGGGGTGAGTGAGGGGGCCAGAGCCCTCTTTGTGGCTTCCCCA  
 CGTTTGGCCTTCTGGGATTCAGCTGTAGTGTCTGAGCTCTCGGGGTTGATGGTTTCTTCTCT  
 AGCATGTCTCTCCACCAGGGACCCAGCCCTGACCAACCCATGGTTGCCTCATCAGCAGGA  
 AGGTGCCCTTCTGGAGGATGTCGCCACAGGCACATAATTCAACAGTGTGGAAGCTTTAGGG  
 GAACATGGAGAAAGAGGAGACACATACCCCAAAGTGACCTAAGAACACTTTAAAAAGCAAC  
 ATGTAATAATGATTGGAATTAATATAGTACAGAATATATTTTCCCTTGTGTGAGATCTTCTTTT  
 GTAATGTTTTCATGTTTACTGCTTACTGCTAGGCGGTGCTGAGCACACAGCAAGTTTAACTTGA  
 CTGAATTCAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPrL  
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV  
QFKPEIAQVGAKYQEAQGPGLLVLFALVRANPPANVTWIDQGPVTVNTSDFLVLDANYPW  
LTNHTVQLQLRSLAHNLSVVATNDVGVTASALPAPGPSRHPSLISSDSNNLKLNNVRLPRENM  
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV  
SSDEIWL

### N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### Glycosaminoglycan attachment site:

amino acids 23-27

### Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

489/615

**FIGURE 485**

AGAGTTCCTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT  
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGCGCGCTTCTGTGGTGG  
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT  
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG  
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCTGTACCCCTCATTCTCGCTGC  
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATCTGTCATGCTTAGTCTAACACCATCAGG  
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATT  
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAACATTTCTGTTATC  
TAAATAAACAGTGAAGTTTGTGTTGACTAAAAAA

1052566\_01522

490/615

**FIGURE 486**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855  
><subunit 1 of 1, 84 aa, 1 stop  
><MW: 9274, pI: 9.70, NX(S/T): 1  
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPGRSRKDasGCHKPG  
YPVPPHSRCPPPPHVQRPRPILHA

**Signal peptide:**

Amino acids 1-21

**N-glycosylation site:**

Amino acids 38-42

**N-myristoylation site:**

Amino acids 27-33

105235.0150

**FIGURE 487**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGCG  
 GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC  
 GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT  
 ACGCACCAACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA  
 TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG  
 GAGGGCGGGTGCCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG  
 CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG  
 AGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA  
 CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA  
 GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCAGT  
 GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC  
 TCTGCAGGTACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGTTGGCAGGTGGG  
 GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCTTTGTG  
 ATTAAGAATGTGGTCTATGAAA

492/615

## FIGURE 488

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAPVLLGLLLALLVPGGGAAKTGAEIVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSAFGEDGEGDDLTLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRQHEVH
GMPSANTHTWKAMEGIFIKPSVEPSAGHDEL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 62-66

**N-myristoylation sites.**

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196

**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

FIGURE 488



**FIGURE 489**

CAGCAGCCGAGACAGCAGCTGAGACGGCGCAGCGCAGCTTCCAGGCCGGAGCCAGCTTCTGGAGGAGACTCTGCG  
 ACAGGGCATTGATCACTGTGGTGGCCCTTTCTGTGCTGTGCTCTGACTTTGCAGAAATGCACCAACAGAGAC  
 ATGGGAACAACTCTTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGAGACTCAGTTTTTTCTCTCTGTGA  
 ACTCCACCACTGGAGCAGATGCTACTGAACACCACTCTCCAGGCTACAACCTGACCTTGCAGACACCCACCAT  
 CAGCTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTGCTGACCACTGCACTCTGAAGCGGGTGGC  
 CCAGGCAGGAGGTCAAGTATGCTGGGCTCAGCAGCCATGCACTTCCCGCCGAGCTGACCCGGGACGCTGCAC  
 GACCCGCCCCCAGGAGCTGCGGCTCATCTGTATCTACTTCTCCAAACCCCTCTTTTCAAGATGAAAACTCT  
 ATCTCTGCTGAATAACACTGCTCTCTGGGGCCAGCTGAGTCATGGGCACGTGAACAACTCAGGGATCTGTGAA  
 CATCAGCTTCTGGCAACACCAAGCTTGAAGGCTACACCTGAGCTGTGTCTTCTGGAAGGAGGAGCCAGGAA  
 ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTGCTACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG  
 CAACCACTCACCCTACTTTGTGTCTCATGCAACTCTCCCGAGCCCTGGTCCCTCGAGAGTGTCTGGCACTCT  
 TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTCTGCTGCACCTTCCATTT  
 CAGGAAGCAGAGTGACTCTTAAACAGTATCCACATGAACCTGCATGCTCCGTGCTGCTCTGAAATCGCCTT  
 CCTGCTGAGCCCGCAATTGCAATGTCTCCTGTGCCGGGTGAGCATGCAAGGCTCTGGCCGCTGCCCTGCAC  
 CGCCTGCTCAGCTGCTCACCCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCTCTCGGGCCTGTCTACAA  
 CATCTACATCCGAGATATGTGTTCAAGCTTGGTGTGCTAGCTGGGGGGCCCCAGCCCTCTGGTGTGCTTTT  
 CCTCTCTGTCAAGAGCTCGGTATACGAGCCCTGCACAACTCCCGCTCTTCGACAGCTGGGAGAAATGGCAGGCTT  
 CCAGAACATGTCCATATGCTGGGTGGGGAGCCCGTGGTGCAAGTGTCTGGTCTATGGGCTACGCGGCCCTCAC  
 GTCCCTCTTCAACCTGGTGTGCTGGCCTGGGCGCTGTGGACCTGCGCAGGCTCGGGGAGCGGGCGGATGCACC  
 AAGTGTGAGGCGCTGCCATGACACTGTCACTGTGCTGGGCTCACCGTGTGCTGGGAACCACTGGGCGCTGGC  
 CTCTTTCTTTCTTTGGCGCTTCTGTGCTGCCAGCTGTTCTCTTCACTATCTTAAACTCGCTGTAAGTTTCTT  
 CTTTTCTGTGGTTCTGCTCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCCTCAGCTC  
 CTCCAAACACACAGTAGTCTCGGGCCTCTGGCCTGGAATCTCAGCTCTCTGGCCGCACTAGCTCTAGGCT  
 ACGGCTCCTGTAGAGAGGCTGGCAGGCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAAGGGGCTTTTC  
 CACTTCCAGGCTCTCTCAGGCACTGAGGGGAAGGCATTGCTTACCTCTCCCTGACATTTTGTCTCGGGGCGA  
 TCCAACTTACCTGGGGCAGCAAACTTTGTCTGTGCTGAGCCAGGCTGCTGAGAGGATGTGGGCAAGCACCA  
 GCTCGGCTATCAGGAAGCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCTGCCACTTCT  
 ACAGACCTCAGGTATCCAGACTGTGACATGGGGCAAGCAGCTTTGTTTCAAGCTTAAACCAGGAGCTTAGTAAA  
 AATTGCATAAGCAGGGGGAAGAGTGTGAGCTGGGGTGGGAATTTCCCGGCCCTCACCTGCTCTGTAGGGG  
 AGATCTCACTCAGGCTGCCCTGGAAGCACTTCTGGCCCTGCACTTCTCCAGGGGAGGGCCAGATGCAAT  
 CTTGCTTGGGCGGCTGGGACCTTACCCAGGCTCTGAGACTTACTGGCCTATGCTGAGGCCCTTTTCTCTTTA  
 ACTCCCTAAATATGATGACTCAAAGTCCAAGCCACCCCTTCCCAAAGATTTGGAGGTTCCGCGTTCACAGAG  
 CTCTCTCTGCGGTGCTCCAGAGACTTCCATAGACCATCTGACACAGTAGGCCATCCCGCACTTTCTTGGGGCA  
 GAGGAAAACGCTTCTTCTCTCAGCTGAATCAGTCCAGTGTCTGGCTTTTGTGATTTGGCCACA  
 TTGAATTTGCCAGGTAGGCGTGGAGTGTGGGTTTTAAATTCGAAGCTCAGGCCATAGTTTTCAGAGAATCACCC  
 TTACCCAGCACTCTCATGAGACAGTGTCTGAAGGCAGTGGCTTTCCAGAACGCAACTAGGCGCACCCGTTG  
 GTCCACATCAGAGGCCCTTGGCGCCAGAGCTGCATAGAATCGCTCAAACACCTGTTTTCGAGCCCACTGAC  
 CAGCTGGAGGGGGCTTAAGCTGCAGGACCTGCGCTACTGAGTGACCCATTTCTCCAGGAGGAAGAGCAGACAG  
 CTTACACGGCCATTGTCTCTTTTCCAAATGCGGGGCTGCACTTCTGCTTGGGGGCTGACCCAGACATGCT  
 TGGCACCAGAGCAGGCTGCTCAGTGGTGGGTGCTCAGGGCCCTGCCCAGGCCACTGGCGGCTTTTGTATGACT  
 CAAAGCTCAGAGCAGAAAATAGAGCAGGATTTCCCTGGGGAAGTATCTCTGGGACATCTTCTGCTCTCT  
 GTACTTTCTAGATGCAAAATACCTGCTTCCACAGGCACTGAGTGGCCTAGGCTCTGGAGCCAGGCTGCTGGGCT  
 CCAATGCGAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCTCAGCCTCTGCTGTGCTCTGTTTCTT  
 TATTTGTAATAATAGACCATATGAGTGTGTAATTTTGAAGACTAAGTAAAAGAAATCAATAAAGAGACTTGGCA  
 CAGAGTAAGTGCTCAGTAAAAA

494/615

## **FIGURE 490**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860  
><subunit 1 of 1, 528 aa, 1 stop  
><MW: 59000, pI: 8.73, NX(S/T): 9  
MDHCGALFLCLCLLTQNAATTETWEELLSYMNMQVSRGRSSVFSSRQLHQLEQMLLNTS  
FPGYNLTQTPTTIQSLAFKLSCDFSGLSLTSSATLKRVPQAGGQHARGQHAMQFPaelTRD  
ACKTRPRELRLICIYFSNTHFFKDennSSLLNNYVLGAQLSHGHVNNLRDPVNIISFWHNQ  
SLEGYTTLTCVFWKEGARKQPPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMLQSPALV  
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNHLASVLLLNIAFL  
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLGRVYNIYIRRYVFKLGV  
LGWGAPALLVLLSLSVKSSVYGPCTIPVFDSEWNGTGFGQNMISICWVRSPVHSLVLMGYG  
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALFAFFSFGVF  
LLPQLFLFTILNSLYGFFLFLWFCSQRCSRSEAEAKAQIEAFSSSQTTQ

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-21

#### **Transmembrane domains:**

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

#### **N-glycosylation sites:**

Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;  
179-183;394-398;400-404

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

#### **N-myristoylation sites:**

86 GLSLTS  
101 GGQHAR  
157 GAQLSH  
255 GCSISI  
311 GSACTA  
420 GGLTSL  
467 GTTWAL

#### **Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

#### **Eukaryotic thiol (cysteine) proteases histidine active site:**

Amino acids 410-421

#### **G-protein coupled receptors family 2 proteins:**

Amino acids 273-302;314-343

1052535.011532

**FIGURE 491**

CTTGGCTGCCCCGACAAACAAGCTGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT  
 GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTGCACACGGGCTGCCCTGAGAGACATTTTC  
 CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA  
 ATACTCCCTCAATCAAGCTATCCGGAAGAATTTACAAGAAATGCCAGAAACTGCTTGGGTGG  
 CCTGAGAAACATCGTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC  
 GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAAATGCTA  
 CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTATGCAAGCCTCC  
 CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC  
 TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG  
 TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCACACAGCCCT  
 GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC  
 TCTCTATAACCCCTCCAACCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC  
 GGGGAGTCTCGTCCCCTCATCCCTGGTGGAGTCATTGAGCATCTTCCGACGCGACTCAGCCCT  
 GCAGTACCACCTCATGCTTCCCAGCTGGTCTTCTGGCACTCAGCCTGATCCACCTCTGTGT  
 TCAACTCTACCGTATGATGGACAAGGCGTCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT  
 GGAGGTAGCCTCTCTGTGTCAATTTCTTTTGAAAAATAACAATAAACTGTTTATATCTTGAA  
 AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC  
 CCTCTGTAGTGTAAATCTCAAAACAGCATTGAGATCAGGTATCATTTAGTGTTGTTACAGTT  
 ACCGTCTATGTACCACAGCAATTTGAGCAAGGTGGTGGTCCCATAGATCATATGGTGCTAAG  
 AAATTTCTGTCACTTAATGACATCTTGATCTGACCTTGATGTAGGCCCTAGGCTAAATATGT  
 CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTAAAAATAAAAAA

496/615

## **FIGURE 492**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDIILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTTLDDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLCVQLYRMDKGVLSYWRKPRNWLEVASLVSFSEK
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-30

#### **Transmembrane domain:**

Amino acids 250-267

#### **N-glycosylation site:**

Amino acids 153-157

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 2-6

#### **N-myristoylation sites:**

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

496/615

**FIGURE 493**

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTCGT  
 CCAAGTTACTAACCAGGCTAAACCATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC  
 CCCACTTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCCAGAGAGGGTCTCACCATTG  
 CGCACAGTTCCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAGAGAAA  
 ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGAATATCTTC  
 TTAGTGGCCGAAGCGGAGGGTGTCTGCTCAACCAACAACCTCATTAAATGCTGCAAACTAGCAAG  
 GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC  
 TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT  
 TGTTCGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC  
 CAGCCTTCTCGCACAAAAGCCTACAGGAAAGAAAACAAATGAGACCAAGGAAACCAACTGTACT  
 GATGAGAGAAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTCGTCCAGTG  
 GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT  
 GGATATCACCTCCAAGTGTTAGTTACACCTGAACCTGACCCTGTTTCAAAACAGGAATAGAAT  
 GCAGTATGCAAGGCAGTTGACAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT  
 TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGACTGTTAAGAGTACATGCCATGG  
 GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGCGCAACAGAGTCTG  
 TACATAGAGCTACTTCTCTGTTCCAGGTGCCAAAAAATCAGCAAAAATATATATTTCCATATATC  
 ATCCTTACTATATTATTTTGGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC  
 AGAAAAATATAAATTGAATAAAAACAGAAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC  
 TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT  
 CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC  
 CAAGAAACAACAACAACAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT  
 GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT  
 CATACCTTTGTATAAATTGGAATTTTGTATTCTTAGCTGTACCAGCTAGTTCTCTGAAGAAT  
 GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCGAGACAGTAAT  
 AATGAAAACCAAATTTCTCAAGAAATAACTGAAGAAAGGAGCAAGTGTGAACAGTTTCTTGTG  
 TATCCTTTTCAAGATATTTTAATGTACATATGACATGTGTATATGCCATGGTATATGTGTCAA  
 TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAAGTGGGAACAATACA  
 CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC  
 ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCATTGTATAGTTATAT  
 CATTTATTTAAATTAATAAACCAACCTAATGATGGATATTTAGATTCTTTTAAGTTTGTGTTATTT  
 CTTTAAAGTTTGTGTTGGTATAAACCAATACCACATAGAATGTTCTTGTTCATATATCTCT  
 TTGTTTTGAGTATATCTGTAGGATAACTTCTTGAGTGGAAATGTGCTGAGCAAGGGTTTGT  
 GCATTTTACTATTGATATATATGTTAAATTTGTGTCAAATATATATGTCAAATTCCTCCAACA  
 TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTTCCTGCTTCTACAG  
 TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA  
 CTATTTAATAAAATGGATTATA

**FIGURE 494**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13, NX(S/T): 10
MLCPWRTANLGLLLILTIPLVAEAEAGAAQPNNSMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIIITWEIILRGQPSC TKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKS AKLYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTFPVVEEDEMOPYASYTEKNNPLYDTTNKV KASQALQSEVDTDLHTL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**Transmembrane domains:**

Amino acids 78-98;267-286

**N-glycosylation sites:**

Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;  
218-222;233-237;247-251;298-302

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

**N-myristoylation sites:**

Amino acids 103-109;259-265

**FIGURE 495**

CCAGGTGCACAGCGCATCGCCCGAGGGCTGTACCGCCCTGCCCCGCCACCCAGCTGTCCTG  
 GACCCAGGGGAGGAGAGGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT  
 TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGGCCAGGAACAGTACCACCTGCACC**ATGGG**  
 GCTGTCCCGGAAGGAGCAGGCTCTTCTTGGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCCTAC  
 GGCACCTATTCTCTCTCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG  
 GATCGTGTGTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACAA  
 GGAGAAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCCTGCCAGGTGGAAGGGCCCTGGAATCTC  
 CTCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT  
 GGTGCTGATCCAGAGGCCCAGCATCGGAAAAACCCACGTTCTCTGGGGGCCACGGCTGGCAT  
 GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTGCAGCAGTCAACCCAGGT  
 CCTGGGCGGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGAGGCCGAAGGTGC  
 CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA  
 ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGTGCCCTGGACATGGGAGGGGCTCCACCCA  
 GATCACGTTCTGCTGCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTCGCTCTA  
 CGGCTCCGACTACAGCGTCTACACTCACAGTACCTGTGCTTGGACGGGACAGATGCTGAG  
 CAGGCTCCTCGTGGGGCTGGTGACAGCCGCCCGGCTGCCCTGCTCCCGTACCCGTGCTACCT  
 CAGCGGCTACCAGACCACTACCTGGCCCTGGGCCGCTGTATGATCAACCTGTGTCCACGCCAC  
 GCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGACAGGCAACCTGGAGCCTGCGT  
 CTCAGCCATCCGGGAACTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCTTTGA  
 CGGGGTCTACCAGCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCTCGGGCAGGA  
 CCCTGGCTGCGGGACTACTGTGCCCTCAGGCCGTGATACCTCCTACCCCTCCTGCACGAGGGCTAC  
 GGGTTACAGCGAGGAGACCTGGCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT  
 GGCTGGACACTGGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG  
 TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG  
 GCGGTGGTGGGGGCTGCCCTTGGTCCAGCTCTTCTGGTTGCAGGAC**TAGTGGGAAGGCGGAGGT**  
 GGGCCCCACAGAGCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC  
 GCCGTGGGGCCTTGCTCTGTGGCTTCCCCACGGTCAAGTGACAGCCACCTCCAGGGCACCGT  
 CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCTCCCGGCGTCCCTCCCCAACCTCC  
 TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCCTTCTGCACACAGGCCGCCAGGACTCGTGG  
 TGCTTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCCTGCAAAACAGGGCAAGACCACGGAGG  
 CACAGGGGTCTGCTCCTGCTGAGTGGGGCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT  
 GCGCCACCTGACACCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCCTGG  
 GGCTTCTGCTGGGCGAGCCCGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT  
 TGTTTTTATTAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAA

500/615

## **FIGURE 496**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870  
><subunit 1 of 1, 458 aa, 1 stop  
><MW: 49377, pI: 4.98, NX(S/T): 5  
MGLSRKEQVFLALLGASGVSGLTALILLVVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ  
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEELVLIPEAQHRKTPT  
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL  
GTLVKYSFTGEWIQPPEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY  
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS  
LPQNLTVEGTGNPGACVSAIRELFNFSQCGQEDCAFDPGVYQPPLRGQFYVEASYPGQDR  
WLRDYCASGLYIILTLLEHGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP  
AQWRAESYGVVWAKVVMVLALVAVVGAALVQLFWLQD

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-21

#### **Transmembrane domain:**

Amino acids 428-449

#### **N-glycosylation sites:**

Amino acids 67-71;135-139;304-308;325-329;410-414

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 133-137

#### **N-myristoylation sites:**

Amino acids 50-56;123-127;165-171;207-213;234-240;  
259-265;311-317;314-320;331-337;398-404;  
413-419;429-435

#### **GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215



**FIGURE 497**

GCCTTATAAGTAGCCTCTGCATCTGCCTCGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG  
 AGTTACACCTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA  
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCGTGGTCGGTGCCTCCA  
 CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG  
 CCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC  
 TTCAGCCCAACAGGATCCGGATTCTGAATGTCCATGTGCCCCGCTCCACCTGAAATTCATTG  
 CTGGTTTCGGAGTGC GCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTGCGCCCCAG  
 AGCCCCCTGGAGCTGACGCTGCTGTGGAACCTGCTGGCTGACACCCGCTGACCCAGAGCTCCA  
 TCAGGACCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG  
 ATGGCAGTAACAGCACCTCCCACGCGCTGCTGGTCCTGGTGCAGAAGCACATTAAAGCTGTCT  
 TGAGTAAACAAGCTGTGCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA  
 CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCCAGATCCGCTATTCCATGGTCAGTGTGC  
 CCACGTGCACCAAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCCTGCTGGGCAACC  
 CCATCATCTGCCACGGATGCCACCCCTTTTGTGTGCCAAGGCATGTGGGTACCGAGGGCT  
 CCATGGCCACCGTGGGCCTCTCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG  
 CCGGTGCCCTCAACCTGGACATCAGGGCAGCTGAGGTGCGATGACAACTGCTGAACACCT  
 CTGCTCTGGGCCGGCTCATCCGGAGGTGGCCCGCCAGTTTCCGAGCCCATGCCTGTGGTGC  
 TCAAGGTGGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAACACACGCCACCTTGCGGC  
 TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACTCGGCTTCCAGTCCCTCTTCTCCC  
 TGGATGTGGTAGTGAACCTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA  
 CGTCTGTGCTGGGGATGTCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT  
 CAGGTGCGCACACTGATGGGCACCGTTTGTGAGAAGCCCTGCTGGACCATCTCAATGCTCTC  
 TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT  
 GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACAGAGCTGAAGGCAAGACCACT  
 GGGAGGCTGAGAGTGGGCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA  
 AACTGAGGCAAAACCACTATTAGTCATCACAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA  
 TCTTCCCTGAGTGCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCTCTCTCTCTCT  
 CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTCTGCCCCACCCAGGGGGGAGCAGACTGCT  
 CCTCCAGGCTGTATAGACCTGCCCTCTTGCATTAAACAACCTTCTCTTGGCTGC

502/615

## **FIGURE 498**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872  
><subunit 1 of 1, 458 aa, 1 stop  
><MW: 49158, pI: 8.72, NX(S/T): 4  
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYSVEIGKAPLQRALQVTVPHFLDWS  
GEALQPTRIRIILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPEPELETLTPVELLADT  
RVTQSSIRTPVVISACSLFSGHANEFDGSNSTSHALLVLVQKHIAVLNKLCLSLISNL  
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSDYISLEVNAVLFLLGNPILPTDAT  
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL  
IPEVARQFPPEPMPVVLKVRGATPVAMLEHTNNATLRLQPFVEVLATASNSAFQSLFSLDV  
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFKEPLLDHLNA  
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-20

#### **Transmembrane domain:**

Amino acids 217-236

#### **N-glycosylation sites:**

Amino acids 96-100;151-155;293-297;332-336

#### **N-myristoylation sites:**

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

#### **LBP / BPI / CETP family proteins:**

Amino acids 22-50; 251-287

2025 RELEASE UNDER E.O. 14176

**FIGURE 499**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAGC  
 CCTTATGCTGCTCACCCGTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCACTC  
 CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA  
 GCAATGCCTGACAAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG  
 CACACCAGAAGAGCCCTGTGAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTGACATA  
 TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCACTCCAGCCCT  
 GGGCCTTGTCTTCCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAGACTCATT  
 CCATTGGCTGCCCCCTCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC  
 CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG  
 GTCTCCTCATCCATCCTTCCACCTCACCCCTTCACTCTCCTTTTTCTGGGTCCCTTCCAC  
 TTCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCCTATACTCTGCTG  
 TCCCCACTTGAGGAGGGATTGGGATCTGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG  
 AAGGCTCCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC  
 ATATGTACCCCATCCCCCATACTCACCTCTTCCATTTGAGTAATAAATGTCTGAGTCTGGA  
 AAAAAAAAAAAAAAAAAA

**FIGURE 500**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQGQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGTLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 77-81, 88-92

**N-myristoylation site.**

amino acids 84-90

**Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

**FIGURE 501**

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGACTGACTGACTGAATCACACCTCTGG  
 GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG  
 GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCCTCAGGAGT  
 CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC  
 AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT  
 CCACACTACCAGGGCCAAGTGAGCTTCTTGGACCCAGCTATTCCCTGCATATCAGCAATCTG  
 AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC  
 ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC  
 TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGTAATTCCTGGCCATGGGACTC  
 TGGGTATCCGAGTCCAGAAAAGACAAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA  
 ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCCGCTGCTGACTGCTCCTTGGGAACCCC  
 AGTCCTGAGCTTGGTTTCTTCCCAGCACCAGAGAATCCTTCTCAGCTCTCTTCTTTCCAGG  
 GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA  
 ATAAAGTCAAATTAAGTGACCACA

506/615

## **FIGURE 502**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENI IWSSHKS
LATVVPKGEGHPATIMVTNPHYQGQVSLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLIFLLLVILAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-18

#### **Transmembrane domain:**

Amino acids 144-165

#### **N-glycosylation site:**

Amino acids 99-103

#### **N-myristoylation site:**

Amino acids 106-112

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 503**

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCAGGATCCGTTGCGGCTGCAGCTCTGCAG  
 TCGGGCCGTTCTTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCCGCCGCCGTAC  
 CGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGCGCCATCTTTCATCGAGCGCCATGCGC  
 CGCAGCCTTCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAITTTGTTTCTGCT  
 GACCGCGGGCCCTGCGCTGGGCTGGAACGACCCCTGACAGAATGTTGCTGCGGGATGTAAAGC  
 TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA  
 ATGTGTTGGAGGCACAGCTGGTTGTGATTCCTTATACCCCCAAAAGTCATACAGTGTCAAGACAA  
 AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT  
 TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG  
 TTCTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC  
 TGGAAAGCAGCAGCGCTTTGCGCTCTTCTCTGATTATTATATAAGTGGTCCTCGGCGGATTC  
 CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA  
 GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA  
 CCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC  
 AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA  
 AGGATATGAAAAATTCAGGACCAGGGTCTCTGGACAGGCTTGGGAACTGGTGGAATAC TAGGATA  
 TTTGTTTGGCAGCAATAGAGCGGCAACACCCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC  
 TCCCTCCTACCCCTGGCACGTGGAATAGGGCTTACTACCCCTTCATGGAGGCTCGGGCAGCTA  
 TTCGGTATGTTCAAACCTCAGACACGAAAACAGAACTGCATCAGGATATGGTGGTACCAGGAG  
 ACGATAAAGTAGAAAAGTTGGAGTCAAAACACTGGATGCAGAAATTTGGATTTTTCATCACTTT  
 CTCTTTAGAAAAAAAGTACTACCTGTAAACAATTGGGAAAAGGGGATATTCAAAAGTTCTGTG  
 GTGTTATGTCCAGTG TAGCTTTTTGTATTTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA  
 AATACTTATGTGTGTATGTAGTCAAGTGAACATGCAGATGTATATTGCAGTTTTTGAAGTGATC  
 ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTAA  
 GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTCAAGTTTTAGGTGGTTGTAGC  
 TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTGATGTTG  
 CTGTTCTTCAAACATTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC  
 TTTTGAGCTCTGAAGCTTTGAATCATTCACTAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA  
 CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG  
 CAAAATGCTTGAAACCTCTATATTCTTTCGTTTCATAAGAGGTAAGGTCAAATTTTTCAC  
 AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATGTTGTAATAGT  
 CTGTTTCAATCTTAAAAAGAAATCA

508/615

## FIGURE 504

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889>  
><subunit 1 of 1, 339 aa, 1 stop  
><MW: 36975, pI: 7.85, NX(S/T): 1  
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO  
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCBGEYESSAQYVL  
RGSCGLEYNLDYTELGLQKLKESGKQHGFAFSDDYKWSADSCNMSGELITIVVLLGIAFVV  
YKLFLSDGQYSPPPYSEYPPFSHRYQRFNTSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG  
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPYPPSYPGTWNRAYSPLHGSG  
SYSVCSNSDTKTRTASGYGGTTRR
```

### Signal peptide:

amino acids 1-30

### Transmembrane domain:

amino acids 171-190

### N-glycosylation site.

amino acids 172-176

### Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

### Tyrosine kinase phosphorylation site.

amino acids 98-106

### N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318



**FIGURE 505**

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC  
 AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTACCTTTTGAAGGACAAGATGCATT  
 GGAAGATGTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA  
 GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCTCATCTACTGCCATTGAACC  
 CAGTCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCTCTGCTGGCCGAACCTTG  
 AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT  
 CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCAGACATCCGCCGGCTCA  
 CGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGTCTGA  
 CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCACGGCCATCAGAAGGACATCTGGGCGC  
 AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG  
 TACCTCCCTGAGAGACTGGCCACACAGGACCTCAGAGCAGGACCAGCACAGTAATCCAGA  
 AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAACACTTACCGCTGACACAGAG  
 CAGCAGAGATCAAAACAGTAACCCCGATGCTCTTTTTCTCTTGTAGTTTCTGGAAGACATC  
 TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT  
 CCATGGGCAGAATGGTTTGCCATATGGCAGGCAGAATTCGATATGCTTCAACCCAGAGCAGTG  
 GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCAGGATCTAAAACTT  
 TCTAAGTTTCTCCATCGTTGGCATCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA  
 CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTCACCTCACTTGAATCTAACAAATCAAA  
 GTATTTCTGCAGGTCCAATGGTCTAAAAATCAAATGCTTGTAAATGACTTTTTACAACACCCCTT  
 ACTTTCCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAACACATCAGTAAAAATG  
 TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTAACTCCATGCATGTTGTGAAAC  
 AGACCCCGGAACCTTTCTCATCTTGTAAATTCGAAGTTCTATACCCACCGAACAACTCCTCTT  
 TTCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTCTGTTTTTGTAGAGT  
 CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTTGTATTCT  
 GGAAAAGTGTTTTCTTCCCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGCTTTATT  
 GTACACTTGCTGTACCTATTTTTTATTTTAAACAAATATTTCATCTATGGTATAATAAAGATGTCAT  
 GGTGGAAAAAAAAAAAAAAAAAAAAAAAAAA

510/615

**FIGURE 506**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893  
><subunit 1 of 1, 173 aa, 1 stop  
><MW: 19733, pI: 8.78, NX(S/T): 0  
MHWKMLLLLLLYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF  
LLAELEISPDLOISIKDEELASLRKASDFRTVCNNVIPSIPDIRRLSASLSSHGILKK  
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFOALRHDLMRSSQPGVFP

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-17

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 36-40;84-88;105-109

10052536-011502

**FIGURE 507**

GCGCGCGGGCTGCGCGGAGCGGCTCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC  
 CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAAACTGAGAAGTGATTGCTCGAGGCCCTTC  
 CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTATTAAAAGACAT  
 CCTCAAATGTACATTGCTTGTGTTTGAGTGTGGATCCCTTATATCCTCAAGTTAAATTATAC  
 TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCCTGACCATGTAAGAGAGCTCA  
 GAAATATGCTCAGCAAGTCTTGCGAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC  
 GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCGAGAAGGCCCCCAAAGA  
 CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCCGGAAGTTCTCCAGTAAAGTCCA  
 GACCCTCTTGAAACTCTTGCCAGAGCACGACCTCCTGAACTTGAAAGCCAAAGACCTGTGCG  
 GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGCTGGGCCACACCCGTGA  
 CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACAGTTGAGGGATATTGAGAATGTTGG  
 AAATAAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT  
 TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTTCAACTGGCTTCAAGCAATG  
 GTAAAAAGGAAACCTGCCATTCTGGGTACGACTCTTCTTTGGAAGCAGGTGGCAGAAAAA  
 ATCCCACTGCAGCCAAAACATTTCAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT  
 GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCGCCACA  
 ATCGGTGTCATTGGCCGTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT  
 GGATATGACCTCAATCAACCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT  
 ATGAACTTTCAGACCATGCATAATGTGACAAACGGAACCAAGTTCTCTTAAAGCTGGTCAAA  
 GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATGATCGTGAATTTTGAACACAGAAAACTCA  
 GTTGAAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGATTTTCTCCAT  
 CCTGCAGATACTTTGAAGTCAGCTCATGTTTTTAACTTTAAATTTAAAAACACAAAAAAAT  
 TTTAGCTCTTCCCACCTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTTGCAACCAT  
 TTTGTAAATGAACTTAAGAATTGAATTGGAAGACTCTCTCAAAGAGAATTGTATGTAACGAT  
 GTTGTATTGATTTTTAAGAAAGTAATTTAATTTGTAAACTCTGCTCGTTTTACACTGCACAT  
 TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACCTTTTGATGGTGGCCCTGAACCT  
 CATTCGTGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCAGGATGACGT  
 GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG  
 GAGAAGGTCAACAACCTTCTCTGTGTTGCTGCTCTGCTGAAAGACTCGAGAACCAACGAG  
 GAAGCTGTCTGGAGGTCCCTGGTCCGAGAGGGGACATAGAATCTGTGACCTCTGACAAGTGTG  
 AAGCCACCTGGGCTACAGAAACACAGTCTTCCAGCAATTATTACAATTTGAAATTCGAAATTCCT  
 GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT  
 CTGAGTGACTTAAAAAATCAGAACAAACTTCTATTATCCAGATCTGGGAGAGTACACCC  
 TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTTGTGTA  
 TTTAA

512/615

## **FIGURE 508**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897  
><subunit 1 of 1, 362 aa, 1 stop  
><MW: 41736, pI: 8.80, NX(S/T): 3  
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTEECMDMKMHYVDPDHVKRAQKYAQQVL  
QKECRPKFAKTSMA LLFEHRYSDLLPFVQKAPK DSEAESKYDPPFGFRKFS SKVQTLLF  
LLPEHDLPEHLKAKTCRR CVVIGSGGILHG LELGHTLNQFDVVIRLNSAPVEGYSEHVGN  
KTTIRMTYPEGAPLSDLEYYSNDL FVAVLFKSVD FSNWLQAMVKKETLPFWVRLFFWKQVA  
EKIPLQPKHFRILNPV IIKETAFDILQYSE PQSRFWGRDKNVPTIGVIAVVLATHLCDEV  
SLAGFGYDLNQPRTP LHYFDSQCMAAMNFQTMHNVITETKFL LKLVKEGVVKDLSGGIDR  
EF

### **Important features of the protein:**

#### **Transmembrane domains:**

Amino acids 11-27;281-297

#### **N-glycosylation sites:**

Amino acids 30-34;180-184;334-338

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 2-6;109-113;223-227

#### **N-myristoylation sites:**

Amino acids 146-152;150-156;179-185;191-197

**FIGURE 509**

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG  
 CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGAGGGAC  
 TGCACCTCCCTCTGAGCGTGTAGCTCCGACTGCCTGACGGATCACCCCTTCCGCTCCAACATGG  
 CTAGTTTCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC  
 CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCGCCAGGCTAGACAGTGGAGTGCCGCACA  
 GCGCGCCTTCCAGCCTCGCAGCGGCCACCCCTAGCGGTTCGACCCGGCGCCAGCAGGGCCTGCT  
 TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG  
 TGCTGCCGCCGGGTACTGTCTGGGTGCCAGTGCTCGTTATTGTCTCTCGTCTGTCTCTGGTCC  
 TACTATGCCTACGCTTTTGAACCTCTGCCTGGTTATTTTACCTCATACTCTACCATGCCATCTTT  
 GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCCAAGCAGCCAAACCAGAAG  
 TTCCACTTGTCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG  
 CAGATGCTTGTTGATATGGCCAAAAGCTACCGGTTACACAAGAACTGGAAGTGGAGGTCAG  
 TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG  
 TTCTCAAAC**TAG**CCCTTTTTTTTCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA  
 CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC  
 TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTGCTATATCACATATCTATC  
 CACATATGCATACCTCTATTTATCTTTCTGTCAGCCATCTTATGTTTCTGATGCATTTCAAAG  
 TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTTAAAAATTTACA  
 TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGATTTTTGAAAAGGTACACATCTGT  
 GTAAC**TAA**CCCCCAATAAAATTGCCATCACCTCAG

20510.955501  
 05555.01501

514/615

## **FIGURE 510**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLSYAYVFELCLVIYLILYHAIFVFFT
WTYWKSIFTLPPQPNQKPHLSYTDKERYENERPEVQKQMLVDMAKKLVPYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

### **Important features of the protein:**

#### **Transmembrane domain:**

Amino acids 24-45

#### **N-myristoylation sites:**

Amino acids 11-17;12-18

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 511**

CAGCCGGGGCGATGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG  
 CGGCAGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCTTGAGCCTGCTGCAGAGGGTGGCGA  
 GCTACGCCCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG  
 GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCTCCTCTGGAGCGCA  
 ACGGGGTCCGACGCCCGTTCCCAACCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG  
 CCGCAGGAGAGAGGAGCCTGTCAACCCTGTGGAGAATGCACTCCAGTTTCTAGTCGTTGCCCTT  
 TGGCACCCGCGACACTGCTAGTGCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA  
 GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCCACTCACCCTGCTCAGCTCTCA  
 AAGCCCTGCGGTTTCCTCTGCTGGCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC  
 ACAGAGCGGTTTTAAACTGGCCAAACACCTTAACGCCACAGAGCCGCCCTCCTCTCGCTGCCACT  
 TTGGAAAATAAGAGACTAGAGATTCACTGGACGCTTCTCTCCCGCATCACAAGACTTGACTGC  
 TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT  
 AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGGTGTCAAACGCCCTTGTTTATTAAG  
 AGTGAATTTTTTAATTAAAAATCATGTTTTAAACAGAGATGGACATTTATTGATGGAAAAAA  
 ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAAGGGAGGGC  
 GAATCGATCTCAGAGTTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA  
 TTTGCCCAAATGGCATATTTTAAATTTGGCCAGACCAGAACCAGTTTCTCTGGGATTAT  
 TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACTAACTCCAAAGCTTGAAGGACTTTTTCTC  
 ATTTTCACTTGTTTTCTCTAATAAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCCTC  
 ATGGAAGAGTGTTTACCAAATATTTAAAAATACTTTGACAGAAAAAATCAAGCGAATCTTT  
 GCCAACCAATATCATCATGACTGATGTAACAAGTAATCCAACAGATATGAAAATCACTGG  
 TAAAAATCATCTCAGTTAATTTCTAAAAGCAGAGCTAACCCACCCCTTTTGTCTTAAGGCTTTAT  
 GGTATTAATAAATAAATGTACAAAAATATAGATTTTCCCTATCCCTTACCCCTGGAAAGTA  
 ATATACTGAAGTCTCATCACTGTTTTGGGGATTCCAGTAATTAATCTCTAGTGAACAAA  
 GACCTGTTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTTCTCTTGTAGTCAC  
 TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAGGGGACTTTTTATTCCACCAACAA  
 ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG  
 AGAAATTTTAAAACTTTAACTTAGAGGGTTTTCTTCTCCTTTACTGTTTAAAGTGACT  
 ATATTACAGAGTCACTTTAAAGGATTAATTTATTGCATGCAAAGTTTCTAGATCACTGCTAG  
 AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC  
 CAGTGTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTGCCAA  
 GAATCTTGCTCTTTCACATACAAGAGGTGTTGCGTTTCATTTTGGGGCTAAATGTCCAAAGCTG  
 GCCTCAGCAATTTCACTTGAAGATTGCAAGTTGGCTTCCAACCTGGCCTCTAAACTCTAATCTA  
 GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCAGCTGTTGGACCTGC  
 TGCCTTAGAACCACAGATTGGTACCTCGTGCC

516/615

## **FIGURE 512**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443  
><subunit 1 of 1, 178 aa, 1 stop  
><MW: 19353, pI: 10.97, NX(S/T): 0  
MAGLWLGLVWQKLLLLWGAASALSLAGASLVLSLLQRVASYARKWQOMRPIPTVARAYPLV  
GHALLMKPDGRGKGRSSWSATGSAAFPFSDQPGTRCLWRWPQERGACHPVENALPVLV  
VAPWHPPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-25

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 75-79

#### **N-myristoylation sites:**

Amino acids 3-9;17-23;145-151

#### **Amidation site:**

Amino acids 73-77

#### **Leucine zipper pattern:**

Amino acids 8-30

205  
204  
203  
202  
201  
200  
199  
198  
197  
196  
195  
194  
193  
192  
191  
190  
189  
188  
187  
186  
185  
184  
183  
182  
181  
180  
179  
178  
177  
176  
175  
174  
173  
172  
171  
170  
169  
168  
167  
166  
165  
164  
163  
162  
161  
160  
159  
158  
157  
156  
155  
154  
153  
152  
151  
150  
149  
148  
147  
146  
145  
144  
143  
142  
141  
140  
139  
138  
137  
136  
135  
134  
133  
132  
131  
130  
129  
128  
127  
126  
125  
124  
123  
122  
121  
120  
119  
118  
117  
116  
115  
114  
113  
112  
111  
110  
109  
108  
107  
106  
105  
104  
103  
102  
101  
100  
99  
98  
97  
96  
95  
94  
93  
92  
91  
90  
89  
88  
87  
86  
85  
84  
83  
82  
81  
80  
79  
78  
77  
76  
75  
74  
73  
72  
71  
70  
69  
68  
67  
66  
65  
64  
63  
62  
61  
60  
59  
58  
57  
56  
55  
54  
53  
52  
51  
50  
49  
48  
47  
46  
45  
44  
43  
42  
41  
40  
39  
38  
37  
36  
35  
34  
33  
32  
31  
30  
29  
28  
27  
26  
25  
24  
23  
22  
21  
20  
19  
18  
17  
16  
15  
14  
13  
12  
11  
10  
9  
8  
7  
6  
5  
4  
3  
2  
1



**FIGURE 513**

GGCGGCTGGACGAGGACGCTCAGAGCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC  
 CCACTGCTCCCAGGAGCGGTTACCTGGGCACCTCTGTGCCCTCCTTCTGTTCGGGCCCA  
 GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTACAGCCCATCCCCAGTT  
 CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCGTGGACTGAGTGGCAGGCCATCCT  
 ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG  
 ATCTGCAAGCCCTGCCTTCCTTCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC  
 ACAGCAAGCCAGTGTCTGTGCTCCGAGTTCCAGGGCGTCTCCAGCTCAGCCACTGCAC  
 TGAGAACATGGACTCTCTGTGGGGCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA  
 CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGTAGGGCCCTCAAGGAGAG  
 CGGGGCAGGGATGCCTGAGCAGGACAAGGACCTTAGAGTCCAAGAGAATCCTGGTGTATCA  
 GAGAAGGGTCCCCAGGATCACCGGGGATGCACGGTCTGCATTTCCGGCCCTGCGGGACAA  
 TGGAGGCCCTCTCCTCCTTTGTGCCGGGCCGGGCTCTGCAGACAGACCTCCATGCCCA  
 GAGGTCAAGAAATCAGATATAACAGACATCCAGACCTCCTGGACGAGCTCCTGCACCAA  
 CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGTCTGGGGCTAAAGCGGAG  
 GAGGGGCCAGGCTCATCCCACTGCCAGCTGACCTCAGTTCTTCAAAGACAGTGAAGTGA  
 GGACAGGCCCTCAGGCTGTCTCTTCAAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC  
 ACCAGGGCAGACACTCACCTCAGGAATGACTCTCCACATCCGAGGCCCTTAGGCCAG  
 TACACACAAGTTTCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC  
 CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGAGAGAAGGAGCGGCCCT  
 CCAGCGCATCAACAGTGCAGCTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCCT  
 ACGGCCCTTCCACACTTTGTCTCACTTGCACACAGGGGCTTCTGGTCTGCCTGCCGTTTC  
 TAAAGCACCCAGTATGGATGCACAGCAGGAGACACAAAGTCCCAAGACTGCCTGGGCCCT  
 ACTGGACCCCTTAGCATCTGCTGCAGGGTCCCCCTACAGCTCCCATGCTTGGGAAGAA  
 GCACAGACCACAGGCCCTCTGTCTCCTCCTCAGATCCCTTCTGCCACCTCTTCTGA  
 TTCCAGGACTCAGCCAGGTCACTCGCTGATTCTGCCCCCTCCAGCTGCAAGCAT  
 GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCTGCAGCTGCCGCAGCAGC  
 CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT  
 TCACATTTCTGGGCCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTGAGAACCAGAGATC  
 CCAGACCTCCTGGACAGCTCGTGCCCCAAATGAAATGCCATCTCGAGCCCTACAGCTC  
 TACGGGAGGCCCTCCCGGAACAAAGCGGAAGAGGGGCCAGCCTCATCCCCTGCCAGCTG  
 ACCCTCAGTTTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTCGGGTCA  
 ACCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCTTCAAGGGGTGGC  
 TCCCCAGATCCAGGCCCTTAGGCCCGGTATATGCAAGTTTCCCTCTGCTCCACGACG  
 CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA  
 GACCTGGACCGGGAGAAGGAGGAGGCATTCAGCGCATCAACAGTGCAGCTGCAGGTTGAG  
 GACCAGGCCATCTAGGACTGCAGACCTCACGGCTTCCACACTTTGTCTCACTTGC  
 ACAGGGGCTTCTGCTGCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG  
 ACACACAAGTCCCAAGACTGCCTGGGCCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCCT  
 GTAGTCCAGCACTACTTGGGAGGCTGAGGCAGGAGAACGCATAAACCCGGAGGCAGAGC  
 TTGCAGTGAGCTGAGATCGGCCACTGCACCTCAGCCTGGGTGACAGCGAGACTCCGT  
 CTC

518/615

## **FIGURE 514**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786  
><subunit 1 of 1, 428 aa, 1 stop  
><MW: 45450, pI: 9.28, NX(S/T): 3  
MDSLWGPAGSHFFGVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR  
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN  
AIISSYSSTGGLLGLKRRRGPASSHCOLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG  
QTLTLRNDSSSTSEASRPSTHKFPLPRRRGEPLMLPPPLELGYRVTVEDLDREKEAFAFR  
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD  
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSLIAPFFPAASMDA  
GMRRTRHGTSAPAAAAAAPRSTLNPTLGSLLEWMEALHISGPQPLQQVPRGQNQRSQT  
SWTSSCPK

### **Important features of the protein:**

#### **N-glycosylation sites:**

Amino acids 105-109;187-191

#### **Glycosaminoglycan attachment site:**

Amino acids 38-42

#### **N-myristoylation sites:**

Amino acids 15-21;130-136;180-186;307-313;361-367

#### **Amidation site:**

Amino acids 315-319

#### **Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 106-117

2025-06-06 10:00:00

**FIGURE 515**

GTCAGGGCCAGGGTGAGCGCCGACTCCGAGCTGTCCCGCTCCCGGCGCGGCGCTCCGCTCT  
 CAGCCACCTCAGGGCTGCCAGGAGTGC GCGGGAGTTTGGCCCGGAGCGCGGGGAAGTTTCTCTC  
 CGAAGCTGCGCTCCTGGAAACAGCAGCACCTGCAAGCGCCCGGCAGCGGCCCGCGAGGTTACTT  
 TATGGAAITGGGCTCTTAGAGAAACAAGAAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG  
 GTCTTCAGATTCTGAAATAAGGAGAAATG CAGCCATCTGAAATGGTCATGAACCCCAACAAG  
 TCTTCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG  
 ATTGAAGAACAACATACAGGGGAGAGTGGAGAAGAGAAGAGAACA AAAAGTAACTTCAGGATGG  
 GGACCAGTGAAGTACTTGC GCGCCTGTACCCAGAATCATGAGTACAGAAAAATCCAGGAACAT  
 ATCACCACCCAGAACCCCAAGTTTACATGCTGAGGATGTACGAGAAAAAAGGAAAAATCTT  
 CTACTCAATTTCTGAGAGATCTACTAGGCTCTTAACAAAAGACCAGTCATTACAAAGGAGGGAT  
 CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTC AAGGAGCT  
 AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCAACCCTTTAAACAAA  
 AGTTTAGTCAAAGATAATAAATGGAAGAAAACTGAGGAGACCCAAGAGAAACGAAGGTCTTTC  
 CTTCAGGAGTTTTC AAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTCATACA  
 GTATCCAGAATCTATGTAGAAGATAAACACAAAACTTTATATTGTGAGGTACCTAAGGCTGGC  
 TGTTTCCAATTGGAAAAAATTTCTGATGGTACTAAATGGATTGGCTTCTCTGCATACAACATC  
 TCCACAATGCTGTCCACTACGGGAAGCATTGGAAGAAGCTAGATAGCTTTGACCTAAAAGGG  
 ATATATACCCGCTTAAATACTTACACCAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA  
 GTATCAGCCTTTAGGGACAAATTTGAAACCCCAATAGTTATTACCATCCAGTATTCGGAAAG  
 GCAATTATCAAGAAATATCGACCAAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC  
 AAGTTCAAAGAGTTTATCCACTACTTGTCTGGATTCCACCGTCCAGTAGGAATGGACATTAC  
 TGGGAAAAGGT CAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT  
 GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA  
 TTTCCCACTTTAAGGATAGGCACCTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG  
 TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTTGGACTAT  
 TTAATGTTTAATTATACAACCTCCACTTTTGTAGT TTTGCAATTCATTTTCTAAAACCTGTATAT  
 ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTTCTCTGTATGACAGAAAT  
 TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTACCAAATAGTATGACACCAATTTGGC  
 ACAAGTTATAGGAAAAATCCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG  
 GAAAAGAGCTGCTTTTGCAATATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA  
 TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAAATAGCATGAGTGTATGTC  
 TATATCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTCAGAGTCTGTGGCATATTA  
 TCAAACTGTGAATGTTTCTTCTTACACCTTGAAATCTTTCTACCACTATACTCAACTATAATAATCC  
 ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTTAGATTGGAAGGCATTATGTGATTTACA  
 ATATGAGAAATATAGCAGAAAAACA

520/615

## **FIGURE 516**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682  
><subunit 1 of 1, 443 aa, 1 stop  
><MW: 52021, pI: 9.63, NX(S/T): 4  
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKREQKVTSGWGPVKY  
LRPVPRIMSTEKIQEHITNQNPKEHMPEDVREKKENLLNLSERSTRLLTKTSHSQGGDQA  
LSKSTGSPTEKLIKRGQAKTVFNKFSNMNWPVDIHPLNKSIVKDNKWKKTTEETQEKRRS  
FLQEFCKKYGGVSHHQSHLFHTVSRITYVEDKHKILYCEVPKAGCSNWKIRILMVLNGLASS  
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAPFRDKFEHPNSY  
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVKSLCYPC  
LINYDFVGKFFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT  
ERQLIYDFYILDYLMFNYYTPLL

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-24

#### **N-glycosylation sites:**

Amino acids 159-163;243-247;324-328;437-441

#### **Glycosaminoglycan attachment site:**

Amino acids 53-57

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 177-181

#### **Tyrosine kinase phosphorylation site:**

Amino acids 329-337

#### **N-myristoylation sites:**

Amino acids 116-122;236-242

520/615

**FIGURE 517**

GGAACTTCCCAGGCACCCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACATGCTCTGTCCAGCCACCTGCTGC  
 CGCCCTTGGTCTGTGTTCTTGGCAGGCTTCCTCAGGCTGGGCTGGGTCGCCAACCACTGTCAGAGAGCCCTGGCCAGG  
 CCGTGTGCAACTCTGTGTGTGACTGCAAGGAGTGTCTCAGATGAGGCCAGCACTGTGGTTTACACGGGGCTCGCCCA  
 CCTTGGGCGCCCTCTCGCTGTGACTCTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACTCTCAGGTACA  
 GCTGGCTCCGAGACAGGCGCAGGCGCCGCACTGGAGGGTCTCTGGGCTCACTCAGACCAACAACCTGGGCAACGACT  
 TGGGCTGGTACATGGCCGCTTGGAAACCCACGAGGGAAAGGACATCCACGCGAGCCCTGCGCTCGCCAAACCCTGC  
 GAGAGGCAGCTCTCCTCTTGCAGCTGAGGCTCTGGTACCAAGCGGCTCTGGAGATGTGGCTGAACTGCGGGTGG  
 AGCTGACCCATGGCGCAGAGACCTGACCTCTGGCAGAGCAAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG  
 CAGTGACCAACAGGCCCATCGGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG  
 CTGTGGCTCTAGATGACCTAGAGTTCTTGGGACTGTGGTCTGCCACCCCCAGGGCCAACTGTCCCCGGGACACC  
 ACCACTGACCAGAACAGGCTCTGGTGGAGCCCCACGACAGCTGTGCGACGGGGAAGACAACTGCGGGGACCTGTCTG  
 ATGAGAACCCACTCACTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCTTGGGCCCATGGAAACCGCTCGG  
 AAGGCTGGTCCCGGAACACCGTGCTGGTGGTCTGAGCGCCCTCTGCGCCACGCCGTGACCAACAGCCGGAACA  
 GTGCACAGGGCTCCTTCTGTGCTCCGTGGCGAGGCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCGAAG  
 CCTCAGGCAACCTCCAATGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT  
 TCTCTGCAGACTCTGGGCGCCGGCGCCCCGGGCCCCGCTCTGTCTGCGGAGGCGCGAGGGGAGCTGGGGACCG  
 CTTGGGTCCGAGACCGTGTGTGACATCCAGAGCGCCTTACCCTTCCAGATCTCCTGGCCGGGACAGCGGCCCG  
 GGGGCGTGTGGGTCTGAGACACCTCATCTGTCTGACCACTGCAGACAGTCTCTGGAGGTCTCCACCCTTGCAGC  
 CGCTGCCTCTGGGCGCCGGGCGCCACAGCCCCCAGCGCTCGCGCCAGCTCGGCGCTCCAGGATTCCTGCAAGC  
 AGGAGGCATCTTGCTCGCGGGACCTGTGTGTGCCCGGAAACAACTGTGTGACTCTCGAGGAGCAGTGCAGCGGGG  
 GCGAGGACAGCAGCCCTGTGGCACCAAGACTTTTGGTCCCCGAGGCTGGGGCTGGGAGGACGCCAGCGTGG  
 GCGGCTGCAGTGGCGCTGTCTCAGCCAGSAGAGCAGGGGTCCAGTGCAGCTGTGTCTGGGCACTTCTGTG  
 CTCTGCACGGGCTTGGGGCAGCTAGGCGCTGAGGCCGCGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA  
 GCTGTGAACTCCACTGGCTTATTATTATTCAGAGCCAGCCCGAGAGGTCTCCTGTAACTTTGAGCGGGACACAT  
 GCAGCTGTGATCCAGGCCACTCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCCGGCGCTGACCAACGACCA  
 CCAAGGCCAAGGCCACTTTGTGCTCTGGACCCCAAGACCCCTGGCTGGGGCCACAGTGCCCACTGTCTCT  
 CCAGGCCCAAGGTGCCAGCAGCACCCACGGAGTGTCTCAGCTTCTGGTACCACTCCATGGGCCCCAGATTGGGA  
 CTTCTGCGCTAGCATGAGCAGGGAAGGGAGGAGACACACTGTGGTGGGCTCAGGACCCAGGGCAACCGCT  
 GGCAGGAGGCTGGGCACTCTTTCCACAGCTGGCTCCCATGCCAGTACAGCTGCTGTTTCGAGGGCTCC  
 GGGAGGATACCAAGCCACCATGGCGCTGGACGATGTGGCCGTGGGCGGGGCCCCCTGTGGGCCCTTAATTAAT  
 GCTCTTTTGGAGACTCAGACTGGCGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGGCGGAGGCCAATGCCCTCG  
 GCGATGCTGCTGGGCGCCCCAACAGACCATACCACTGAGACAGCCCAAGGCACTACATGTGGTGGACACAA  
 GCCAGAGCGCACTACCCGGGGCAACAGCGCTCCTCCTGACTCCAAAGGACCAAGGCCACTGGCCAGCCGCTGTT  
 GTCTGACTCTCTGATACCAAGGAGGCTCCGAGCCACGGCACCTTGGGGGTCTACCTGGAGGAGCGCGGAGGCG  
 ACCAGTGTCTGACTGCTCAGTGCACCGCGGCTTCTGCTGGCGCTGGGACAGTGAAGCTGTGACGCGCAGAGCG  
 CTTGGAGGTTGGTGTTTGAGGCACTGGCCGAGGCGTGGCACACTCCTACGTGGCTCTGATGATCTGCTCTCT  
 AGGACGGGCCCTGCTCTCAGCCAGGTTCTGTGATTTTGGAGTCTGGCTGTGGCTGGAGCCACTGGCCGCGG  
 CGGCTCTGGGCGATACAGCTGGAGCTGGGCGGGGAGCCACCCCTCTGCTGTACCCCGAGCCCTCTGTGGAC  
 ACACCTCTGGGACAGAGGCGAGGCCACTTTGCTTTTGGAACTGGCGTGTCTGGGCCCGGGGCGGGCGCGCT  
 GGCCTGGCAGAGGCTCTGGCGGCAACCCAGCCCTCTGCTCGCTTCTGATACCACTGAGTGGTTCTCTGAGC  
 ACTTCTACAGGGGGAGCTGAGAGTACTGCTGCACAGTGTCTCAGGGCCAGTGGCTGTGGGCGGCGAGCGGGC  
 ATCGCGGCAACAGTGGCTGGAGGCGCAGTGGAGGTCCAGGTGCCAAGGATTCAGAGTCGTGTTTGAAGCCA  
 CTCTGGGCGGCGAGCCAGCCCTGGGGCCATTTGCCCTGGATGACGTGGAGTATCTGGCTGGGCGAGTATGCCAGC  
 AGCTCTGCCGCCAGCCGGGGAACACGCGCACCCGGGTCTGTGCCAGCTGTGGTGTGGCAGTGGCTCCTTATTTG  
 TCAATGCTCCTGGTGTCTGTGGGACTTGGGGGACGCGCTGGCTGCAGGAAGAGGGGAGCTGCCCTTCCAGAGCA  
 ACACAGAGCAGACCCCTGGCTTTGACAACATCTTTTCAATGAGTGTGCTACCTCCCGGATCTGTCA  
 CAGTGTATCTCGTAGACCAACCCACAGAGGCCCGGCTTCTCACTGCTGACTCAGACACTGGTTCAGACCTCAGCC  
 AGGACCGGACACTGCCCCCGCCAGCTGGGACAGGCTGCAAGTCTCAGGATATGCTGAGGCTGGGCGCTTCCC  
 TGCCCTGTGCTGACTCTGTGCTCTGTGAATAAACCCCTGGGCCATGAGGGCGCGCCCAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAA

522/615

## FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFPLAGSSGWAWPVNHCRSPGQAVCNFVCDRCDSDEAQCGYHGASPTL
GAPFACDPEQOPCGWRDISTSQYSWLDRAGAALGPGPHSDHTLGTDLGWYMAVGTNRG
KEASTAALRSPTLREAASSCKLRILWYHAASGDLVAELRVELTHGAETLTLWQSTGPGWPGW
QELAVTTGRIIGDPRVTFSSATRNATHRGVAALDDLEFWDGCLPTPQANCPGPHHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGFWNNRSEGWSRNHRAGGPERPSW
PRDHSRNSAQGSFLVSVAPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRRGELGTAWVRDRVDIQSAYPFQILLLAGQTPGPGVVGDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPSSRLQDSCKQGHACGDLCPVPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRLLQWRRVSAQESQGSAAAAGHFLSLQRANG
QLGAEARVLTPLLGPSPGSCELHLAYYLQSQPREVSCNFERDTCWYPGHLSDTHRWVVE
SRGPDHDHTTGQGHFVLDPDTPLAWGHSALLLSRPQVPAAPTCELSFWYHLHGPPQIGTL
RLAMRREGEETHLWSRSGTGQNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAGWPPTDHTTETAQGHYMV
VDTSPDALPRGQTSALTSKEHRPLAQPACLTFWYHGSRLSPGTLRVYLEERGRHQVLSLS
AHGGLAWLGSMDVQAEARWVVFEEAAGVAHSYVALDDLQLGQGPCPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYQPQPPVDHTLGTAGHFAFFETGVLPGGGAOWL
RSEPLPATPASCLRFWYHMGFFEHFYKGLKVLVLSAQGLAVWAGGHRHQRWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCCQPAPSPGNTAAPGSPVAVVGS
LLLLMLLVLLGLGRRWLQKKGSCFPQSNTEATAPGFDNLINADGVTLPASVTDSP
```

**Important features of the protein:**

**Signal peptide:**  
Amino acids 1-20

**Transmembrane domain:**  
Amino acids 1075-1092

**N-glycosylation sites:**  
Amino acids 203-207;281-285;339-343;756-760

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**  
Amino acids 514-518;1100-1104

**N-myristoylation sites:**  
Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;  
523-529;540-546;678-684;707-713;791-797;870-876;921-927;  
937-943;954-960;1036-1042;1071-1077

**Amidation site:**  
Amino acids 1093-1097

**Cell attachment sequence:**  
Amino acids 191-194

2025SEP-07T15:02

**FIGURE 519**

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAAGTATCAGCTCTGGCATCTGTAAGGATGCT  
 GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG  
 GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT  
 CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA  
 TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACACAGACCTTCTGTGACATGACTTC  
 TGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC  
 GGTGGGTGATCGCTGGTCCAGTGCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA  
 CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACC  
 TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCAACAAAGTCCCCAT  
 GCAGCATTTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT  
 GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG  
 GAATGACAATGGCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC  
 TTATTACTCACCGTATGGTCAACGGAATTTGTTGCAGGATTCGTTCAAGTCCGGGTGTTTAA  
 TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACTAGCA  
 TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAAACCCCGTCAGTGTGGGGACTTCTC  
 CGCCTTTGACTGGGATGGATATGGAACTCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA  
 GGCGGCTGTACTCTTGTCTATAGATGAGACAGAGCTCTCGGTGTGTCAGGGCGAGAACCCATC  
 TTCCAACCCCGGTATTTGGAGACGGAAGAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA  
 ATCACATCAATTGCA

43051586.014537

524/615

## **FIGURE 520**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSLRLTMTRLCLLLFFSVATSGCSAAAASLEMLSRFPETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGNKA
DYPEGDGNWANYNTFGSABEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYYSPTYGO
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCQGFSAFDW
DGYGTHVKSSCSREITEAAVLLFYR
```

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-26

**Glycosaminoglycan attachment site:**

Amino acids 86-90

**N-myristoylation sites:**

Amino acids 23-29;88-94;127-133;136-142;265-271



**FIGURE 521**

GATCAGTGTGTGAGGGAAC TGCCATCAT **TGAGGT**CTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT  
 GTGTTGGCTGTGGATCTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA  
 TTCTAGAAGAGCTCATGATGAGAGGCCATGAGGTAAACAGTATTGACTCACTCAAAGCCCTTCGTTAAATTGACTACA  
 GGAAGCCCTCTGCAATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAAACAGAGAAATTAATTTGTTGTTG  
 ACCATGCTCTGAATGCTTGGCAGGCTTATCAACCTGCCAATCAGTTATAAAATTAATGATTTTCTGTTGAAA  
 TAAGAGGAACTTAAAAATGATGTTGTGAGAGCTTTATCTACAATCAGACGCTTATAGAAGAGCTACAGGAAACCA  
 ACTACGATGTAACTTTATAGACCCTGTGATTCCTCTGTGAGACCTGTATGGCTGAGTTGCTTGCAGTCCCTTTTG  
 TGCTCACACTTGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCAGCTCCACTTCCCTATG  
 TACCTGTGCCATGACAGGACTAACAGACAGAAATGACCTTTCTGGAAAGAGTAAAAATTCATGCTTTTCAGTTT  
 TGTTCACACTTCTGATTCAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA  
 CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAAATATTTGGGATTTTGAATTTCTCTCAAC  
 CATACCAACCTTAACCTTTGAGTTTGTGGAGGATTGCACGTGAACCTGCCAAAGCTTTGCCCTAAGGAAATGGAAA  
 ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGTGTTTTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG  
 AAAAGGCTAATATCATTTGCTTCAGCCCTTGCCAGATCCCAAGAGGTGTTATGGAGGTACAAAGGAAAAAAC  
 CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTCTTTGGTCATCCCAAAACCA  
 AAGCTTTTATCACTCATGGTGAATGAATGGGACTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTT  
 CCATATTTGGTGATCAGCTTGATAACATAGCTCAGATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA  
 CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCCTCTTATAAAGAGAATGCTATGA  
 GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCCTAGATCGAGCAGTCTCTTGGATCGAGTTTGTCTATGC  
 GCCCAAAAGGAGCCCAAGCAGCTGCGATCAGCTGCCATGACCTCACTGGTTCAGAGCACTACTCTATAGATGTGA  
 TTGGGTTCTGCTGACCTGTGTGGCACTGCTATATCTTGTTCACAAAATGTTTTTATTTCTCTGTCAAAAAT  
 TTAATAAAACTAGAAAAGATAGAAAAGAGGGAAT **TAGAT**CTTTCCAAATTCAAGAAAAGCACTGATGGGGTAATCTGT  
 TTAATTCAGCCACATAGAATTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT  
 ATATAGCCTAGAATTCCATGATCATGAGGTGTGTAGTATATCTCATTCTTCGTGTGATTTTCCTAGGTGTCTTT  
 ACTCTCTTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGAGTGTTTTGA  
 TGATGTCTTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATCTCGTGTGCGCCCAACAC  
 ATGGATATAAAGAGGTAAAAAATTAATAATTCACAAAATTCAGTAACCAACACAAATCAGGTAAAGTGTCTATGA  
 GATTAGCTGGCTATGAGAAAACATAATGATGTTCTTTTTCAAATTTAAATTAAGCCCTTTCACATAGCCAGCATCAG  
 TGATCTCAGAAAATAAATTTGCTTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGGCTGATTTCCATAGAC  
 CTCATCTAGATGTCATGGCCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTGTTTCTTGATGATAAAAA  
 GACCTTTTCTCATGATTGCCATCAAAATAACAAAAGAACTATTTTCTTCTCACAATAGAGAACATGTCAGTAAGAT  
 ATTCAGGTGAACAGATATTTTGGGATTAGTAACCTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT  
 TTAATTTGATAGTACACTTAAGAAAGATTATATGTTTATTCTTTAAAAATGATGAATATCTCATATTTCTTATCT  
 TATAATCAAAAGTATAATTTACTGTAGAAAAATAAGAGATGCTTGTCTGAAGATAGATCAGTAACTGCTTT  
 TCAGTCTCAATCTTTGAGAATTTGTAATTCATCAATAATTTGCTTACATAGTAAAAATTAAGGTATTAGAAAAC  
 CTGCTATAACCAATAGTATTATATAATTAATTTTATATGTAAGAAAGCTACACAAAGCTAAAATATAGTGATAATA  
 ATGTTTCTACAGTAGTAAGCAAAATGTGTAATCTCTCATTTTCTTATCTGTCATATTAATCTTAGTGATAGCTTAT  
 AATGATTTTAAATAAATAAATTTGGCTTATCTGGCTTTTGGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA  
 TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAAATATAAGTATTTTCTGTGTATGTATACA  
 ATAAATATAAATAAATTTGTTACTGTTTTGAAAGTTTCTTAAGTTTTA

526/615

## **FIGURE 522**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720  
><subunit 1 of 1, 527 aa, 1 stop  
><MW: 60284, pI: 8.31, NX(S/T): 3  
MRSDKSALVFLLQLFCVGCFCGKVLVWPDCMSHVLNVKIVILEELIVRGHEVTVLTHSK  
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNLVLPGLSTWQSVIKLNDFFVEIRGT  
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER  
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR  
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED  
GIVVFSLSGLSFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYLDWIPQNDL  
LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKMTS  
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAHD  
LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-21

#### **Transmembrane domain:**

Amino acids 489-510

#### **N-glycosylation sites:**

Amino acids 131-135;313-317;518-522

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 67-71;340-344

#### **Tyrosine kinase phosphorylation sites:**

Amino acids 122-131;136-144

#### **N-myristoylation sites:**

Amino acids 19-25;276-282;373-379;377-383

#### **Amidation site:**

Amino acids 338-342

2025-09-25 09:50:53

**FIGURE 523**

GGCTGCGGGGTGCGCACGGAAG**ATG**CACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC  
 GGCCGAAACAGAGCGCGCGCTTTACACCGTGGCTTACTACTTACCACAGGACGGCTTCTGTG  
 GGGGTGGCTGGCCCTTGCTGTCTCTCTGCCCGGGTTCCTTGGTCCAGGCCCTGAGCTACCTGTG  
 GTTCCGAGCAGACGGGCATCCAGGGCATTTGCTCTTGGTGATGCTGCACCTCCTACAGCTTGG  
 TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACCTGGAGGCTCCCCA  
 CCGAGGCTGGCTGCACTGTCAGGAGGCCGACCTGTGCGCCCTTCGACTCTTGGAGGCCCTGTCT  
 GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTCTTAGCCTCAGACTTCACAGATATT  
 GTGCCAGGGGTGAGCACCTGTTTTCTGTGCTCTCACTCTCCTGGGCACTGGTGTCTTACACT  
 CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG  
 CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGTCTGAGTCTGGTTCTGTTCTACAAAGCC  
 TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTGTCT  
 GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG  
 GCCGTGTACATCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG  
 TTCTACATGGTACGCTGTTGGAGAACATCATCTGTTGCTGTTGGCCACCGACTTCTTCCAG  
 GGGGCATCGTGACAGCCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCGTGATTGGCAGT  
 GTCTCACTGGTAATTTATTACAGCTGTGTCATCCAAAATCCACAGACATCTGGCAGGGCTGC  
 CTAAGGAAGTCTGTGGCAITGCAGAGGTGATAAAACAGAGAGAAAGAGATTCTCCCCGGGCC  
 ACAGATCTAGCTGGGAAGAGAAACCGAGAGCTCAGGCTCATGCCAAGGGCCGAAGTTATGAACCA  
 ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG  
 GTTGCTGTGGAGGACTCTTTCTCAGTCATCACCACTGGCTGTGGGTGAAACTTGCCCTAAAA  
 ACAGGAATGTGTCTAAGATCAATGCCGCTTTGGAGATAACAGTCTCTGCCTATTGTCCACCT  
 GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCCTGTCTGCCCAGCAAGAGCTC  
 CCATCTCATCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA  
 GCAGAGGCCGACCCATTGGAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA  
 GCACCTACCCAGAACCAGCAGCCACGAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT  
 GTTCTTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT  
 TCCACGTTGTACTTCAGCGCCATGTCAGAAGTGGCCACATCTCACAACAAGAGGACAGCCCA  
 GCTACTCTGCAAAACGGCCCATCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA  
 TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA  
 GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTCAGGCTTCCTCGGAAGAACCTCAGTATC  
 TCAGAGCTAGAGGAGCCGCTGGAGCCCCAAAGGGAGCTAAGTCAACCATGCAGCTGTGGTGTG  
 TGGGTGTCTATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCAGTCCACCCCTAAGTCT  
 GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAGGATTTTTCATC  
**TGA**CCACAGTCTATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTGGTACCCT  
 GAGAAAGGAAATCCCACTTCTGACACCTGTGTCTTGGGCACATCACTGTCACTCTGTAATCT  
 CCATCTGCATCCTGAAATGAAGAAACAGGCTGGATGATTTTGAGGTTCTGTGTACAATT  
 TCACAGACCCACCCATGCATAGGAGAGACTTAACATACCTTTAGAGAGAGAGAAGAGATT  
 CAGTCAAAATTTGCTGTCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTCTGTG  
 GCTTCTAGGAACACAAAGGTAAAACCCAGATTCTTATTTATTGAGGTTCTGTGTACAATT  
 AGCTTTGCTCATCATTTAGCGGTTATGAATCTCATTTTAAATATATTCTAAGTGTATATGTGA  
 TGAATCTCTTGGTAAGATATTGTCATGCTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTGA  
 ATAATAACATAACTGAAAGTGCAATGTCA

528/615

## FIGURE 524

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726  
><subunit 1 of 1, 686 aa, 1 stop  
><MW: 74981, pI: 6.60, NX(S/T): 2  
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD  
GHPGHCSLVMHLHLQLGVWKRHWDAALTSLQKELEAPHRGWLQLEADLSALRLLLEALLQ  
TGPHELLLOTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF  
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF  
NLLGVAVIILCYLSFWSDSPSRNRMVTFYVMVLENIILLLLATDFLQASWTSLTQTIAGV  
LSGFLIGSVSLVIYYSLHHPKSTDIWQGLRKSCGIAGGDKTERRDSPRATDLAGKRTES  
SGSCQGASYEPTILGKPPTPEQVPEAGLGTQVAVEDSFLSHHHWLWVKLALKTGNVSKI  
NAAFGDNSPAYCPPAWGLSQODYLQKALSQQELPSSSRDPSTLENSSAFEGVPKAEAD  
PLETSSYVSFASDQQDEAPTQNPAAATQGEPTPKEGADAVSGTQGGTGGQQRGGEQQSS  
TLYFSATAEVATSSQEGSPATLQTAHSGRRLGKSSPAQPASPHPVGLAPFPDTMADISP  
ILGTGPCRGCFCPSAGFPGRTLSISELEPLEPKRELSSHAAVGVVWVSLPQLRTAHEPCLT  
STPKSESIQTDCSCREBQMKQEPSFFI

### Important features of the protein:

#### Signal peptide:

Amino acids 1-17

#### Transmembrane domains:

Amino acids 35-50;269-287;293-313

#### N-glycosylation sites:

Amino acids 416-420;467-471

#### cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

#### N-myristoylation sites:

Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;  
390-396;473-479;529-535;536-542;558-564;603-609;  
643-649

#### Amidation sites:

Amino acids 354-358;568-572

#### Leucine zipper pattern:

Amino acids 112-134

10052536-011502

**FIGURE 525A**

AGTGCCCTCTGTCACTTTAACTCCACCGAGTCTCGAAGTGCTTCCAGGTTTGTCCCCATCACACAGATGAGGCC  
 AATCGTTTCGTAAAGACTGTCTTGGGTCACTTATGTACGCAATGAAATCGGTGTGCCATTACTAAACCCCTTACT  
 GTGTGCTGGCATTTGTGATGCATGCATGTGTGTGGCTGCACAGCTGTGTGTTGGCTGTGATGTGTCATGTGATGTGTG  
 TTTGTGTGCTGTGTGTCACATGTGAGAAAGAAAGTGTGTGTGGGAATGGGAATTTCCAAACCCAGGAGGACTGT  
 TGCTCTGGGGCTGCCACGAGCTGGGTGACACTTCGAGAAACGGGTTCCAAATGCAGTGTGCTCTCCAGTTCTCTGT  
 TGTGACCTTGGGCAAGTCACTTCAGCTCCCAGGCTTTGTTTTTAAATATTTTTTAAATGTATAAAACCATGG  
 ACCATTACATATGAAGAGAAATGTGTGTGCACAACTTCAGTTAAATATCAACAGGTGTGAGGAGTGTCTGCTCAGA  
 CCCAGAGCTGCACACAGGGAACTCTCCACAGAGGCTGCAGGGCTTCCCTCCCAACCTTCAACGGCCCACTTGTCTGT  
 AGCCCGTGCTTATCTGTTCAGTGGAAATGCCATGTGCCACGTTCTCCAGAAAGTAAAGCACTAGGTAAAGTGTGAC  
 ACTCTGTGCCAGCTTGTGTCAAAAGCCCTTGTGTGTGCTATCTTATTGACCTCCAAATAGCATGTGTAAGGTCA  
 GTACTGTCACTTCCCCACCTTTGAAGATGAGGAGAGCACAAATCTAGATGGAATGGAGGTTCACGCGATGTGAA  
 TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATCTTCCATTCCACGTACCGTTGAAGCTCAATCTCTCT  
 TTCTGTGTGATTTCTCCCACTTCCCCACCCAGATATATCCCATCCGTGCTTGTGTGGACAGTAGCCATGACTG  
 GGTTTTGTGAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTCATTTTACATTTTCCCAAGTGAATGGGGC  
 CCGATGAAAAGGCGACTCAAGTTGTAATTTACTCAAGGAAGGACAGAAAGGCTTCTGTGTTGCACCTACCCCTA  
 AGGATTTGGGGTAGACACTGGGAATTTACTAATTTATGAATTCAGTGCTTCTTGTCTGAAAAGAGGCGTGGAA  
 TCAACGCTGATGAGAAGGCTCAAGTTTAAGCTGCTAATTACTTCTCGATCATGCAGAAATAAAGCTACGTCCTCT  
 GAAATACACAGGCGACTAAACATAATCTTTCGCTTTCGGTAGTGTGGTAAAGGAATCCAGATGTTACTGCAAT  
 AACCATCCATTAACAAAGGAACACCCAGCTGTGAGAACTTGCTTCTCAGCATCTCTGCCAGCAGAGGCTCTTC  
 CGGGGCGCCCTTGGAGAACCCATCAGGGTTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTTGGCAGGACG  
 ACGGCTACGCGGACAGCCAGGCTGAAGGTGAGTCCAGCACAACTTTCTGACAGTGAAACAGGAGTAAACATG  
 GGACCCACCCGAAACCTTTGTCTGTGACTTCTTAGCAATGGAGGAGCTCTAGGCTCTGGAGAGTTCGGGTAT  
 AGGAGCCATGACTTTAGAGCAGCTGATATAAGTGAATGCAACATATTTAGATGGCACAACCTTAATTTAGATTT  
 ATCAGTGTCTAATAGTAAAGAACTGATTTATTTGGGGCTTATAGATTTTATGCTGTAATCTTCAACCTTACG  
 AGGGGCTGCTTTTTCAGACATATGATCTTGCAATGATTTCCCCAAAGATGCTCATTAAGTATATGTTGAAGATAGA  
 TTTTGAATACAGAAGACCTGGTTTCTGCTACTTTCTGTGTTTCTTATTTGGTTCAAAACCGCTCTTTCTCTTTCAAA  
 ACAACTTCAGTGCAATTCATGTTTGTGGAAAAATAAATGATTTTGAATTTGAGATTCAGACAATAAGTGCAATTTTAAATG  
 TTTATCTTTTATCTTGAATAATGATATATTTATGAAATGATATGTGCTCACTCACTGTGTCAACACTTCAAAACA  
 CACAGCAGTACAATGACAAATTTGGAGTCACTGCTCTAATCTCGGCCCCCAATTTAAATGATTTGCTGAATATCTCT  
 CTGAACATAGTCTACATCCCACTGTGCCATGACACAAGACGCTCCAGGGGCTGAAGATAGAGGCACTCTGCAG  
 TCAAGAGAGCTGGGAACTCTTGTGACAGTCAATGTGCAATTTGGGTATTAAGGCTCTGCAAAAGTCTGCAACCA  
 AATAAACCTCTGATTTGGTGTGATCTCAATGCCATGTTTCCAAACCTACTTGTGCCGTGGAGCACTTAGTGCATA  
 ACACAGGTTGGCACTTCTCTAGAGAGTGTGCTGTGAAAAACACTGCTCTACAGCACGTCGATTTCTCACAGCA  
 GGTATTTACCAAGCAGGACTTTGGGCGAGCTCCAGGCTGTGCTGTGTTTGGAGCACTTCTTCCGACATGAGATA  
 GAATGAACCTGCAAACTTTGGGGGCTACGATGGTTTGTAGAAAGAGCTAGAGTGAAATACCTTTGACATATAT  
 ACATACAAATAAAGATACATGTGTATTAATTTATGTAATTTGACATCAATATATGCTGGCACTGCTCTTTTGT  
 CTTAATGAAATGTCAAAGGTAATATACCAATCAATCAATATTTCCACATGCTGTTAAATTTCTGCAGAGCA  
 TTTTCTTCAAGCACATATGCAATTTTCTTAGTCACTCACTGTTGGGAATAGAAAGTTTCTCAGGCATGCAATTT  
 TCCACTCTTGAATGATCTCTTGAATAAATTTCCCAAAATGTATTGTGGGTTCAAAGCAGTGAACATTTTAA  
 CATTTTATACAAATATGTCAAACTCACTTCCGGAATGATGCTCACTTTTACTTTCCCTCCAAAGCTGTGTGAA  
 ATGCCATCTGTTTAAATGCTTACTATGACTGGTTTCCAACATCATTTTAACTTTCTGTGTTGTTGTTGTTGTTGTTG  
 AAATGATATTTAAATTTTATTTGATGATATGACCTTGAAGCGTGGCCATTAGCTTTTGCATGATATTTCTTTAT  
 GAAACATCTGTCTCTATCTGCTCAATGTCTCTTCTCATATGTAACTTTTCTTATTTGATTTGTTTAGAGCACTT  
 TGTATTTGTAATATTAGCTTTTGTGATCAGAAATTTGGAATTTGTGTTGTTGTTTGTGTTTGTGTTTGTGTTTGTG  
 AAAGCACTCAGAGATGTGTGTAATGTGATGTTGTTAAATTTATGCTTATTTTGTGTTTGTGTTTGTGTTTGTGTTT  
 GTTTAGATGTGTCAAGCAATCCCACTATGATATACATAAATATTTCCCAATTTTGTGTTTGTGTTTGTGTTTGTGTTT  
 TTTTCTATGTAACCTCTTTGTTCTTTCAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCAGTTTCTTATGTTT  
 CCAATGGTGTGATCAGCTGTGCTTATTTCCATTTCTCTCTTATAGAAATGACCACTATTTATGTTTGTGTTTGTGTTT  
 TCTGCTACTTGTGCTGCTTCTCTATACTCAGTTCATCTTGTGACTTCTTGTGATTTGTTTGTGTTTGTGTTTGTGTTT  
 ACTGCTTTTACTGAACTGTCACTCATCTTATACATTTTAAATACTCAGCAAGACAAGTTTCTCAATGGCACTCTTTT  
 TCGAGTTTCTTGTGTTGTTGAAGATGTTTATCTTCTGTTGATAAATTTGAATCACTCTTTTGTGTTGTTGTTGTTGTT  
 AAATATATCCCACTTGAATCATACTGAATATACAGACTAATTCAGGAAAAATGATGCTTTTATTTGCAATTGA  
 GTCTTCTTATCCCAATAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTATTTTGTGGCTTTTCA

1052586.01502

530/615

**FIGURE 525B**

CATGTCCTGCAAATGATTTGTTAAATTATTTTATAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC  
TAGCTTGTATATAATTTACATATGAGATAGTCATTGTTGTATATTTATATACTGATCATATTACTGTATTGTGA  
TTGTTTAAATAGTTTTTCTATATTTTGGGTTTTCCGGAATACAACCTTATTATCTACAAATTATGATTGTTTT  
GCCTTTTCCAATGTTTCATAACIGTTTTTATATTCTTGTCGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT  
GCAATACTAATGA

2015-04-23 15:55:00

531/615

## **FIGURE 526**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728

<subunit 1 of 1, 100 aa, 1 stop

<MW: 10922, pI: 8.81, NX(S/T): 0

MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVVMCMCVLCACVCTCRKKVMCGNGEFQ

PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-28

#### **N-myristoylation sites:**

Amino acids 80-86;94-100

#### **Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 13-24;34-45

108728

**FIGURE 527**

GTGAGACTTCTTCTTCATTGTGGCTAGCTTTGAAAAGACCCCTCTGAACTTCCTAAAGATATC  
AAG**AT**GATATCACCAGACTTGCCCTTTTTGACAATTGCTCTTGATCATAGTTAGTTGGACAAC  
TGTGGAGCACTAGCCATACTTCTTCTTATCTTTACTATGTGTTAAGGTTGTTTCATCTGCAA  
GCCAGCTTAACAACTTTTAAGAATAGCCAGCCTGTGAATCCCAACACTCTAGAAGAAGTGAA  
AAGAATCCAATCATATAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT  
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACCTTACTAACATGGATTGTATTACTCAGC  
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA  
TGTAACCTTTGGCATTATCCTTATTCCGACTATGGCAATTCTTGGAAATACTTACACTGTT  
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT  
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCTCTTTTA  
CTCCATGCATTATGCAACTTTATG**TAA**GATTGGACTTAAGGAATGATGAAGATAATTTATGTG  
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA  
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG  
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC  
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT  
ATCAACTGTAAA



533/615

## **FIGURE 528**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLNLRYYFK
LNPDPCCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLRPLP
CFVFIPLLLHALCNFM
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-25

#### **Transmembrane domains:**

Amino acids 91-108;128-143;167-186

#### **N-myristoylation site:**

Amino acids 141-147

108738.DNA108738

CCGAGCCGGGTCCTCCCACTATGGCCGCGAATTATTTCAGTAGCACCAGTACCCGGAGAGAACATGTCA  
AAGTTAAAAACCGACTCCCGACCGAGCTTCCTGGAAACGGCTGAGCGAGACCTCGGGTGGGATGT  
TTGTGGGGCTCATGGCCTTCTGCTCTCTCTTCACTTAATTTTCAACAAATGAGGGCCGCGCAT  
TGAAGACCGCAACCACTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA  
TGTGTGGCTCCGGAGTAAGGAAGGCTGTGCATCATCATTGGGCCCTTACGCACATCCAAGCTT  
TGTCCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTCGGAGGCGACGTGGAGAT  
TACCAATTTGGGTAGAAACTGAGGAGTTCGAGGAGTACACCGAGGATGGGCGAGGTGAAGAAGGAG  
CCAGGATTATCTCTACAACTGAATGGAGGTGAGAATCATCAACGAGCAAAACCTTCGACGAG  
GAGATTGGCCACAAAAACCCAGTGCATTTGGCAGTGGAGTCATTATGGCAACAGCCCCCTTT  
GTCCAAATTTGGCAGGTTTTCCTCTCTGTCAGGCTCATCGACAAAGTCAGCAACTTCAAGTCT  
CTGACCTTACAAGCTGGAAGGACCTCATGTTGGACATCATTCGCCCTGGGAGACTTTCCTTAC  
CACAGCGAAATCCCAAGTATCTCAGAGGTGGGAGACTTGGCTGTCTCCTTTTCTTATGCTGGA  
CTGAGCGCGGATGACCTGACCTGGGCCAGCTCACGTGTCTGATTGGCCGCGACGG  
GGTGACGAGCTAGTCCCATCTCCACCAAGTCTGGGGATCCTTACTGCTCTGCGACACGGG  
GACTTCTCAGCAGAGAGAGTGTTTTCATAGAGAATAAGGAGCAACTCCATGAAGACTCTGGGCG  
CTCGGGGACGCTGGTGGATGGCCATGTTTCATGGGCCCTCAACCTTATGACAGGATCCTCTAC  
ACCTTGGTGGACTGGTTCCTGTTTTCCGAGACCTGGTCAACATTGGCCCTGAAAGCCTTTGCC  
TTCTGTGTGGCCACCTGCTGACCTGCTGACCTGGCGGCTGGCTGGCTCTTCTACCGACCT  
CTGTGGGCTCTCTCATGGCCGCTGGCCCTTGTGGCCATCTTGTGTCCTGGACACGGGT  
CCAGCCAAAAAGTTGGAGTGAAGAACCTGGCACCTGGCCGCGACCTGCGTGGAGCCTGAGG  
CTGGTTGTACAATGGCCACGCTGCTGGCTGCTTCCAGCTGGGAGTGGTTTCGATGTGGGCA  
CTGGGCTTTCCTAGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT  
TCCTTAATTAAGATCAACCCACCACTAAGTTCAGATAAGTAATTTAAGTCCCCCACTACTCTACA  
CCCTTTTAAAGATTAAGTATGTTGTAACAGGACGCTTAAATGATCTTTGTGTACTTTTTC  
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG  
TAGCTGAATAAAGGGTCAGAACTTCTGAACACAGAGATCTGTAAATCATCTTATTTGCTGGG  
GTGCTGTGCTATAAATGAGTTTCTTCATGATAAAACACAGCCAGCCCAAGTACATTAATCT  
GGGTTAGGATTCAATGATATTTCTACTAATCTGTTATTACATGAGCAATTTCAATCAAACTCCA  
AACTCTTAAGAGTATCTTTCCGAAAAACCGCTGTTATCTAGATGACTACATGCAAAATCT  
CTGGGCTTTGGTTTTTTCTAGTAGGAATTTTAAATAAAGTGGCACTTCAAAGTGTCTTTA  
AAACGAAAGATAGATTGAAGAAATTTGAAAGCTTTGGAAGAACCAAAATTTGTAATATCATTG  
TATTTTCTTAAAGAGTTTGAATAAATTTCTAAATATCA

535/615

## **FIGURE 530**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743  
><subunit 1 of 1, 400 aa, 1 stop  
><MW: 44876, pI: 8.32, NX(S/T): 2  
MAANYSSSTSTREHVVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT  
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPAVKLRRHVE  
MYQWVETEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVBSFMA  
TAPFVQIGRFFLSSSLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR  
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEVFHRE  
LRNSMKTWGLRAAGWMAFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFAPCVATSLT  
LLTVAAGWLFYRPLWALLIAGLALVPTILVARTRVPAKKLE

### **Important features of the protein:**

#### **Transmembrane domains:**

Amino acids 34-53;365-388

#### **N-glycosylation site:**

Amino acids 4-8

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 140-144

#### **Tyrosine kinase phosphorylation sites:**

Amino acids 99-107;220-227

#### **N-myristoylation sites:**

Amino acids 35-41;93-99;310-316

#### **Cell attachment sequences:**

Amino acids 221-224;268-271

10052536.01430

**FIGURE 531**

AAAAAAAAAAAAAAAAAAGAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG  
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGGGAACTTGAGAGAAATGGGCAATAA  
CTGTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT  
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTCCCTCTCTCTCTTCCCCCCTCTTT  
CCCTTCTGTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTCAGA  
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCTGCAGTTTAAACAGGCTCAGGAAT  
TAGGTGCGATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG  
GACCATTTCTGCCTTTTCACTATTACATCCCCCGCTGTAGCCAGCCTGCCATACAGTAGA  
TACTCAATAAATATTTGCTGAATGATAACCAATAA

537/615

**FIGURE 532**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10316, pI: 8.52, NX(S/T): 0  
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFSLFPPSPFSPVFLRSKGYNGGA  
NCLAISDKTSLSDCSAHDLPCLSLTGSGIRSHQLSAGHLGL

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-47

**N-myristoylation site:**

Amino acids 58-64

2025.03.03.08.00.00

**FIGURE 533**

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG  
 CTGAGCCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG  
 TAGTCCCCATCTCTGGAGGGGAGGCTCTGCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTC  
 GCCCTCCTGGCTGGCCTTCTCGTGGGAGTGCAGCAAGTCCATGGAGAACACGGCCAGCTG  
 CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT  
 CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA  
 ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC  
 ATGAACAGAAGCTCAGGGACCCCCCGGGCGGCCACATCCTGGGGCTCCGCGGTGGCCGCCTCC  
 CTCCTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTCTCTTCTAC  
 CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAGCTCCGGCCCTGCAG  
 CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG  
 GAGGACCCACACGACAGGGCAGACCCCCAATACCTGCTCCTCCTTGAAGTCCAGCTCCACCC  
 GAGGACAGACGCAGCCGGCCTCCGCGAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG  
 GTCAGGCGGACCCAAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTGAGGCGGGAGCGGCCCT  
 GGCAGGGCCACGGATCCCGCTGCTTCCCGGGGAGGCCCGTATCAGCAATGTCTGACCTGG  
 AGGCCGAGACCACGCCACGCACTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC  
 AGCACAAAGTGTGGCATCGCCGGCGCCCGGGACAGTCTTGGGCACAGCCTCGGCTCTGGGT  
 CCTCCGCTCCACAGCAGCGACGCCAAAGGGTCCGGGCCGCTGAGGCTCTCCCCACCAC  
 AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC  
 CTTGGGGGGTCCGGGCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG  
 CACGATCTATGGGGCAGGTGCCGCTCTGCCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC  
 CAGAGCCCACAGCGGCAGGACTCCTCCAGCACCACCAACCCAGTGGCCCCGAGACCCCTCTG  
 AGAACAGTGAGGCTGGTCTCTCGTGCCGTTCCAGCCGCTGCCCGCCAGTGGGGAGGACACAGC  
 CTAGGAACCAAGCTGCCCTGAGACCAGGGTGCCCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC  
 AAGCACGCAGCCACCATTTCCGGAGCTGCAGSATAGAGCTTCTCTTGATCTCTGTTTTTAAG  
 CAGAAATTCAATTGTGCAGAAAAAGTCCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC  
 CCCATGCCCTGGCTGATCCCTGCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG  
 CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCTGGGGTCCCTCCCGGAGTTCCCTGG  
 GAGAAAGCGCCGTCGTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA  
 CGCCTTCGGGCACCCGACCCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC  
 TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG  
 GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

539/615

## FIGURE 534

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
>>subunit 1 of 1, 189 aa, 1 stop
>>MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLALVGVASKASKEINATQLPBCCVDVVGVNASCPGASLCPGPGCYRRWNADGS
ASRCVCGNGTLPAPYVSGSEKSFAGTAPGPPFMMNRSSGTPGRPHPGAPRVAASLFLGTTFIS
SGLTISVAGFFFYLRSSSKLPACRYRKNKAPALQFGEAAAIPIPPQSSDVSGSAGKEDPPRQ
GRPPIDAPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

**FIGURE 535**

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCTGCGGTGGTACCAGCCTCCAGCCTGCCCCCA  
 GGACTGCCCTGACCCAGGCGCGCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**  
 CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC  
 TGGTTGTGCGTCTTGTAAGTGAAGTGAATTTCCCATTGCTACTAACTGCTTTGGACAACCTG  
 GTACAAAGTGGATACCATTTCTCTACACATACAGCGCGCCCTTCGAACCTCACTATGGATACA  
 TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT  
 CAGGTGAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA  
 TGAACAATGCCCCACCAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTCGAGTTG  
 TGTCCCATACCAAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA  
 CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT  
 ACAACATGTTGAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA  
 AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAGT**GAC**  
 CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCTCTGCCCCACCACAAAAGGA  
 AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA  
 AAACAAATACCCATGTGAGTGGTTCAAAGATTAAAGATTGTGGCTTTGTGTAAAGTTCCTTCCC  
 TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA  
 TTGTGGTATGTGGTATGTAAATATTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTGTT  
 TATTCAAITTTGCTTTATTAAATCTTATCAAAGCA



541/615

## **FIGURE 536**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783  
><subunit 1 of 1, 210 aa, 1 stop  
><MW: 24022, pI: 9.51, NX(S/T): 1  
MACILKRKSVIAVSFIAAPLFLLVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT  
HYGYINVKTQEPQLQDLCDLCAIVSNSGQMGVQKVGNEIDRSSCIWRMNNAPTKGYEEDVG  
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGII  
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-27

#### **N-glycosylation sites:**

Amino acids 148-152

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 6-10;191-195;201-205

#### **N-myristoylation sites:**

Amino acids 41-47;87-93;91-97;167-173;178-184

**FIGURE 537**

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT  
 CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA  
 ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCCCTGGGAGCCTGGGGTTGGCCT  
 TCTACCTGCCTTTGGTGGTGACTACACCTAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG  
 CTGTGGGAAAAGTTATCATCAATGCCACAACCTGTACTGTCACTGTGGCCTTGGCTATAAGG  
 AGGAGACCGTCTGTGAGGTGGGCCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA  
 TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTCAACATTCTCATTGGCAAGGAATTTGAG  
 CTTAGCTGTCTGAGTTTCAAGCATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACTGGAGA  
 CTTGCTCGAGGTGTCTATCTCCACTGACGATGAGGTCTTCAAACCTTTCAAGCCAACCTCCAC  
 TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG  
 GTAAAAAATCTGAGACTTGTCAAGAGGCTCTATTTTGGGTGAGGGTCCTTCCTCCTAACTTG  
 GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA  
 GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAAAAGAAGGTGGCGTCAGCC  
 TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTTGGTGAGGATTGTCCTCTGTGCG  
 CTAAGGGGGGGCCTGCAGCAGTGAAGCTTCAAGAAGCTTAACAGCCTTGTCTCTGAAGAAGT  
 GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT  
 TAGAGGGAACTCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG  
 AGCTATGCGCAGTAACCTAACTTCCTTATGTCCATGGATCTCTTCTGATCTTCCCTGCCCA  
 TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTCTGGGAAGAGTTCTAAGAAGCTTGCA  
 TTCATTTTCTACCTTTTATGACTTGGATGCCTCCCACTCCATTTCCCTCTTCTGAGCTGT  
 GTATTCATGTAGAGGGATGTATTACGCTTTTTTAGTGAACATTTTTTTTCAATAAAGTAATT  
 CACAGTAA

543/615

## **FIGURE 538**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVTPKTLAIPEKLQEA VGKVIINATCTVTCGLGYKEE
TVCEVGPDPGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEA FRPT
WRLARGVISTDDEVFKPFQANSHFVKFKYAEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-30

#### **Transmembrane domain:**

Amino acids 225-244

#### **N-glycosylation site:**

Amino acids 45-49

#### **N-myristoylation sites:**

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

**FIGURE 539**

GCCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG  
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGC**ATG**AAATTCAGCCAGCGCAC  
TACCTGCTGCCTCTCCTGCGCTGGTCCTCAGCACAGACAGGACTATGAAGAGCTAGAA  
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTTCTCGTCAGCTGACAAAGACATCA  
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAACGATGAGCAGTCTGCCAAA  
ACTGATGTTCAGAAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG  
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT  
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT  
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC  
TTATTGATGTATCTCT**AG**TACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT  
GTGGAATTAATTAATAA

545/615

## **FIGURE 540**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL
```

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-22

**N-myristoylation site:**

Amino acids 54-60

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 541**

CTCCACGAGGCTGCCGGCTTAGGACCCCAAGCTCCGACATGTCGCGCCTCTGGTCGCGCTGTGTC  
 TTCTCACCATCGTTGGCCTGATTCTCCCCACAGAGGACAGACGTTGAAAGATACCACGTCCA  
 GTTCTTCAGCAGACTCAACTATCATGGACATTCAAGTCCCGACACGAGCCCAGATGCAGTCT  
 ACACAGAACTCCAGCCCACCTCTCCAACCCCAACCTGGCCTGCTGATGAAACACCACAACCCC  
 AGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACA  
 AGAGCACCAAAGCAGCTCATCCCCTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAA  
 GCACAGACGTCCAGACAGACCCCCAGACCCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCT  
 TCTTCTATGATGAACACACCCCTCCGGAACCGGGGCTGTTGGTCGCAGCTGTGCTGTTTCATCA  
 CAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGGTTATGCCGGAATCGTT  
 GCAGGTGAGTCCATCAGAAACAGGAGCTGACAACTGCTGGGCACCCGAAGACCAAGCCCCCT  
 GCCAGCTCACCGTGCCCAAGCCTCTGTCATCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACAC  
 AGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCTGCCCCGCC  
 CTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAG  
 TAAAGCACTGTGGTCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

**FIGURE 542**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
>>subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPSTRGTDLKDTSSSSSDSTIMDIQVPTRAPDAYVTELTQVTSPT
PTWPADETPTQPQTQQLGELDGLPLVTDPETHKSTKAAHPDTDDTTTLDERPSPSTDVQTD
PTLTKPSGFHEDDPPFYDEHTLRKGRGLVAAVLITGIILTSKGRQLSRSLCRNRCD
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

**FIGURE 543**

CGGCTCGAGGTGAGAAGGAAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC  
 TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCAGTCCC  
 GCTCCGCCCTTTGAAGGGTAAAAACCAAGCGGGGCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**  
 CCGCAGAAATTCCTCTCCCTGCTTTGCCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA  
 ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCAGCTCGGTGGTTGAAGCCGAGAGCA  
 ATGTGACCCTGAAGTGTGAGGCTCATTCCAGAATGTGACATTGTGTCTGCGCAAGGTGAACG  
 ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAAACGAAGCTGAATTCCTTCACGGACC  
 TGAAGCCTAAGGATGCTGGGAGGTACTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT  
 CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACCTGAAGCTCCCT  
 CAATGAAAACAGACACCAGAACCATCTTTGTGCGCATCTTCAGCTGCATCTCCATCCTTCTCC  
 TCTTCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA  
 CCAAGAGAACCAGCCATTCCAACCTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA  
 TGGAAAGGGTATCTCTCTCGACGGCAGACCCCAAGGAGTGACCTATGCTGAGCTAAGCACC  
 GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCAGGATCTCATGAATATGCGG  
 CACTGAAAGTGT**AGCA**AGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGTCTGGCCAAG  
 GTTATCGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCATATCAATAAAAT  
 TAAGTTTCTCGTCTTA

1005236-01501



**FIGURE 544**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFDLKPDKAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSESSESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSSEAASDTTQEPPGSHEYAALKV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**Transmembrane domain:**

Amino acids 135-153

**N-glycosylation sites:**

Amino acids 44-48;55-59;64-68

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 171-175

**Tyrosine kinase phosphorylation sites:**

Amino acids 61-69;87-95

**N-myristoylation sites:**

Amino acids 12-18;203-209

**FIGURE 545**

GGCGGCCCGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGGATCCTG  
 CTCTCTCTCAGCCGCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGTCTCAT  
 ACCAATGGCTTCAGTGATGGCGGTGACTGAAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCT  
 CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGTGCTGCCCCTGGGGGC  
 TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGCCCTCTACCTGCTCAGGAGCAAACCGGACAG  
 GGCGCAGCATGCCGCCACCAAGTGACACGAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG  
 CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC  
 CCTGAACCAAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT  
 GCACGCCCTCAAGATGGACCCGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA  
 AGAAGACAAGGACATCATCCAGGCGGACTACTGTACACCAGAGCATTGACCATCTCACCTTA  
 CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG  
 GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACTCAGC  
 TCTGCGCAGGGTCATGGAGGAGCCTACTACCATCAATCTACCACACAGTGCGCCATCGAGGG  
 CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA  
 GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC  
 TCTGGTTTCGCGCATCGGCTCCGTCAACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT  
 GGGCTACGTGGACCCCGTGGAAAGCCGGCAGGTTTCGGACAACACAGGTCTTGGTCGGACCA  
 CATCCCTCCCATCCGCAAGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC  
 GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCCATTATAAACTCGTTTAC  
 ATCCACCCCTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG  
 CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG  
 GAAGCTGCCAACGAGGGCGACGTGAGGCCCTTCATTTCGCTTCATCGCCAAGTGTACTGAGACC  
 ACCCTGGACACCTGCTTTTGGCCAACTGAGTACTCGTGGCACTGCCAGAAGCCCCAACCC  
 AACCACTCTGGGTTCAAGGAGAGCCTTCCTGTGAAGCCCTTAACCCTAGAAATCCTCAGTGACA  
 AAGGCTGTCTGAGGTAGGAAA

551/615

## **FIGURE 546**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517  
><subunit 1 of 1, 458 aa, 1 stop  
><MW: 51778, pI: 7.81, NX(S/T): 2  
MMLIPMASVMAVTEPKWVSWSRFLWVITLLSMVLGSLALLLLPLGAVEBQCCLAVLKGLYL  
LRSKPDRAQHAATKCTSPSTELITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG  
KREKAQKLFMHALKMDPDFDALTEFGIFSEEDKDI IQADYLYTRALTISPYEKALVNR  
DRTLPLVEEIDQRYFSIIDSQVKKVMSIPKGNLSALRRVMEETYYHHIYHTVAIEGNTLTL  
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRLVGY  
VDPVEAGRFRYTQVLVGGHIPPHPQDVEKQMQEFVQWLNSEEAMNLHPVEFAALAHYKLV  
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQQRSDYYHVLEAANEQDVRPFIRFIK  
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-46

#### **N-glycosylation sites:**

Amino acids 275-279;446-450

#### **Tyrosine kinase phosphorylation sites:**

Amino acids 216-225;217-225;244-232

#### **N-myristoylation sites:**

Amino acids 35-41;235-241;266-272;368-374

#### **Amidation site:**

Amino acids 119-123

2025 RELEASE UNDER E.O. 14176

**FIGURE 547**

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA  
 TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG  
 CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG  
 GCATTTCACAAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC  
 CTCCTGCTCTCAGCCTCAATCCTGGTCTCTGGATGCTCCAAGGCTCCAGGCAGCTCTCTAC  
 ATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTCCTGTGCTCAGTCCAGGGTGTG  
 CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA  
 TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC  
 ATCGTGGGCTTCCCCAATGGTTCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC  
 TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA  
 GCTGAAAAGAATAAGGAGCTGCCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC  
 ACCATCATTTGGATCTCTGTGCTGCCGGGCCCTTCTCATCAGCTGCATGCGCTATCTCCTGGTG  
 ACAAGGAACTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCC  
 ATCTTGTGCTCGGCTGTATCCCCAGTGCCCTTCAGTGACGCCCCAGCACATGGATGGCGACCACA  
 GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCC  
 TCTCCAGTCTCTCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCCGGCCCCCTG  
 CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACAGTACCAGCAGGACCTGCTAAAC  
 CCGGACCTGCCCCCTACTGCCAGCTGGTGCCAACTTCTGATGGGTCTGGGCCAGGCCAGC  
 CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCCTCACACCTGAGACCAGCAGGACAAG  
 GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCATGGGGCA  
 GGTGTCTGTGCGCAGGGGGACAGGAGACTGTAAACAGGCCCAGGTCTTGTGCAGCCCCCTGAATGC  
 ACGCCCGCCTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCTGTGAAAGGCAG  
 GCTCTGGCCCCCTTCCATGCCCCAAAGTCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC  
 CTCAGGCCCTGCTCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC  
 AACTCCACTAGTGACCTCAGAGTCTTCTCCCTTTAGGACAAGGCAGACACCCACCATGCGG  
 GCCTCAGGTGGCAGAGAGGGCCAGCCTCACAGGCCTGTGGCCCCACACACAGTCCCAGCAAG  
 GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAAGCAGGCCCAGCCCCCTCTCAGAACCTGCTG  
 CCAGCTGTGCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT  
 CTCACCCACCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAACT  
 ATGCATTCAATCAGCAATAAATGAGCCTTGTCTGCA

**FIGURE 548**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIIPMGTOGCFKSLLSASILVLWMLQGSQAALYIKIPEQPQNQDLLLSVQGVPTDF
CDFNWYLGEEITYGGRLLFTYPIGQIQQRDGSAMGQRDIVGFNPGSMLLRRAQPTDSTGY
QVAITINSEWMTMAKTEVQVAEKNKPELSTHLPTNAGILAATIIGSLAAGALLISCIAYL
VLTRNRWQSHRLPAPRGQGSLSILCSAVSPVSPSTWMTATTEKPELGPAAHDGNNI
LEYVMPSPVLLVSPISDTRSINPARPLPTPEHLOAEPENHOOYODLLNPDPAPYCOLVPTS
```

Important features of the protein:

Signal peptide:

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

**FIGURE 549**

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA  
 AGAGCTTCCCTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTTCTGCCTGGTC  
 TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCCTTACCACCTTGTCTT  
 CACCAGCCCCCTGCTCCCCCTCTTCCCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTGTT  
 GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACACAGACACTTTTGTCCC  
 TGGAGATGTTGGCAGTGTCCAGAGGCGTGTGATGGTCCCACTGGGGTTGGGGGTGCTGCTGGCA  
 CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCCTATGGGACACTGCACAGTACACC  
 TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG  
 GTTGGGATCCTCCACAGTGACAGACGGTGGCTCTGCCCACGTTTCCACACAGCTCTTTTGCT  
 TGTGGAGCTCACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA  
 TGAAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACCTCAGGAGTGAGAATTTGT  
 GGAGAGCAAGAGAGGTGAGACTGGGGTGTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCGTGA  
 GAAGCGGGTGGGGCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC  
 CTCCAGTCACTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTTCAGTATTT  
 GCGCACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG  
 CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG  
 GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGAGCTCTTCCAGCTGAAGCAG  
 AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC  
 AGCAGCTCTGTTCTGGAGTTTCATGTGATGAAGTCCATCCCGACGTTTCTGTGGATATCTCC  
 ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCTGACGACAGCCATTTGAACCTTG  
 GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCAGGCGGAGCGCGGCGGCTCTCGG  
 CCGTGTGCCAACCCTCAGCTCCCTGTCCAACGCTCCGAGAGGGACAGCACCACCTGGGAAGC  
 CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGAGCTCACCCAGACCCCTATGAGTTTCTTCAG  
 TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTAGACCACCTTCAGCTCTTTTATTTTAA  
 TTTTTTATGTTTTATTTTGACAGTGTAGAGTTTTTGTCTACAGCAAGGACTTTGATCCTGTCT  
 CCGTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTACGCA  
 GAGTCTCCAAGCCCCACGAACCCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT  
 GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCTGAGGAGTGGAGTCATACACGAAG  
 GCGTGTGGCCATCGTGTGACGAGAGAGTCTCTGTACACAGCCCCGTGAACCTGAGGAGTGG  
 AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA  
 CGTGTGGCTCCAGCCCTTGTCTTCTGCCAGTGTAGACACCTCTGTCTGCCCACTGTCTGGGG  
 TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTTGTATCAGTCCAGTGTGTCT  
 CTGTCTATAGTTTGTGTCTCCAGGCAGGCCATGTTAGGGGCTCGCAGGGGCCATTGGGGAGC  
 ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA  
 GGAGTGTGTTCTGCTGCCCCGTTACAGTGGAGCGTTCGTGTCCATAAAACGTTTTCTAACTG  
 GGAA

555/615

## **FIGURE 550**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537  
><subunit 1 of 1, 104 aa, 1 stop  
><MW: 11136, pI: 8.20, NX(S/T): 0  
MLAVSRGVLMMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPTARAGPGQAWSLRC  
VLVGILHSDRRCALPTFPFHSSFACGAHPFAESSFP CGLWPAEVK

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-20

#### **N-myristoylation sites:**

Amino acids 53-59;64-70;97-103

#### **Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 74-85

2025 RELEASE UNDER E.O. 14176

**FIGURE 551**

CGCCCTTAGCATGCGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCTGGTGAGGCCATCATGCTGGCCAT  
 GACCCTGGCCCTGGGTACCTTGGCTGCCCTTCTTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACCTGCAACTG  
 GCTGTTCTGAAGTCTGTGCCCACTTCTCCATGGCAGCACCCCTGGCAATGTACACGAGCCTTTCCTTGTCTCT  
 CAACGCGATCCACCACTCCATAGTTCTGACTTTGCCCACTTGCACGCCTGCGGCATCTCAACCTCAAGTGGAA  
 CTGCCCGCGGTGTGGCTCAGCCCATGCACTTCCCTGCGACATGACCATCGAGCCACGACCTTCTGGCTGT  
 GCGCCACTGGAGAGCTAAACCTGAGCTACAAACATCATGACTGTGCTCGCTGCCAAATCCCTCATATCT  
 CTTGTCCTCAGCCATACCAACATCTTGATGTAGACTCTGCCAGCCTCGCCGCGCTGCATGCCCTGCGCTTCT  
 ATTATGGAGCGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCATGGAGGTGGCCCGGCTGCCCTCCTTGG  
 CTTGGGCGACCTCACCACCTGTCACTCAAGTACAAACCTCACTGTGGTGCCCGCAACCTGCCTTCCAGCCT  
 GGAGTATCTGCTGTGTCTTACAAACGCGATCGTCAAACCTGGCGCTGAGGACCTGGCCAATCTGACCGCCCTGCG  
 TGTGCTCGATGTGGGCGGAATTTGCCCGCGCTGCGACCAAGCTTCCCAACCCCTGCATGGAGTGGCCCTGTCACTT  
 CCCCCAGCTACATCCCGATACCTTCAAGCCCTGAGCCGTCTTGAAGGCTTGGTGTGAAGGACAGTCTCTCTCT  
 CTGGCTGAATGCCAGTTGGTTCGCTGGGCTGGGAAACCTCCGAGTGTGGACCTGAGTGAGAACCTTCTCTACAA  
 ATGCATCACTAAACCAAGGCCCTCAGGGCCCTAACACAGCTGCGCAAGCTTAACTGTCTTCAATTACCAAAA  
 GAGGGTGTCTTTGCCACCTGTCTCTGGCCCTTCTTTCGGGAGCCTTGTGCGCCTGAAGGAGCTGGACATGCA  
 CGGCATCTTCTTCCGCTCACTCGATGAGACCAAGCTCCGGCCAATGGCCCGCTGCCATGCTCCAGACTCTGGC  
 TCTGCAGATGAACCTTATCAACAGGCCCAAGCTCGGCATCTTCAAGGCCCTTCCCTGGCCTGCGCTACGTGGACCT  
 GTCCGACAAACCGCATCAGCGGAGCTTCCGAGCTGACAGCCCAATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG  
 GCTGCAGCCTGGGGAACCTTGTCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAAGCTGCAGC  
 CCTCAACTTCACTTGGATCTGTACGGAACAACCTGCTGACCGTGCAGCGGAGATGTTTCCGACGCTCTCGCA  
 CTTGCAAGTGTCTGCGCTGAGCCAACTGCACTTCCGAGGAGTCAATGGCTCCAGTTCCTGCGCTGACCCG  
 TCTGCAAGTGTAGACCTGTCCCAATAAGCTGGACCTTACCAAGGACTCATTACCGAGCTACCAAGCT  
 GGAGGCCCTGGACCTCAGCTACAAAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACCTTCAAGCTTCTGGC  
 TCACTTGCACACCTTGCGCCACCTCAGCCTGGCCCAACAACATCCACAGCAGTGTCCACGACGCTCTGCAG  
 TACGTGCTGGGGCCCTGGACTTCAAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTTATCTGCA  
 CTTCTTCCAAGGCTGAGCGCTTGAATCTGGCTGGACTTGTCCAGAACCCGCTGCACACCTCTTGCCTCCCAAAC  
 CTTGGCCAACTCCGCCAAGAGCTTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTAAAGTGGTGGAG  
 CTTCACTTCTGCCCCAACTGGAACTTCTGACCTGGCAGGAACAGCTGAAGGCCCTGACCAATGGGAGCCT  
 GCTGCTGGCACCCGCTCCGAGGCTGGATGTGAGCTGCAACAGCATCAGTCTCTGGGCCCCCGGCTTCTTTTC  
 CAAGGCCAAGGAGCTGCAGAGCTCAACCTTAGCGCCAAACGCCCTCAAGACAGTGGACACTCTGTGGTTTGGGCC  
 CTTGGCGAGTGCCTGCAAAATCTAGATGTAAGCGCCAAACCTTCTGCACTGCGCTGTGGGGCGGCGCTTATGGA  
 CTTCTGCTGTGAGGTGCAAGCTGCGCTGCGGCTTGCACGCGCGGTGAAGTGTGGCATCTCGGCGGACCTCA  
 GGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCTGAGTAGGGCCCTCTCTCGGAGCTGTTTGCCTCTCT  
 GCTGCTGCTGTGCTCTGGCCTTGGCTGGCTGTCGCCATGCTGCATCACTCTGTGGCTGGACCTCTGGTACTGCTT  
 CCACTGTGCTTGGCTTGGCTTGGCTTCCCTGGCGGGGGCGGCAAGTGGCGAGATGAGGATGCCCTGCCCTACGATGC  
 CTTCTGTGCTCTGCAAAACGCGAGCGCAGTGGCAGACTGGGTGTACAAAGACTTCGGCGGCGAGCTGGAGGA  
 GTGGCTGTGGGCGCTGGGCACTCCGCTGTGCTTGGAGGAACCGGACTGCTGCTGGCCGCAAAACCTCTTTGAGAA  
 CTTGTGGGCTTGGCTTATGGCAGCGCGAAGCGCTGTTGTGCTGGGCCCAACGAGACCGGAGTCAAGTGTCTT  
 GCGCGCGAGCTTCTGTGCGGCCAGCAGCGCTGCTGGAGGACGTGCTGGAGTCTGTGGCTGTGATCTCGAG  
 CCTGACCGGCGCGCTCCCGTACGTGCGGCTGCGCGAGCGCTTCTGCGCCAGAGTGTCTCTCTTGGCCCCA  
 CAGAGGAGTGTGTCAGCGAGCTTCTGGGCGAGCTGGGACTGGCCCTGACCGGGAACAACCACTCTATATA  
 CCGGAACCTTCTGCCAGGACCAACGCGCGGAATAGCCGTGAGCGGGAATCTGACAGGTGCCACCT



557/615

## FIGURE 552

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714  
><subunit 1 of 1, 1032 aa, 1 stop  
><MW: 115799, pI: 8.61, NX(S/T): 12  
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAA  
PRGNVTSLSLSSNRIHHLHDSDFAHLLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFL  
AVPTLEELNLSYNNIMTVPALPKSLISLSLSTNIMLMLDSASLAGLHALRFLFMDGNCY  
KNPCROALEVAPGALLGLGSLTHLSLKYNNTLVVPRNLPSSLEYLLLSYNRIVKLAPEDL  
ANLTALRVLVDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSLSLWLN  
ASWFRGLGNLRLVLDLSENFLYKCIKTAKALQGLTQRLKLNLSFNQKRVSAHLSLAPSF  
GSLVALKELDMHGIFFRSLDETTLRPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYV  
DLSDNRI SGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNF TL DLS  
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS  
FTELPRLEALDLSYNSQPFQMVGHNFSFVAHLRTRLRHLSLAHNNIHSQVSQQCLCSTSL  
RALDFSGNALGHMWAEGLYLHFFQGLSGLIWL DLSQNR LH TL PQTLRNL PKSLQVLRL  
RDNYLAFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRRLDVSCNSISFVAPGF  
FSKAKELRELNLNLSANALKTVDH SWFGPLASALQILDV SANPLHCACGA AFMDFLLEVQAA  
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCG  
WDLWYCFHLC LAWL PWRGRQSGRDE DALPYDAFVVF DKTQSAVADWVYNELRGQLEECRG  
RDALRLCLLEERDWLP GKT L FENLWASVYGRKTLFVLAHTDRVSGLLRASFLLAQORLLE  
DRKD VVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHF  
YNRNFCQGPTAE

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:

Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;  
469-473;474-477;513-517;567-571;694-698;731-735

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:

Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;  
563-569;607-613;695-701;794-800;929-935;945-951;  
1010-1016

Amidation site:

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

**FIGURE 553**

GGCGTGGGACGTGCTGCGGCGTCTAGCTGGCTTACAGGGCGGCGGGGTGTGTCTCTCT  
 GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGTCATGCCACTCTCTGGGTGAGACGGTGAGGT  
 CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCTT  
 CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATC**ATGG**CATTGCTGGTGGAACCGAGTGCGGGGC  
 CACTGGCGAATCGCCGCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCTC  
 AACAAATGGATTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCCTGGTGCATTCTGTG  
 GTCACCTGGCTGGGCTTGATATCTGCCAGAAGCTGGACATCTTGGCCCCAAAAGTCTGCCG  
 CCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT  
 CTGCAGAACACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA  
 GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCT  
 ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGAATGGTG  
 TTTGCTGCTCTTGGTGTCTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT  
 GAATTACAAGTGAACCTAATGCAGCTGCTGTACTACCAGGCTCCGATGTCTATCTGCCATGTTG  
 CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA  
 GTTTCGTCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTTCATGGTGAACCTTATCAATT  
 TATTGGATCATTTGGGAACACTTCACCTGTCACTATAACATGTTTCGGACACTTCAAGTTCTGC  
 ATTACTTTATTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC  
 ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA  
 AGTAGGAGTAAACTGGCACAACGTCCT**TAA**TTGGGTTTTTGTGGAGAAAAGAAATGTTGTCCCA  
 AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

559/615

## **FIGURE 554**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSI C I V F L N K W I Y V Y H G F P N M S L T L V H F V V T W L G L Y I
C Q K L D I F A P K S L P P S R L L L L A L S F C G F V V F T N L S L Q N N T I G T Y Q L A K A M T P V I I A I Q T F
C Y Q K T F S T R I Q L T L I P I T L G V I L N S Y Y D V K F N F L G M V F A A L G V L V T S L Y Q V W V G A K Q H E L
Q V N S M Q L L Y Y Q A P M S S A M L L V A V P F F E P V F G E G G I F G P W S V S A L L M V L L S G V I A F M V N L S
I Y W I I G N T S P V T Y N M F G H F K F C I T L F G G Y V L F K D P L S I N Q A L G I L C T L F G I L A Y T H F K L S
E Q E G S R S K L A Q R P
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-27

#### **Transmembrane domains:**

Amino acids 46-60;75-90;153-167;192-208;221-237

#### **N-glycosylation sites:**

Amino acids 43-47;92-96;97-101;238-242

#### **N-myristoylation sites:**

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 555**

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG  
 CAGGAATGTAAGCACTGTTTCACAGAGATTTTCGTCTTTGGCTTATTGTGCTGCAGAGTCTAG  
 TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCTCTTTTCTGGAACCAAGTCCCTGGA  
 GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCAGCAAGTACTCTACATGCAACCCCC  
 CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC  
 AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCAGGTTCTTCAGACCCA  
 AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT  
 TTTCTACGGGGTCTCTGCGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC  
 CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACCTCAGTCTTTGCTGGCCAC  
 GCTCATGCCCTCCCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCAGATGCACC  
 TACTGCCCTCACCACCTGAACCCCGGCTCTGCGGACTGAGTGAGGGCCCCAAGCCTGGCTGT  
 TGCAGCGCCAGAGTCGCGCTCTCTTGAGTGCCTGCAGCGAGTTACCCGTGTGGGTTCTTG  
 AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG  
 GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC  
 GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCCTTGAGAGGCGCTCTTAGAGACCGAGGCTCT  
 AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCTGTTGCAGCAGCTGAA  
 GGGCGCACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGGCCACGCTCTCTGGAAGTGGCCG  
 CCTACCCCTTGCCCTTGCGGACCTCATGCGCCGGCCGGTCCGACGCCCTTGCGCACTGGCTGGC  
 ACAGTTGTGCGGCCGTGGGCAACTGTTGGTTTCGTTACTTTGGGCGTGGGCGCGGACGCGAGCAG  
 TGATGTACCAGAGCGCTCTTCCACCTGTGAGCCTTTGCCACCCCGCGCCGCTGCTGCTGGC  
 ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG  
 CTCGGTCTCCAGTCAGCTCCAGTATAAACGCTCTGGAGATGAACAGCAACCCCTCTGCACTTCAG  
 GGTGGAGAATGGTCCAAATCCACGCTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT  
 CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGACAGGACAGTCTTCCAGCCAAACCCAG  
 CCCTCTGCCTCCCGTCAGCATCAGCACAGGCCCGGGGCACAGTGACCTGCCAGCCCCAGC  
 CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA  
 GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACCTGTGTCCA  
 AAGGAGGGTCCATGTGTGAGCCACCCCTGTCTTGAGCCGCTTACCAAAATAAAGTTGTAG  
 TGATTCCA

561/615

## **FIGURE 556**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594  
><subunit 1 of 1, 162 aa, 1 stop  
><MW: 17598, pI: 6.58, NX(S/T): 1  
MPVFWNQSLLELGHVLIDSVELAQQVLYMQPPPTQALPLLLHGLLLHRQLYGTRLQAHRRG  
WSQVTLTQVLQTDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS  
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-45

#### **N-glycosylation site:**

Amino acids 6-10

#### **N-myristoylation sites:**

Amino acids 97-103;144-150

2025 RELEASE UNDER E.O. 14176

**FIGURE 557**

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC  
 AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTGAGCATTTC  
 TCCAGGACCAGCCTACCCAGGACGGTGTGGTACCCAGCACATTACCTGTGACCAAGCCACC  
 ACTCTGGTTCCAAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTGAGTGTCTGCTCT  
 TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG  
 CCCTCACCCGTGCAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA  
 CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC  
 TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTGACCT  
 GGGTGCAGCACTTTGATTGTGTGCCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG  
 TGAGGGGGGATGAAGGATAAGCCCATTTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT  
 CAGAATTTATTTGTTGAGGAAGAGGTTTGAAGAGTTAGGTTTCGACCAATTCGTGAGTCTGTGTT  
 CCATACTCCACTGAGTGTGGGCCTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG  
 CTCATGTTGCCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTGAGGATAAGAGC  
 ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGTCATGAAGCTCGAAAG  
 TATTCCTTTGGAACCTCCCATTTCTTGTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC  
 TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT  
 TGAGGAAAGCTGGATTTAGACAAGTTCATTTAGGGAGTTCTCCTTGTGTTGTGGATTAAAATA  
 TGACAGATTGCAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA  
 AAGTATAAGACTAAGTGATAAACTGTCTTCCACCGTGGGAGTTGTTAATGAGAAAGAAAGT  
 TACTCTGAAAAACAAGGGG

563/615

## **FIGURE 558**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSVLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTTFAGLCYFNYHDVGICRAVAMLWKL
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-15

#### **Transmembrane domains:**

Amino acids 71-88;126-140

#### **Glycosaminoglycan attachment site:**

Amino acids 12-16

#### **N-myristoylation sites**

Amino acids 8-14;58-64;78-84;108-114;148-154

**FIGURE 559**

CCCAGCCCCGCGTTCCGGCTGCTCTCGAGGAGGCCGAGTCCCCGGAGACGATGCGCCCCGCGC  
 AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCCTCTTTGGCTCTGC  
 CTGGGTTTTCACCTTCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC  
 CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCAGGGCAGAGCCTCGCTTCGGTG  
 CCCAGCAGCCTCCCGCCCCACGCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG  
 TGAATCACTCCCTCCAGCCTTACCCTCTCTCGGAGAGCCTCAGCCTGCACAGCTGCCACCTG  
 GAGCGCATCAGCCCGCGCGCCTTCCAGGAGCAAGGTCACTGCGCAGCCTGGTCTCGGGGAC  
 AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG  
 AGGCTGGACTTGTGAGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCCT  
 TCCTCGCTGCGGTCCGTGTCTCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC  
 GAGGGCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACATACATCTTCGAGATCGAGGGC  
 GCGCTTTCGACGGCTGGCTGAGCTGAGGCACCTCAACCTGGCCCTTCAACAACCTCCCTGC  
 ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCTCAACGTGAGCTCAACGTCTCTGGAGTGG  
 TTCTCGCGACCGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAAACAG  
 CTGCTGTTCTTCCCGCTGCTGCCCAAGTACAGCAAGTTGCGGACCTCTCTGCTGCGCGACAAC  
 AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCAGTTC  
 CTCCTCGTGGACGGCAACGTGACCAACATCACACCGTACGCTCTGGGAAGAATTCTCTCC  
 AGCGACCTCGCAGATCTCCGCTTCTCGGACATGAGCCAGAACCAGTTCCAGTACCTGCCAGAC  
 GGCTTCTGAGGAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG  
 CTTCACATTCGGGAGCAGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAAG  
 CTGTCGGAGCTGCACCTGGCTCCGGGCTGGCCAGCTGCTGGGCAGCCTGCGCTTGTTCAAC  
 CTGAGCTCCAACAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC  
 ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCCTGGACCGGGTGGG  
 CCCCCCTAGCTGTGTGGATTTCAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG  
 TGGCTTGGGGGCAATTGCCAGACTGCCATTCCAAGGACCTCCCTGACCTACTTAGACCTCTC  
 AAGCAACTGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA  
 GGTCTGTCTCTCAGGAACATGGGCCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT  
 TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCAAAGTTTGGGGG  
 CAGCCTGGCCCTGGAGACCTTGATCTCCGTAGAAACTCGCTCACAGCCCTTCCCCAGAAGGC  
 TGTGCTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAAGATCCATATGACTG  
 CTGTGGGTGGATGGCTGGGGGCCCCGACAGCATGGGCAGCGTGGCCGACTGGGCCATGGT  
 CACCTGCAACCTCTCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCTCGGGA  
 CTGCAAGTGGGAGCGGCTGGAGCTGGGCTGCTTACCTCGTGCTCATCTCTCCAGTGCCT  
 CACCCTGCTGGTGGCCTGCACTGTCATGCTCTCACTTTTAAAGAGCCTCTGCTTCAGGTCTAT  
 CAAGAGCGCTGCCACTGTGCTCCCGTTTACCTGACCTGGCTGTGTGCCAAGACTCGAATTCG  
 GTCGCGACACAACAGGACACTTCTCTGCGCAGCTTCAAGATGTGATGCAGAGGCCAAGTCTG  
 ACGAATTGAAGTTTCAATTAAATTTAATATGTTTCATTCCTCATCGCCACCCCAACCCCG  
 CCCCCACCCGCCCCAAGTCTTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAT  
 ATTTTAAAGTGACTTTTTCAGAAATAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA  
 AAAAAAAAAAAAAA



565/615

## **FIGURE 560**

><subunit 1 of 1, 692 aa, 1 stop  
><MW: 76366, pI: 6.07, NX(S/T): 11  
MELLPLWLCLGFHFLTVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR  
MLTLDANPLKTLWNHSLQYPPLLESLSLHSCHLERISGAFQEQGHRLSLVLGDNCLSEN  
YEETAALHALPGLRLDLDSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG  
ERLRELDLQRNYIFEIEGGAFDGLAELRHLNLAFFNNLPCI VDFGLTRLRLVNLVSYNVLEW  
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRTLTLRLDNNMGFYRDLYNTSSPREMV  
AQFLLDVGNVTNITTVSLWEEFSSDDLADLRFLDMSQNFQYLPDGFRLKMPSSLSHLNLH  
QNCMLTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVPFG  
LFANARNITTLDMSHNQISLCPLPAASDRVGPPSCVDFRNMA SLRSLSEGCGLGALPDC  
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD  
LDLSGNCCLTTFPRFGGSLALETDLRRLNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG  
VDGWGALQHGQT VADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVILPSC  
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSVY

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-18

#### **Transmembrane domain:**

Amino acids 651-672

#### **N-glycosylation sites:**

Amino acids 21-25; 74-78; 155-159; 232-236; 292-296; 309-313;  
312-316; 408-414; 427-431; 500-504; 622-626

#### **Glycosaminoglycan attachment site:**

Amino acids 533-537

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 566-570

#### **N-myristoylation sites:**

Amino acids 24-30; 39-45; 45-51; 141-147; 199-205; 245-251;  
308-314; 396-402; 416-422; 420-426; 471-477;  
484-490; 497-503; 522-528; 545-551; 555-561; 610-616

#### **Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

#### **Leucine zipper patterns:**

Amino acids 48-70; 492-514

2025-01-15 10:00:00

**FIGURE 561**

TGGCCTACTGGAaaaaaaaaaaaaaaaaaaaaAGTCACCCGGGCCGCGGTGGCCACAACAT  
 GGCTGCGGCGCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG  
 CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG  
 CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT  
 GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGGATCCCTTGAAC  
 TTGGGCTGGAAGTGTGAACACAGTTTTGGATATTTTCCAAAGATTGTGATCAAGGTACTTCA  
 TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG  
 AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA  
 CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA  
 GGAGTCTCGGGGGCGTGAACCTTGACCTGTGCTGAGCCCGAGGCATTTCAGAGCTGATTCAGA  
 GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA  
 GAGCCACCTCACACGAGCGGTCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC  
 TTTTGAAGAAATTCGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAAGTGGCAATAG  
 TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCTGAAAAAGAAATGAG  
 TCAGAGAGGAAGTGGACAGTGCGTTATTTCATTACAGCAAAGGATTTGTTGGCATCAAATCT  
 AAGTTTGTTTTACAAAGATTGTTTT**TAG**TACTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCC  
 AAACAAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAA

1055555.011555  
 205110.005555

567/615

## **FIGURE 562**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFWLGGALWVPGQSDLGSHGRRFSDLKVCGDDECSMLMYRGKALEDFTGPD
CRFVNFKKGGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPPEESRGRELD PVP
EPEAFRADSEDEGAFSESTEGLCQGPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGSESRTGNSSPASVEREKTDAYKVLKTEMSQSGGQCVIHYSKGFRWHQNLSLFYK
DCF
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-22

#### **N-glycosylation site:**

Amino acids 294-298

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 30-34

#### **Tyrosine kinase phosphorylation site:**

Amino acids 67-76

#### **N-myristoylation sites:**

Amino acids 205-211;225-231;277-283

#### **Amidation site:**

Amino acids 28-32

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 563**

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG  
 TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT  
 GCTCCTACCTTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT  
 GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTGAGCCCAGGCCTGGTTGCTG  
 GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTACCACCATCTGCACAATGTC  
 TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTAAGAATCAACAAAATGGCCCTCTGG  
 GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT  
 GACCGGCAGTTCTCAGCTCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG  
 GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTCCTG  
 TGGTTCGTGAGCATGGACCTGGTGCAAGTGCAAGTGGCTCACGCCTGTAATCCAGCACTTCGG  
 GACGCCAAGGTGGAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA  
 CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG  
 CTGTACCTAAAAATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTATGTTAT  
 GAAAA

569/615

## **FIGURE 564**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649  
><subunit 1 of 1, 153 aa, 1 stop  
><MW: 17603, pI: 7.42, NX(S/T): 0  
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLYYVDTFVSVYKINKMAFWVGETVFL  
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEADSI TLGRYLRLARHRNFLWFVS  
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-20

#### **N-myristoylation sites:**

Amino acids 4-10;12-18;93-99

#### **Leucine zipper pattern:**

Amino acids 102-124

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

570/615

**FIGURE 565**

CGGCACGAGTAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA  
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA  
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA  
CCCACCCTGAGGTCGGGACCTGGGTTCCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC  
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA  
TCTCC

202110-4825001

571/615

## **FIGURE 566**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGPSPSQWALPCL
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-18

#### **Glycosaminoglycan attachment site:**

Amino acids 58-62

1062586.011503

**FIGURE 567**

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT  
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA  
**ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCTGGCTAGGGGGCCAGAACGCC**  
**TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC**  
**CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGACCTGCACTCCGCCGCCTGCAC**  
**ACATCCTCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT**  
**GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG**  
**GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG**  
**GCCAGGCTGCCGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT**  
**GATGACTTGCATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAGTGA**CCGTGGCTC  
CAGCCACCCCGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC



573/615

## **FIGURE 568**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSSLGLAASSWLGGQNADHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRMLAMPIDLDTL
SPEERRARLRKREQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-18

#### **N-glycosylation site:**

Amino acids 20-24

#### **N-myristoylation sites:**

Amino acids 5-11;9-15;17-23;18-24

AD573-615.F01

**FIGURE 569**

GGTGCCAAGGGTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTCAT  
 CCTCCTGTAGCAGCTGGAATAATCAGATTACAGGTGAAATCCCTGGCTGGCAATCTTCTGTAT  
 TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT  
 GGAGCCCTCCACACCTTGCTGTGTGGCTCTCATCTTGATTTGAATCTTATTTGGCTATA  
 TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGGTAGAAATAGG  
 CTGTCTTATGGAACGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG  
 TTCTGTACACTGATTCTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA  
 CAACTACAATTTGTTGTGCGATTAGAGTTAACTTACAGACTCTCAAAACCCCAATTCTTTGGGTT  
 TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTAGTCTAAGATCAACTGAATTAGGGAG  
 GTTTGAAAGTGTAAGCAAAATCGTACATTCCAAACACTTTGTAAAGAAGGAATGGGTAGTG  
 TCAACTAAAGGAAATGGTGTGCATCCAGCAAAAGAAAGAGACCGAAAGCAAAAGTCATAAAACC  
**ATG**CCACGAGCTCAGCTGCTGCTCCGTGCTCCTCCATACCCTTGTTGACTGTGCTCAT  
 TTAGCCAGAGACCTAAGTGCTCTTTGGAGGATGCTCCTCGGGCCCCCTCCCCCTCCGCTGCAC  
 TGCTACTTCTGTATCCTCTCTTCTGTGCGAGGAGGTCAGGCCTTCTATGAGGACCTGAGT  
 GGCCGGCAGTAGCTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC  
 ACCAACTCGCCCTTCCAGCGGATTTTCATGGAGCAGCGCGCTTCTCTGATATCATCTTCCAT  
 CCATGGAAAAAGGAGGAGAATTGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC  
 AACCTCTGGCTCCCAAACTGCCACTGTGCGGGAGACACAGACCATGTACAAGCGAGCCAG  
 GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCAACCCAGACGTGCCCTACCACGACTAC  
 TTCTACACAATCAATCGCTACACGCTCACCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC  
 TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAACGTTTCATCGAGAAGAAC  
 TTCTGGAGTGGGCTGGAGGACTACTTCGCGCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC  
 ACTTATTTGGCTGAGATGCACAGACAATCTCCAAAGAGAAGGCCAGCAAGACTACAACGGTG  
 CGGAGGAGGAAGCGTCCCATGCCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG  
 GTCACACGCCCCACAGATGAGGATGTGGGCCACAGGATCAACATGTGGCAGGTTCCACACAG  
 ACGCGCATATCCCGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGGTGTCCAAGCTGCTG  
 CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTACAAACT  
 TGGATGTTGGAATACACCACGACACCTCCTGCTGGCAGGGTCTAAGGCTCCAAGAAAGG  
 TTACCCAGTCTCAGACAGAATGGGCCAGCTCTTAGAGTCCCAACAAAGTACCACGATACT  
 GAGCTCCAAAATGGAGGAAATCATCAAATCCTCAGTGATGCTCTTTGACCAGATGAAGGAC  
 TCGCTCATCAACCTTCAGAACGCGCATCAGGTCCCGGACTACAGTTCGGAAGTGGAAGAAAG  
 AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT  
 ACATAGACATATAAAATATATATATAATAATATATATATATAAATAAATAATATATATAT  
 ATATACAGATTTTAAAAAGAGATAATGCCATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC  
 GCCCTGTGCTGGCCGGAGCAGCGTTTCTTATGGTGGAGCAGCTGAGGAGGGGAGGAACCGCC  
 TCTCAGACCCGACCTCCCTGATCTCCTCCTCCACCTCTGTGTTCCCAACCCCTTCCCTTGC  
 TGGCCATTCTTGGCTTTTAGAAGGGAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCCTAAG  
 GTCTCAAAAGAAGCTTAAAGACGGCATTGCTTAAAGTGCTTCATTCCCTAATCCCTTTTGA  
 TTTGTTTCCAAAATAAAAGAGAATCTTTTCTCCGTAAAAAAGAAAAAAAAAAAAAAAAAAAA

**FIGURE 570**

><subunit 1 of 1, 425 aa, 1 stop  
 ><MW: 49786, pI: 8.84, NX(S/T): 3  
 MPTSSAVLLRLVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE  
 DLGSRQYVNEVFNFISVDKLYDLLFTNSPFQDFMEQRRFSDIIFHPWKKEENGNSRVIL  
 YTTITLTNPLAPKTATVRETQTMYKASQSESECYVIDAEVLTHDVPYHDYFYTINRYTLTRV  
 ARNKSRLRVSTELRYRKQPWGLVKTPIEKNFWSGLEDYFRHLESELAKTESTYLAEMHRQ  
 SPKEKASKTTTIVRRRKRPHALRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE  
 DTPNGPHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWOGLRLQERLPQ  
 SQTEWAQLLESQQKYHDTLQKWRETIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEK  
 RNRYP

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 312-334

**N-glycosylation sites:**

Amino acids 73-77;114-118;183-187

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 97-101

**Tyrosine kinase phosphorylation sites:**

Amino acids 144-153;188-196

**N-myristoylation sites:**

Amino acids 201-207;291-297

**Leucine zipper pattern:**

325-347

**FIGURE 571**

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT  
 TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAAATCCCTGTGGATAAGGGTGGACGGCTGCTGTCAACTT  
 TGACCAATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCATCGTCGAGAAGCGAGAC  
 TAAGAAATATTGTCACATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGTTTCGGAATGTTTTCCG  
 GGAGCTGCAGATGCAGGAAGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCTCTCCAGGATGAGGAGGA  
 CATGTTTCAATGTTGTTGGACCTGCTCTGGAGGCGACCTGCGCTACCATTCTGCAGAGCAAGTGTGCATTTACAGA  
 GGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTACTCTGCAGGTTACCAATCATCTCCACAG  
 AGACATCAAGCCAGACAATATCTGCTGGATGAACACGAGACATGTTTACATTTACAGACTTCAACATAGCGAGGT  
 AGTGAAGAGGAGCAAAAGGGCTTCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGAGTGTA  
 CATGGACAGAGGCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG  
 GGGCTGGAGGGCCGTACGAATCCACTCGGTACAGCCCATCGATGAATCCTTAACATGTTCAAGGTGGAGCGGTGT  
 CCACTACTCTCTCACGTGGTGCAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG  
 CGTGTCCAGCTTTCATGACATACAGAGCGTGGCCCTACTTGGCCGACATGAAGCTGGGACGCGGTGTTCAAGAAGCC  
 ACTGATGCCCGGCTTTGTGCCAATAAAGGGAGGTTGAACTGCGATGCCACATTTGAGCTTGAAGAGATGATTCT  
 AGAATCCAAGCCACTTCACAAAAAGAAAGCGATTGCAAGAAACAGATCCAGGGATGGCAAAAGGACAGCTG  
 CCGCTGAATGGACACTGCAGCACTGTTGGAGACTGTCGGGAGGAATTATCATATTTCAACAGAGAGAAGCT  
 CAGGAGGCGAGCAGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT  
 CCAGGACGGGTGCAACAACACTCTCTCACCCACACCTGCAACCGTGGCTGCAGCAGCTGAGCCCACTTTGTTG  
 CTGCTCAACAGGACTGCACTGCTCTGCCCCGCCACCCAGAGCCCTCTTTGTGCCCTGATGGTCCCTGTCTC  
 ACCCTGAAACATCATGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCCTGGGTCTGGTCCCATCTCCAT  
 GACTGATTACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA  
 AACACTTCTGCCCACTTCAAATTAAGATTATGGGGAGAACCAATTAGGTAGGAAACATGAAAAACCTTTGA  
 TATTTATAAAATCATTTTACGTGCAAAATATAACCTTAATTTTGAAGTGACCCCATTTCCCCAAAGCAATCAA  
 ACCGTCATGAATTTGCAATTTGGCACAATCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA  
 AATAAAGTCTGATATGTTGGCCCTTCTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGGAAGTGTCTT  
 CATGTGCATTTCTCTGGCAGGCCACAGTCTTCTGAGCTTGTGAAGTGGTGACAGCATGCAACCCAGACTTGTCCCC  
 AAGGCTCAGCGCTGGGGTCTCACTCTCCCTCATTTAAGAAAGCTATCTTACCTTTTAGTTTTCAGCAGTCTCT  
 CACCCACCATATCCCAGTGTGGGATGGCACACAGGTGTCCATTAGATGAGAGTTGGTGGCTGCTGAGCATGT  
 GTTACTCTCTGCAGAGTGTAACTCAGCACCCTCATCAAATGGGCCGAAAGCCAGACCTGCAGCAGAACTTCCAAC  
 TCTCTATCAGCTTTCAGGGTTTCTCTCTCGGGGAAGGTGTAATAACAGCTTGTGAGATTCTTCTTACAGAGAT  
 ATCCAATCGGTATTTGGTGGACGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAGTTTATTTTCAGG  
 AGGAAAGGATTTCACACAAAAAGCAAACTACATTTCTGATCTGCTCGAGGAGAAGCTTGGCTTTGAACTGGAAGA  
 TGTGGGATGAGCAGGGAAGCTTAGACTTGGAGTCAGGTTTGTGTTCAAGATTCAGCCCTGTGGCTACTAAC  
 TAACTGGGAGCCTTAGGCAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTAAACAGGATATAA  
 ACTAATATTGACGGGGATTACAGGGTTAAATAAGATCTGTGTGTAACCCCAAGCATTTGGATGACTCATGAAT  
 GGGCTTTTGTGTCAGCATAACTCGTACATTTATTTAGATACTTTCTTCTCTCACTACCCAGCAGGCTTCTT  
 TGTGCAAAACAAACCTGTTTAGAGATTCTTCCAAATGTCTTCTGGGGCTTTGTAGATATTTGTTTGTACATCTCTG  
 TGAAGTTCGACATGTGTTTTATTTTTCATCCAACTTCCATTTTTCACTTTTCATACATGATACATCACTCTCGG  
 CTGTGCTCATGTCACTCTTAGATTCTTAAAAAGACATTTAATGATGTGTAGGTTTTATATTTTATATTTTAA  
 AAAAGAAATAGTCAGTGTTTTCTCTCTTCAACCGAGACTATTTCTGGATTTGTGTCTCTGTCAGTGACTGT  
 TTGTCACATTTTCTTTTACTTCACTGTCCCCATCAACACCGTCTGCTCCCCACTCCCCCGGAAATAAGGGGC  
 CTGCTCTCTCTCTCATGTGACCTCGGAGGCTCTTAAGATGATGATGTTTTTTTATTTGGGCTGAGTTCAGAA  
 TTAGGGGAGGAGCTGGAAGTGCCTTAGGAACACAGATTTCTCTGGTCTGTTCAAGTTGGCATTCTTGTGTTG  
 GAATAAATATTTCTTGG

577/615

## **FIGURE 572**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHI IHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHSV
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGRNLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDKSCPLNGH
LQHCLETVREEFIIIFNREKLRRQQGQGSQQLLDTDSRGGGQAQSKLQDGCNNLLTHTCTR
GCSS
```

### **Important features of the protein:**

#### **N-glycosylation site:**

Amino acids     285-289

#### **N-myristoylation sites:**

Amino acids     123-129;290-296;337-343;339-345;348-354

#### **Serine/Threonine protein kinases active-site signature:**

Amino acids     92-105

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 573**

CTCCAGTTCGCCGACTGTAAACATGTTTCATCCAGTTCAGTATGTTTGTATGCAAGTTGGAAATAAATAAACGTC  
 CTGAACCTGGATGAACCATGTTACAGTCCGCCGAAACATGAGAGGCTGTGTGAGAGCTGCAGCCGCCGAGAGG  
 AGACCTCAGCATCTATAGAGCCGAGGCTGGCCCTGCCTCCGCTGCGCCGCCGCCGCCGCTGCCGTTTCTGTT  
 CTTGCTACTGTCCCACTAAACAACTCCGCTTACAGGCCAAGTGAACATCTGTGGCTGTCTCTCTCTTTCTTC  
 CTCTCTTCCAACTCTCTCTCTCTCTCTCTCCACTTCCAGGCCGACAGAAAGCCCACTGACCGCTGGCA  
 CAACTGCAACCGGTGTCACTCCGCACACTTTATCTCGCTCTCTCGGCTCCCTTAAGGCATTGGACCCATCGCCGC  
 GTCTTTTATTTTTGCAAGTTGCATCGCTGTACATATTTTGTGCCGCCACCTCCCTCTGTCTCTGGAGTGCCC  
 TACAGCCCCGCAAACTCCTCTGGAGCTGCGCCCTAGTGCCCTCTCTGGGCAAGTGGGTTTCCCCCATCTCTCC  
 GCGCCGAGCCCTGTCTGTCTGGGCGAGAGTGTGAAGATGTCTCTTTAAGCTGTCTGTCTGGCCGTGGCT  
 CTGGGCTTCTTTGAAGGAGATGCTAAAGTTTGGGGAAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAAGTGTCTG  
 AATGGGAACCCCCCGAAGCGCTGAAAAGGAGAGACAGGAGGATGATGTCAGAGCTGGAGCTGTCTGAGTGGGGGA  
 GAGATGCTGTGCGGTGGCTTCTACCTCTGGCTGTCTCTGCTGCGGAGTGACAGCCCGGGGCTAGGGCGCTG  
 GAGATAAGATATTTTCTGTTACCAACAAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGACATTTGC  
 TCTCCACATTTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAACTCTGGAAAGAGACTAGTACTTCTCTGCTC  
 TGCAAAGACTATTGCAAGAAATCTTTTACACTTGGCCGAGGCCATATTCCAGGTTTCTCTCAAACAACTCGGGAT  
 GAGTTTGTCTTTACTATGCAAGAAAAGATGGTGGGTTGTGCTTTCCAGATTTTCCAAGAAAACAAAGTCAGAGGA  
 CCAGCATCTAACTACTTGGACAGATGGAAGAATATGACAAAGTGAAGAGATCAGCAGAAAGCACAAACAAAC  
 TGCTTCTGTATTCAGGAGGTTGTGAGTGGGCTGCGGCAGCCCGTGGTGCCCTGCATAGTGGGATGGCTCGCAA  
 CGTCTCTTCATTCTGGAAGAAAAGAGGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTCAAGGAGCCTTAT  
 TTGGACATTCACAACTTGTTCAAAGTGAATAAAGGGGAGGAGATGAAAGAGGACTGCTAAGCCCTCGCATTTCCAT  
 CCCAATTACAAGAAAATGGAAGTTGTATGTGTCTATACCACCAACCAAGAACCGGTGGGCTATCGGGCTCAT  
 GACCACATTTCTTAGGTTGTGGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTTGAGAACAGCCAGA  
 GTCTTTCTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAACTGCTCTTTGGCCCTGACGGCTTTTGT  
 TACATCATTCTTGGTGTGGGATGATTAACCTGGATGATGGAAGAAATGGATGGGTTAAGTGATTTACAGGC  
 TCAGTGCTACGGCTGGATGGGACACAGACATGTGCAACGTGCCTTATTTCCATCCAAGGAGCAACCCACACTTC  
 AACAGCACCAACAGCCCCCGAAGTGTGTGCTCATGGGCTCCAGCATCCAGGCAGATGTGCTGTGGATAGACAT  
 CCCACTGATATAAACATCAATTTAAGGATACGTGTTCAGACTCCAATGGAAAAACAGATCATCAGCCAGAAT  
 CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTGAATTTAAGCATCAAGCCATTCAGTAATGGTCT  
 TTGGTTGGTGGATTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGTCACTGTGTGGAGATCGTAAT  
 GGGAAATTTCTAATCTCCAGCAAGTCTGTGCAAAAGCAGTGGCAAGAAAAACCACTGTGTCTCGGCACATG  
 GGGCTCTAGAGGCTACTTTTCCGGTCACTCTTGGGATTTGGAGAGATGAACTAGGTGAGTTTACATTTTA  
 TCAAGCAGTAAAAGTATGACCAGACTCACATGGAAAACTCTACAAAATTTGATAGTCCCAAAAGACCTTTAATG  
 CTTGAGGAATGCAGAGCAACGGTACAACTGCACAGACACTGACTCAGAGTGTCTCAGGCTCTGTGCAAAACGCG  
 TACTGCACCCCAACGGGAAGTGTGCTGCAGTCCAGGCTGGAGGGGAGCTCTGCAGACTGCAAAATGTGAG  
 CCAGCATGTCTGTAGAGGTTGTCTGTGTAGACCGAACAGTGCCCTCTGTAAGAAAGATATTCTGTGCTCTCAA  
 TGTGAACAAAGTGCACAGAAACATCCGCAAGTGACCAAGGCAGTATTTCTTGATCAGATCATTGACATGACATCT  
 TACTGTCTGGATCTAACAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTTCTATTCCAATGGGCATTTAT  
 TTTTATCTCTGTCATTAAGAAAAAAGAGCTGTTATCTCTGCTACACACTCTGTATTTCTATTCTCTTTATTAAC  
 TTTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTGCAGCATGTTGTTCACATATGCACATGAC  
 ATACTCATAAACCCCTATATGCGTGTGTGCATAACAGATGATTTTAAAAATATATCTTCTTTATGCAAAATGAT  
 TATACAGAAATTCATTGTGATTTTATATTTGATAATGGATTTTTATGTTTACTAGAAAGATTAATTTGATCTTCCAGGAA  
 TTTTCTGTCTGATACATTAAGTCAACTTTAATAGATTTTGAACAGTATCTGTGCAATCCGATGGATGATTAAT  
 AAAAAAAGGCAATATTTTATATTTAAGTACTATACATAGGAGAGAAATGTTTCAGAACTCCCTGATGAATTTCTA  
 AGTGAGCAACTTGATATAAAATTTGATATCTTCAATTTTGTGAGTGTATCCAGTTACAGAAATGCTACACACTTACC  
 TTTTATTTGGCTGAGAAATCTGGTTATTTCACTTAATCTCAAGATTGTTTCAAGTGTTTTATAAATAAAATCAT  
 AATAGCATATTTTAAAAACAAAAA

579/615

## FIGURE 574

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592  
><subunit 1 of 1, 882 aa, 1 stop  
><MW: 98428, pI: 8.89, NX(S/T): 5  
MKHVTVGNNMRGCVRSRQRPPQHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG  
QVNICGCPLLFFLLFQLLLLLPLPSRSRKPPTQLTLAQLQTVSSAQLYLAPRAPLRHWT  
RRVVFYCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSGVPPHPAPSPCCSG  
QTMKMLSFKLLLLLAVLGFEGDAKFGERNEGSGARRRRCCLNGNPPKRLKRRDRMMMSQ  
LELLSGGEMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNNTTECGKLEELKCALCSPH  
SQSLFHSPEPEREVLERDLVLPPLCKDYCKEFFFYTCRGHIPGFLQTTADEFCFYARKDGG  
CFPDFPRKQVRGPASNYLDQMEEDYKVEEISRKHKHNCFCIQEVVSGLRQVPGALHSGDG  
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLSLAFHPNYKKNKG  
LYVSYTTNQRERWAIQPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQL  
FGPDGFLLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVDTCMNVYPSIPRSPHFNST  
NQPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIKGKDYSESP  
SLLEFKPFSNGPLVGGFVYRGCSERLYGSYVFGDRNGNFLTQQSPVTKQWQEKPLCLG  
TSGSCRGYFSGHILFGGEDELGEVYIILSSSKSMTQTHNGKLYKIVDPKRLPMPEECRATV  
QPAQTLTSECSRLCRNGYCTPTGKCCCSFGWEGDFCRTCACEPACRHGGVCVRPNKCLCK  
KGYLGPQCEQVDRNIRRVTRAGILDQIIDMSTSYLLDLTSYIV

### Important features of the protein:

#### Transmembrane domains:

Amino acids 63-80;186-201

#### N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

#### Glycosaminoglycan attachment site:

Amino acids 417-421

#### cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

#### N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

#### EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

2025-10-10 14:50:00

CGGCTCGAGAGCGGGGCAAACTGCTTGGCACCCTCTTAATAGGTGACATTCAATGATAGATCT  
CAGGCTTCTCGTCTGTTGTTGTTCTGGTTCTGGTGGAAAGCGCTGCTGCTACGCCCATGCCCGG  
GACTTCTTCCACCTCAACAGGACATTTTCCATCTCTTGTCTCTCTGTGTGCAAGTCCCTTT  
CTCTCTGGATTTCATGCTTGAATTATTTCTTAATTTACTTCTCATTTTGTGTCAGAGGATGTCTT  
CCAGTTGTTTCTGGGAATGCTAATATGCAAGTGAACCACTGCACTTGCGAGTTCTGCCCAACA  
GGTTAATAACCAATCAGATTCTCTTTTCAAGATGGTTAAACATAACAGACACCAAGAAAGG  
GAAGAGGAGCGGACAGCAGGAGGGGGAAGCTGAAAGAACGCAACAAGAAATGGCCATAAAGAGATA  
TAGCAACCCGAGTTTTCAGACAGTCACTTTTCCAGTGGTCTACTGTTCTGGAAGATT  
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACCTCATGAGAGAGACCGAATGGAGTGA  
CCAGCAGGGCATCTGGGCAAGAGAGGATCCCCCGAGTCCGCAAAATAAGAAATTTCAACTAGTATA  
AAACGAGGCGAGGCAACCCACAGTGAAGTCTGATACCGCTTCGACAGGGAATTTGAATAGAT  
GTCTCTCTTATGGTAGAGTATGGTGTGTTTATGAATCAACAAAGCCGCAAGCAACAACT  
TGATCATCCGCGGATGCTGCGCAAGGAATAATTGAACTCATTTAGACACAGGGAACAACT  
ACTGCCTCTTTTCTGCTTTTCTCCAGATTCCAACAGTCTGAGTGTACAGCATTTCACCTTGTTT  
ACCTCCCTTGAGAAGAGCTTGACAGTCACTACCCAGTGGGCACTGGGAGCCTTGCTCAGGT  
GGAGACAGATGCCCCCACTGACATCTGTGTTTATGAAAGCATACCTGGGCTTCATTA  
ACAACAAGAGGGGCGAAGGATAGCCCCAGGCAAGTGTGGGGCTCCTGACATAAAGTAGCTT  
GCAAAACCCCTGCTCATACAGCCACTTCTGGCAGTATTGTGCCATTTAGGAGCCCTCTCTCA  
CCGCTCTTCTTTAGTTTCTTCACTCTGTATAGACCTGCGACAGCAGCTCAGGGTGGAGCAG  
CTGACGAGCTGGGACCTGCTCCAGGCAAGCCCTATGCTACACAGTCTCGGGGTGAGGATT  
CCAGAGGATCAATTCCTACCCGCTCTCCAGGGAGTGCCCGAGATGAGCTTCCCAAGG  
AAAGTGAAGAGCTGCAAGGCTGTGCGGAAACACAGGGGTTCCATTTAGGCTTTGCTGCTCAT  
CTCACAAGAGCCAGTCACTGAGAACAAGTATTCAGGGGAAGAGGCTTTATCCAGTGTCTAC  
AGACAGGGTGAACAAGAGATCAGTCTCAAAATCCATCATCATCACTGACTAAAAATTAGGGGTT  
TATATAGCAGGAAGAAATGTAACTACATGTGCGGAAACAGGAGATTAAAGCGGGGCGAAGGAG  
AGGAGTTGGCCCAAGCAGCAGGAGTGTGCTCACTGGGGAATCATGATGGGTAGGGGTTGCTCT  
TCTCACTTCCAGATGTGGGATCTGGTAAATTTTCAAGTTTCTGTAATACCGTCTGGAGAGATT  
CTGGCTGGTTTCTCGAAGAAAGGAAATTCAGATGACATAAATGTAATTTCTCTTGGGTTTCAA  
GACTGAGAGGGTCAATTTCTAGGTTTATTCAGAAAGAAACCAATAACATCAGTTCTATGGGACA  
ATTGGGCCCTTCAAGGCTCTGAGAGTAAAGGTTAATGAGGGGACAGAGTGCCTGGAGAAG  
TTCACTGGGCTTCAAGAAATCAGAGAGGCTTCTGGCAAGCTCTATGCTGTCTATCTCTCT  
CTTCTCTCTCTGCAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATA  
AGTAAAGAAATGAAGGGGGTGGGAGGCACTAGGATTTGAACACAGAGACCGCTTGGCCCTGCAG  
GCAAACTGCTGATCTTCAAGTTCAGTCCACCCCTCACTTTGTTACAGCTGTTCTGTAAGACATTGT  
GAGCCCTTACAGCACTCGATTCTTCTTCTGTGTGAGTCCATGGGACAGGCCCTTCAACAAACA  
CCCATTCGCTCTCTCTTCTTCTTCAACTCAACCTCTGCTACCTGGCAGTCCACAGGCC  
TACAGCTTCTCTCAGTGGGGAAGACATCAGCTTGGAAAACCACTTGGAAAGCAACGTTATC  
CTAGAAAGCTTTTAAATGACCAAGCAGCAAGTCTCCGAGTGGCCTTGGCCCAACCCGGT  
CTTCCCTCTTTTCTGGTGTAGTTCTGACAAATACTAGAAATGTACTGGGAGTGTGCTCT  
GAGATAAGGAGGAACCTGCTTAAACTGGACTCTGTTTCCCATCACACCTAGAACAGGATGCTC  
TGCAACGCTTTAGCCCAATGATCCAAGTGTGCCCTTGGGGTATAAACTTGCAGACAGAGGGCG  
TTAGGGTCTCTCAGTGTGAGTGTGAAGTGGGACACAGAGTGAGACTCCATCTGCCCTGGGC  
AGGTTCCTGAGCCTTGGGGACAGCTTACCCCTACATCCCAAGGCTTCTGTGTGCTCTGCTGCTG  
CCTGTTAAGGAATAAAGTTGCTTTTCTTAA



581/615

## **FIGURE 576**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFPPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-29

#### **Transmembrane domain:**

Amino acids 47-62

#### **N-myristoylation sites:**

Amino acids 25-31

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80

**FIGURE 577**

ATCGGTTAGCGCCTTGCCATGATTAAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA  
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT  
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA  
TGTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTCCTATTTTCTGATGATACCAGAAAT  
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAAGTCTGCTCAGATTGATACACAA  
GAAGACATGGAATTTTGAAGAGGTACGCAGGAAGTGCATGCACTGGATTGGACTAAGCAGG  
AAACAAGGAGATTCTTGGAAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC  
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC  
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTGACGAGGAAGCAGTTAA  
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA  
TTTATCAATTGAGAGCAATTCATCCTCCTCTTCCATCTTTGATTACAGTTAATAGGCTATA  
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

583/615

## **FIGURE 578**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292  
><subunit 1 of 1, 160 aa, 1 stop  
><MW: 18576, pI: 9.29, NX(S/T): 3  
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG  
DWLGVRDKCFYFSDDDRNTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR  
KQGDSWKWTNGTTFNWGPSNSKWSCNWSLRQWLLLLGLPLR

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-42

#### **N-glycosylation sites:**

Amino acids 78-82;130-134;146-150

#### **N-myristoylation site:**

Amino acids 131-137

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

**FIGURE 579**

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC  
 TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTACAGTTCCAGGATTCCTGCAATGAGC  
 TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG  
 GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC  
 AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG  
 CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG  
 GAAGCCCCAAGTCAGCCGCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT  
 GTTTCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAAT  
 ACTGAAAAGCATCATTTTGAACAGCCATTTCTTCTTTTGGCAAACTGAAGAGGGTTTAC  
 ACAACTTATTTTAAACAAATCAAGAATGGTTGAACCTCAGTAGGTCTCTGGGCCCTGAAAGCC  
 AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC  
 TCGGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG  
 TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCACC  
 TGTGGGAAACTACTCATTTCTTGGCATTCCTTCCCCCTTCATTCCTTGGTTTGCATGGTTC  
 TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

585/615

## **FIGURE 580**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844  
><subunit 1 of 1, 145 aa, 1 stop  
><MW: 16618, pI: 5.26, NX(S/T): 1  
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH  
KQVDEEKMYENVLNEPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNNKTVS  
IPSYIEPEDDYDDVEIPANTEKASF

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-35

#### **Tyrosine kinase phosphorylation site:**

Amino acids 61-70

#### **Amidation site:**

Amino acids 48-52

0052556.01502

**FIGURE 581**

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA  
 CCTCCCTTTCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG  
 GCCCGGTGTCCCCTCCGAGCCTGTCTGCACTCCACGTCCCCCTACCAGGGGCTCCAGCCCCAG  
 GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCTGGAAGAACCATGTCCGGC  
 AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGTGTTTGAATTATCTGTG  
 AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAAACCAAGAGAAATCTGCAGG  
ATGGACTTTCGGTCTCTTCTTGTTCACCTGGCTTCGGTGTCTGATGGGTCTTGTTCATTATC  
 TGGTCTGTCTCGAAAACCCATAGCTTGAAAGGCCCTGGCCAGGGGAGGAGCACAGATATTTCC  
 TGTATAATTCCAGAAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTCCATACG  
 AGAAACCACACCTTCATTGTCTGCACTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC  
 TGGGAAGTATTTGGCTACTGTGAGGAGCTGGAGTTGTCTTGCATTACCTTCTTCGCCCTAT  
 CTGCTGCTAGGTGTAAACCTGTTTTTTTTCACCCTGACTTGTGGAACCAATCCTGGCATTATA  
 ACAAAGCAAATGAATTATTATTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG  
 AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT  
 AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACTGCATCGGGGCTGG  
 AACATCAGGTACTTCTCATCTACGTCTTGACCTTGACGGCTCGGCTGCCACCGTCGCCATT  
 GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGATGTGAGATTATACAGGAGACTTACATC  
 GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTAGTACCTGTTCTGACT  
 TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTCTCTGAGCTTCTCTGGGTGGCTAC  
 CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC  
 TGGGCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTGAGCAGAGCCCCAAGTCCAC  
 CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTCTACCTGCCCTTCCA  
 TGTGATGAGAGGAAGAAACAAGAATGACAAGTGATGACTGCCTTTG

587/615

## **FIGURE 582**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFIFYLASVLMGLVLICVSKTHSLKGLARGGAQIFSCI IPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCYQELELSLHYLLLPYLLLGVLNFFFTLTG
TNPGIITKANELLFLHVYEFDEVMPKPNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHC
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETIYIDDLGHLHVM
DTVFLIQYLFVLTFFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFFCHERKKQE
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-29

#### **Transmembrane domains:**

Amino acids 100-116;201-217;256-275

#### **N-glycosylation sites:**

Amino acids 65-69;284-290

#### **N-myristoylation sites:**

Amino acids 32-38;77-83;120-126;322-328

#### **Cell attachment sequence:**

Amino acids 292-298

#### **DHHC zinc finger domain:**

Amino acids 140-204

**FIGURE 583**

CCGCGGAAGCTGGCAGGCGTTTCAGAGCGTCAAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT  
 AGGCTGGGCGAAGAGTGTAGCGCTGAAGGGGGCTCCGGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT  
 GACGGGAAGGCGCAGTGCAGCGGCAAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCGCCCTC  
 CTGCTCCTCCTCTTCTGTGCTTCAGAGGGAGAGCAGGCCCCGTGCGCCCCATTCTCTGCAACAGCCAGAGGACCTGGTGT  
 GTGCTGCTGGGGGAGGAAGCCCGGTGCCGTGTGCTCTGGGCGCTACTAGGGGCTAGTTTCAGTGGACTAAGAGTGGG  
 CTGGCCCTAGGGGGGCCAAAGGGACCTACAGGGTGGTCCCGTACTTGGATATCAGGGAAATGACAGCCAAATGGCCAG  
 CATGACCTTCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAAGGTACACAAAGCAGGCCCTC  
 CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAAGCCCCCAGGTGCTGGCGGCCCTCTGTGTCT  
 CTGTTGTCTGGAGTTTCTGTGAACTGTGACATGTGAGAGCCGTGGGATGCCCCGCCCTACCCCTGAATTGTCTGTGG  
 TTCCAGATGGGGTCTGTGTGGATGGAGCCACTTTTCATCAGACCTGCTGAAGGAAGGGACCCCTGGGTGAGT  
 GAGAGCACTTAAACCTTGACCCCTTCAGCCATGATGATGAGAGCACCTTTGTCTGCCGGGCCGAGGCGAGGCC  
 CTGCCCCAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA  
 CACACTGTGACAGGAGGAGAGAAGGTCAATTTCTGTGCCAGGCCACAGCCCCAGCCTCCTGTACAGGCTACAGG  
 TGGGCAAAAAGGGGCTCTCCGGTGTCTGGGGCCCCGGGCCAAAGTTAGAGGTGCTGGCAGACGCTCGTCTCTG  
 ACTGAGCCCGTGTCTGCGAGGTGACAAACCGCGTGGGTAGCGCCAAACCGCAGTACTGCGCTGGATGTGCTGTTT  
 GGGCCGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGACGTGGGGGAAGACGCTTCCCTCAGCTGCGCCCTGG  
 CGCGGGAACCCGCTTCCACGGGTAACTGGACCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG  
 CGTCTTCCGTGCGTGGGGCCCCGAGGACGAGGCCACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCTCGCG  
 GCGCGCGCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCCAGTAGTGACCGCCCTGCACTCTGCGCTGCTCTC  
 CTGAGGGGCCCTGCTCGCTCCAGTGTCTGTTTTCGCTCTCCCCCCCCAGATGCCGTGGTCTGGCTCTGGGAT  
 GAGGGCTTCTGAGGCGGGGTGCGAGGGCCGGTTCCTGGTGGAGACATTCCCTGCCCCAGAGAGCGCGGGGGGA  
 CTGGGTCCGGCCCTGATCTCTGTGTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC  
 AGTGGCCGGAACCGGCTGGCGAGGGAGGTGCCCAGGCCAGCCTGGGGCTAGAGACTTGTGCCCCACTGTGCGG  
 ATAGTGGCCGGAGTGGCCCTGCCACCACTCTCCTTATGGTTCATCTAGGGGTGGCCCTCTGCTGCTGCGCG  
 CACAGCAAGGCTCAGCCCTTTTCTCCGAGCAAAAGAACCTGATGGAATCCCTGGCAGCAGCGACGGCTCCAGT  
 TCACGAGGTCTGAAGAAGAGGAGACAGGACGCCCGGAGGACCGGGGCCCATTTGTGCACACTGACACACAGTAT  
 CTGGTCTGAGGAGGAGGAAGGACTCTGGAGCAACAGGACCAACCAACCGTTACTCAAGGTTCGAGGAGTCACT  
 GTGAGCTGAGGCTTGGCAAGCCCCCTGGAGGAGGTCTCTTCTGCGCACACCCCTCCCCCTTGGGGCCCCAGGG  
 ACCCTTACCTTCTATGACTTCAACCCACACTGGGCTAGGTCCCCCTCTGAGACTTTACAGAGCCAGGGCAGGC  
 TATCTCACCAACCCACCCCTCGAGCTTTCACACGCTACATCAAAACCACTCTTTTGGGCCCCAGATCTGGCC  
 CCGGGACTCCCCCTTCCCATATGTGCTCTTCCCAACACTAGGCCACCCCGTCTCCAGACTCAGCTGTGACAT  
 CTTTTCCAAATGGAAGAGTCTGGGATCTCCAATTTGCCATATGGATTTCTGATTTCTGAGGAGCCAGGACAAG  
 TTGGCGACTTTACTCTCTCAAAACTGAACACAAGGGGAGGGAAGATCACTTACATTTGTGAGGAGCATTTGTATA  
 CAGTCAGCTCAGCCAAAGGAGATGCCCAAGTGGGAGCAACATGGCCCAATATGCCCCACTTATCCCCGGTG  
 TAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG  
 GCGCGGATGGAAGTGTCTTAGCCACTGAAAGAAATATTTCAAGATGACCATCTGCAATTGAGAGGAAGGTAG  
 CATGAGATGAGATGAAGATGAAGACATACAGGCCCAACCTGGCTCTCCCTGAGGGGAACTTTGCTGCGCCAAAT  
 GGAAGATGAGCCAGATATGCCCATATATCTCCCTAGGAACCCAAATGGCCACCATCTTATTTTACTTTCTCTTAA  
 GACTCAGAAAGACTTGGACCAAGGAGTGGGATACAGTGAGAAATACCACCTGTTGGGGCAAAATATTGGGATAA  
 AATATTTATGTTTAAATAATAAAAAAAGTCAAGAGAAAAA



```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
```

Important features of the protein:

Amino acids 1-20

## Amino acids 511-531

Amino acids 143-147:301-305:484-488

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;  
387-393;460-466;473-479;494-500;495-501;514-520;528-534;  
554-560;592-598;608-614

## Amino acids 500-504

Amino acids 149-152

## Amino acids 445-466

## Amino acids 326-377

CCGCCGCTGAGGAAGCGTGTGCTGGGATGCCAAGAGCCAGAGATGGATCTTCTCCGAGTGGGACGATCTGTGCAACTCCCGCTTCCCGAGCGGGCTAAGAACAGGCAGTTTGTCTCGGCTGGCTGCAGATACCGAGAGCCAAAGAGACCGAAGCACCCCGAGGGAGCCACGAGCAGACAGATGGTAGGCGCGAAGCCGAGAGGACCGCGGAGGCTGAGCACCGAGAGCGCCGAAGAGAGAGAACTAACCCAGCCCAAGTTACCCCGCCGGCTTCTTCTCTGCTGCGCTAAGGAATGAACCTTCAGCTCGATCTGCTCTTCTGCTGCTTCTTCTCTTCTCAGTCAAGAGCTGGGGCTCCAGAAGAGAGGATGCTCTCTCTGGTGTGGGCTATCGCCACAGGACAAGTTTCGGAGAATGAATGAAGCCCAAGCTATTCTTCTCAGCCAGCAGCCACCGAGACCGAGTGGTGTGCGGACAGCCAGTGAAGCTACTCTGCGCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGTGGGCAAGGACCTTCAAGTTTACCACAGCTATCTGGTGTGGGACCAACCTGTTCAGGGGAGCACCACTGAAGATCTCTGAGGACAGAGCTGCAAGACAGTCTCGGTGTACAGTGTCCAGGCCATCCAGGCCCATCCGCTCCCGCCCGCACGCTCACAGTCTCTGTGTCCGCTGTATGAACCCGTCATCTCTGGGGGGCTGTGATCAGCCTGCGTGCGGGGACCTCTCAACCTCACCTGCCACGACAGCAATGCCAAGCTCTGCAGCTTCCATCTATCTGGTTGCGAAAGGGAGAGGTCAATCAATGGGGCCACTCTCTCAAGACGCTGCTCTGGGACGGCAAGCGGGAGCATCGTGACACCTTCTTCACTCTCCGTGGTGAAGTGGAGAATGGCCAGAGCATCGGTGTGCTGCGCCAAACCAACCGCATCTCCGGAGGAAGGAGACGTGCGTCAACATTGACATCCAGCACCTCCACTGTCAACCTCTCGGTGGAGCCACAGCGAGTCTGGAGAGCAACGTCGTCATCTTCCATGCTCTGCAAGAGCCAAACCCAGCTGTCAACCGATACAGTGTGGGCCACAGCGGGCCAGATCATCAAGGAGGCTCTGGAGAGGTGTACAGGACACAGTGGATCACTGACTTCTCAGAGCCCGTCTCTGTGAGGTGACCAACCGCTCCGCGAGCAACACTCAGCCGACGGTTGACGTCTACTTTGGGCCCCGATGACCAAGCCCAATCCTTGTCTCGTGGATCTGGGGCTGTGATGCCATCTTACGCTGCGCTGGACCGGCCAACCCCATCTCTGACCATCGTGTGATGAAGAGGGCGCTCCGAGTGGTCTGAGCAATGAGAAGACCCGTACCTTCAAAATCGTCTGCAGGAGGAGCGGGACAGTACGTGTGCGGGCTGTGGTGGCCCGTGTGGGAGCGGGGAGAGAGAGGTGACCTGACCGTCAATGGACCCCCATCATCTCAGCACCCGAGACGAGCCCTCCAGCGCGAGGAAGGGCCAGATCAAGTGTCTTATCCCGGACCGCCGCGCGGAGCCGATCGCTGGTCTGGAGAGGACAGCTTCTGGAGTCGGGCACTCGGGCGCTATATACGGTGGAGACCATCAGCACGAGAGGGCGTCACTTCCACCTGACCATCAGCAACATCTGTGGGGCGACTTCCAGACCATCTACAATCAACGCGCTGGAAAGCACTTCCGCTCCGACATGAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAATGAAGTCCGGAGCCGGGCTGGAAGCAGAGTCTGTGCGCGATGGCCGTCATATCTGGGTGGCGCTAGGAGCTGTGTGGCTTCTGTCCTTATGCAACCATGTGTGCTGTCGCGTTCACAGAGAAGTACGGGAGGAGATCCGGATCTCAGGAGGGGGACAGGAAGAGCCAGGCTTAGGCTTCCCGGAGAGCAAGTATAGCACGAGTGCAATGAACAGGGGCTTAAACAGTGTCTGAGCTCTGGGGCAGGAGTGGGTCTGTATCATCGTGTATGTGAGCTCTGGGCACAACTGGCGCTGGCAGATGGGCGTAGCTGAGTTTGAACCTGAGCTGACTGACTTCTATCTGCAAGGAGATGAGGGGAAAGCGGTTTGTGTTTGTATCTTGTCTCTACAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAATAAAGAGCTGCTAGTCTCACCAAGAAACGAGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAGGCAATAAAGGAATTGCTTTGAGAAAATCTTAA

591/615

## **FIGURE 586**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCVLVGYMAKDKFRMRNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLKKEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAIPGGKET
SVTIDIQHPPVLNLSVEPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSLTI VVMKRGSGVVL SNEKTLTLKSVRQEDAGKYV CRAVVPRVGAGEREVTLT VNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPDRIAWSWKENVLESGTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTA WNSFGSDTEI IRLKEQGSEMKS GAGLEAESVPM AVIIGV
AVAGGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-17

#### **Transmembrane domain:**

Amino acids 534-555

#### **N-glycosylation sites:**

Amino acids 167-171;253-257;324-328;498-502

#### **Glycosaminoglycan attachment sites:**

Amino acids 523-527;574-578

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 204-208;370-374;588-592

#### **Tyrosine kinase phosphorylation sites:**

Amino acids 40-49;300-308;389-397

#### **N-myristoylation sites:**

Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;  
374-380;436-442;478-484;539-545;543-549;  
568-574

#### **Amidation site:**

Amino acids 202-206

#### **Leucine zipper pattern:**

Amino acids 8-30

2025-01-06 15:00:00

## FIGURE 587

CAAAAAGAGGAGCATGTCATCATCATGAGAGGCCCTCGAAAAATCAATGGTATTCGCAATTTCTC  
CCAGAAGAGGTGCTGTGCCAAACCTTTGGCCACTTTCTGCTTTCAGATGAGACAAGAGTCA  
AAATGACAGCTGTGCAGCTCATGGAAGCAGTAGATACCTCGCTCGAGGTACCACTTATCCC  
CCACAGAGGGGTTGTGTTGTCACTGTGTAGTGACTTGAGGCCAGATAGTCTTCTGGCTATG  
TTAAATAACTCAGATCAGCTACCGAGTCTGAGATCTCTTCTCATGGCATTTGGAGCTGGCT  
GTGCTCTGAGGCAGACCTGAGCCCTGGACATGGGGCAATGCTCTTGACGGGAAGGGGAAGCCACT  
GAATTTTGGGTGTACCCAGGTAAACAGAGCCCTCAGCATCTGAATAGAAAGTGAACAGGAACA  
GAAGAGATTACACTACATCTGAGATGGAGACCTTCTCCTGTCTGCTCAGCTGGGCCCTGG  
TTCTTGCAAGAGCATCAGAAGAACAATGAAGATAATTAAGAGAATTTACAGACGAAGAAGA  
TGCAATATGACATGGCAAAAAGTGCCCAAGAAAAACAGACATTGAGATTAAATGAACCGGA  
TCCTTGTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATAGTATGTTCCACATTACTGCA  
CATTCAGAAGTTTACATTATAATGACCCCAAGGAAACAGTTCGGGTAAATGACAAAGAGTGT  
GCAATGACAGTGACAGTCTGGAGAAAAATTTCAAGAACAAACGGATCTGCAAGTGGAGCAATA  
ACTTCACTCCGCAAGCTCAACAAGATGATGCGCAGAGGTCACAGGCCCCCAGCTCGAAGTTTGA  
CAGAACTCTGGCATAAGCTCTGTGAGAGCCTAGAAGCTGAAAATACAGTGTGCGAGTTCACT  
ACAGGCCAAACAGTTCCCCAGGTGCCAATACGATAGTTGTACTCATTAGAAGAAATATTGACA  
GTGTGCAAGAGTCATTCTCTGATGAGCTGGTTAGTTTGTGCTCTAAGTTGTAATCCCCAC  
AGCTTTAGAGCTAGGGTCTTACTAAAGAGGACCTCTCTGTTCATTCTGTTTAAACCTTT  
CCTTAATATCTACTCTCTTAGCAATATAGTGAACCTCGTATATTATTCTTAACCTGGAGGATG  
AAAAATCAAAAATTTGGGATAATTAATCAATTAAGGATATGACTGATACCG

593/615

## **FIGURE 588**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893  
><subunit 1 of 1, 199 aa, 1 stop  
><MW: 22427, pI: 6.46, NX(S/T): 3  
METFPLLLLSLGLVLAEASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK  
NTLSMSKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNF  
IRSTEVMRRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI  
LTVLTGHSLMSWLVCGSKL

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-16

#### **N-glycosylation sites:**

Amino acids 61-65;89-93;111-115

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 105-109

#### **N-myristoylation sites:**

Amino acids 12-18;88-94;144-150

#### **Microbodies C-terminal targeting signal:**

Amino acids 197-201

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**FIGURE 589**

CAGTCCTGCCGGACGGTGAGCGCATTACAGCACCTGGACAGCACCGCGGTTGCGCTGCCTCC  
 AGGGCGGGCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC  
 TGCACCTTGCCCGCGCTTTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG  
 AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCGCCCGAAGCA  
 GAGCCATGAGAACCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGCCCCGGCGAGGCGCTG  
 CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT  
 TGTTGCGCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCTCCTGGTGAATCTGTCT  
 CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTACAGCTGCTCGGTGTGATGCGCGGG  
 CGGACACCGTCGGCGCCCGGCGCATGCCAAGTCATTGGCTTCTTGGACACCTTCTTGGCGTCC  
 AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCACTGGCTGGCAGTGGGCTTCCCACTG  
 CGCTACGCCGGACCGCTGCGACCCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCTTGGGGACAG  
 TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG  
 TCCTGTTGCTGCGCTGCGCCTGCCGCCGAGCCTGAGCGTCCGCGCTTCGAGCCTTCACCGCCACG  
 CTCATGCGGTGGGCTTCTGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC  
 CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC  
 GCCGACCTGCACCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC  
 GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCGTATGTCATG  
 ACCAGGCTGGCGGAGCTCTGTGCCCTTCGTACCGTGAACGCCCACTGGGGCATCTCAGCAAG  
 TGCTGACCTACAGCAAGCGGTGGCCGACCCGTTACAGTACTCTCTGCTCCGCCGGCGGTTT  
 CGCCAAGTCTTGGCCGGCATGGTGACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC  
 CATGACAGCTCTCTGGATGTGGCCGGCATGGTGACACAGCTGCTGAAGAGAACCCCGCGCCCA  
 GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGTCAGCAGACACACTGA  
 GGGCTTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAGGGCACTGGCCCTG  
 CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

595/615

## **FIGURE 590**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930  
><subunit 1 of 1, 363 aa, 1 stop  
><MW: 39332, pI: 10.42, NX(S/T): 3  
MGGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLslGHLlLLAALDM  
PFTLLGVMRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPPLRYAGRLRP  
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG  
FVLPLAVLCLTSLQVHRVARRHCQRMDVTVMKALALLADLHPSVRQRCLIQKRRRRHRAT  
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRP  
FRQVLAMVHRLLRTPRPASTHDSLDVAGMVHQLKTRPRPASTHNGSVDTENDSCLQ  
QTH

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-24

#### **Transmembrane domains:**

Amino acids 46-60;85-103;130-150;175-192;246-264

#### **N-glycosylation sites:**

Amino acids 47-51;348-352;355-359

#### **Tyrosine kinase phosphorylation site:**

Amino acids 286-295

#### **N-myristoylation sites:**

Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;  
349-355

#### **G-protein coupled receptor proteins:**

Amino acids 72-112

#### **7 transmembrane receptor (rhodopsin family):**

Amino acids 22-294

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted May 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

AA AATGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGT  
CCGGCGCCAGCTGACCCACGACATGGCCGGCGGGTCTCGGAGACAAAACCTGCGCGGACGAC  
GAATGCAGCATGATGTACCGGGTAGGCTCTTGAAGATTTACAGGCGCGGATGTCTGTTT  
GTGAATTTAAAAAGGTGATCTCTGTATATGTTACTATAAACTGGCAAGAGATGGCCTGAA  
GTTTGGGCTGGAAGTGTGGACGCATCTTTGGATATTTTCCAAAAGATTTAATCCAGGTAT  
CATGAATATCAAAAGAAAGAGCTACAAGTTCACACAGATGAGACGGATTTGTTTGGTTTGA  
GGAGGAAGAGATGATTTTATAATTATAATGTAGAAGAACCTTTAGGGTTTTGGAACTGTAC  
AATTCCTCAGCTACAGATTTGAGAAGCTGTAGAAAAAATTTACAGGATATGGAATAAA  
CCTGAATTTACTAAGGAAGGGAACTGAACCTGAACCAAGTAGAAGCCAATCAGAGGAAAGT  
GATAGTGATGATTTCCAGAAAACACTGAGGATCTTCAGGAACAGCTTTCAACTCAGAAGCACAC  
TCCCATCGAAACAGCCAAAGCAATCATGCTCAGGAGAGCAGGCTCTTGAATCTTTTGA  
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAAACAACAAACCAGCAATAGTTCT  
CAGGCTCCAAATGAAACAGGATAAGATGATGCCATAAACTTTGAAAAAGAAATGACTCTA  
GACTTGAAAAACAAATTTGGCTCAACAGCTGATGCATCTGTATGTATGATAGAGACAACCA  
CTCGTTACTCTTATAGAAGATGATTTTGTAGGAAATTTGGATCTGAGTATTATGCAGTTTGA  
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTTACTTACCTTTACAGATGGG  
GAAGATATGAAAACTCCAGCAAACTGCGCGTTGAGAAATTCACAAAGATAGAAAGCAGAAAT  
TCAATAGAGAGGACAGAGGTTGACGTAACCTGTGCCCTTGGCATCAAAATGATGATAAAAT  
ATACTAACCAAGCTGGGGGGACACTATCTCTTATTTGTCAAGGAGGTGAAGAACCAAGAT  
ACGATGGATTTAGAGAGCTCTAGTTTCAGAGGAAGAAAAAGAGATGATGATGATGCATTAGT  
CCAGATGACCAACAGGGGAAACACAGCTCAGCAACAGATATATAGTGACCTTGACATATGAT  
GATGGTCCTTTTATTGTAGACATCTCTAAACAAATATGACAAGAAGTAAACGCAAGCAAT  
CACATTAAAGGAAAAAGGGAGGGGAGTTCAGGAATCCAAGAGGGGCTGGTACAAGATGAGACA  
GAATTAGAGATGAAAAATCAAGAAGTTTAAAAACAGAGCCCAATAAACTATGACATCTGAGG  
TTTCATTGGGAAGAAGTGTACTGTGCATTATCCATTACAGTAAGAGTTTCAATTGCTCTCAA  
AATCCAAAAGTTTATTTTAAAGGTTTGTGTGTAGAATAGCTGCCCTGGCAGTGTCATT  
TTGAGCCAAACAAATCAAAAATGTCATTTCTCCCTAAATAAAATCACCTTTAAGCTAGAG  
CGTCTTCAACCTTTGAAATGTGCAATAAAGAACTACTGTTGTTTAGCTAATGTAGCATATGT  
AATGTCAAATGATTTAGAATGTATGAAAAAATGAACATTTCTCTGGGAATGCTTTTAAGA  
ACATGTATTTCCATATCTTATTTTGTAGTACACAGCTGAATACGGAGCAATGGTGTATT  
AAGCGTTTTTTTAAACTATCTGGTCACAAAGACTGTTACGCAAAAATGTTTACTAAAAAGATC  
ACTAAACTATCTCCCTCTGTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT  
AATATTTAAAAAATAAAAAA



## FIGURE 592

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLVLVLLVLLPLRWPRVQGLDPSTGRRFSEHKLCAADCESSMMRYGEALDFTGPDCC
RFVNFKKGDPVYVYVYLLKARGWPEVWAGSVGPRFGYFPKDLIQVVEHYTKKEELQVPTDSTD
FVCFDGGRRDDFVFNVEELLGFLELYNSADSEKAVEKTLQDMEKNPELSKEREPPEP
VEANSEEDSDHSENTEDLQCFOTYTKQHHSHANSQAHQAQGCQASPEFSEFMLQDKLVPR
ESENKNTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKEFGSTADALVSDDETTRLVTSLED
DFDEBLDETTEYAVGKDEDEENQDFDELPLLTFTDGEDMKTAKSGVSEKYTEKDKQNSNEE
DKVQLTVPPGKIKXNDKKNILTLTGGDTI FSVTGEETERTDMLDSESSSEEEKEDDDALV
DSKQGLKQPSATSDSDPNVDGLFIVDI PKTNNNDKEVNAEHHI KGGKRGVQESKRGLVQD
ETGEEDENQEGFKEPTIKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249; 249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

## Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

GGGGCAGTAGAGTGTGCTCTGGGTACGCTGAGTGACCTACATCAAAGCTCCCGAGCCTGAAAAAC  
ACATGCTGTTTCCCGAGCCCTCAAGATATTTGAACATTATAGATATTTAAAGTAGCGTTTCTT  
TCTTACAATGCTCTGAAGAAAGTGACCTACGCGCACTCACATTCTCAGGATTCTGCTGGAGCAAG  
GAATTAACCGAGATGGAAATAACCTTAAGAAAAAGAGGCGCTCCAGCTCCATCTCCCAATTTGGCT  
TCAATGCTCTCTGGGTCTGTGAATCTTTTGCTGATGTGTGCTGATTGGGCTGTGAGCTTGGG  
GATGATGTTTTTGCAGATATCTAATGACATTAATCAGATTACAGAGAAATTGATCAACTTCA  
GAAAACCCATCCCAACGAGCAGGATAACTTATCCCGACACTGGGCAACTCCAACAATTTGCT  
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCAGTCTACTGAAGAGCGAGGAACAAATGGC  
CATCAAACCTGTGCGAAGAGCTAATCACTACTATCTCAGACCAGATGTAATCCATGTCCTTAA  
GATGTGGCAATGTGTACAAAATAGTTGTCTACTATTTTACAACAATGAGGAGAAAACCTGGG  
TAACAGTAAAGAGGATGCTATAGACAAGAACTCCACCTTAGTGAGATAGCAGGATTTGATCAAG  
AAAGGATTTTATGCTACAGCCATTACTGTTTTCTGTTCTTTGGCTGCTGATTTGATGATG  
GGACTCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTGTCCCTCTCATCTGTGACGT  
CTCTAACTATTGAGGGTAAACACAAGCTTTTCATGGAATCTGGGAAATTAATGATGTTGT  
GAGAAATTAATAATACAGACATAAAAGAGGAGTACACAATACTGAGAAAGAGCTCCAGTAAC  
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAGGATGTGC  
TTATTTTCAAAAAGGAAATTTATTTATTTCTCGCTGTGCTGCTGAAATTTTTTGGATTTGCGA  
GAAGACAGCTGCCAGTGAAGATCAGGATTTGGATTAGTATGCTCTTCCAAATTCCTCAA  
GAAGTAAGAGACTTGTGATGAAGCTCATATGAGGAAGAAGAGGAACTACGGTACCAGAGCAAGG  
GCGAATCTTCGCA

599/615

## **FIGURE 594**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80, NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLKRGRHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINSDSEKLSQLQKTIQQQDNLSQQLGNSNNLSMEEEFKQSIISSLLKRQ
EQMAIKLCQELIHTSDHRCNCPKMWQWYQNSCYFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

### **Important features of the protein:**

#### **Transmembrane domain:**

Amino acids 42-62

#### **N-glycosylation sites:**

Amino acids 91-95;101-105;176-180

#### **N-myristoylation sites:**

Amino acids 17-23;97-103

**FIGURE 595**

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCATCCTACCCAG  
AACACCTGCGCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTTAGGAGAACC  
**ATG**GGGGGCTGCCAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCATATGCTGACA  
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTGCTTGATACAACAAC  
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG  
GATGAACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAACCAAAAC  
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAAATTTATGTGGAAATGAAA  
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT  
CTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAATTCAAGCCAAACCAAGTATACAAG  
ATCGACACAATTGCTGCTGATGAGAGTTTACCCAGATGGATTGGGTGATCGCATCCTCAAA  
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTCAA  
GACATTGGGGCGTGCATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT  
GTTTCGTAACCTGGCCATGTTTCTGATACCATTCCAAGGGTTGATTCTCTCTTTTGGTTGAA  
GTACGGGGTTCTGTGTGAAGAGTGCTGAAGAGCGTGACATCCTAAACTGTATTGTGGAGCT  
GATGGAGATTGGCTGTTTCTCTTGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG  
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTT**AGT**TGGCCATCTTGGCCCCACCCCGA  
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTAATAAATATTAACGG  
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 597**

A C A C T G G C C A A A C A A A A A C G A A A G C A C T C C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A  
 G G A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G  
 A T T C C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G  
 C A G C A C A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A A T G C C C T G T G C C C T G G T T C T T  
 G C T G T C C T T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A  
 G G A C G C T A C C C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T  
 G C C T G G G G A C A T C G T G C C T G C T C C G G G C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T  
 G G T G C T G A G G T G C C A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C  
 C G T G C A T G G G C A C T G G G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G  
 G G T G G A G G A G C C T A G G A A T G C C T C T C T C C A G G C C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C  
 T A C T G C C C G C T G C G T C C T G C T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C  
 T G T G G G C T C T G T G G T A T A T G A C T G C T T C G A G G C T G C C C T A G G G A G T G A G T A C G A A T C T G G T C  
 C T A T A C T C A G C C C A G G T A C G A G A A G G A A C T C A A C C A C A C A G C A G C T G C C T G C C C T G C C C T G  
 G C T C A A C G T G T C A G C A G A T G G T G A C A A C G T G C A T C T G T T C T G A A T G T C T C T G A G G A G C A G C A  
 C T T C G G C C T C T C C C T G T A C T G G A A T C A G G T C C A G G G C C C C C A A A A C C C G G T G G C A C A A A A  
 C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A  
 G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A C G A A C A C T C T G C C C C T T C A G G G A G A C C C C G  
 C G C A C C C A G A A C C T C T G G C A A G C C G C C C G A C T G C G A C T G C T G A C C C T G C A G A G C T G G C T G C T  
 G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T G T G C T G G C G G G C T C C G G G T G G G A C C C  
 C T G C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G T C A C T G T G G A C A A G G T T C T C A G T T  
 C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G A A C A G C T C G G A G A A G C T G C A G C T  
 G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T A A A G A C G A T G T G C T A C T G T T G G A G A C  
 A C G A G G C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A G T G G C T G T A C T T C A C T A C C  
 C A G C A A A G C C T C C A C A G A G G C A G C T C G C C T T G G A G A G T A C T T A C T A C A A G A C C T G C A G T C A G G  
 C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G C C C C A T G G A C A A A T A  
 C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G C T G C G C T T T C C C T  
 C A T C C T C C T T C T A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A C A G G A C G T C C G  
 C T C G G G G G C G G C C C A G G G G C G C G C G G C T C T G C T C C T C T A C T C A G C C G A T G A C T C G G G T T T  
 C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C C G T G C G C G T G G C C G T A G A  
 C C T G T G A G C C G T C T G A A C T G A G C G C G A G G G C C C G T G G C T T G G T T T C A C G C G C A G C G G C G  
 C C A G A C C C T C A G G A G G G G G C G T G G T G G T C T T G C T C T C T C C C G G T G C G G T G C G C T G T G  
 C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A G G C C C G C A C A G C G C C T T C C G  
 C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G A G G G C C C G G G C G C C C G A G C T A C G T G G  
 G G C C T G C T T C G A C A G G C T G C T C C A C C C G G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T  
 C T T C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G A G C C T C G C G C C C C G G  
 T T C G G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T C A G C A G C C C T G G A T A G  
 C T A C T T C C A T C C C C G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G G C G G G A C C T G G  
 G C G G G G G A C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A

**FIGURE 598**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLSERLVGPQDATHCSPGLSCRLWDSIDLCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWST
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVNLVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEALCWAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEALEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLFLFAAALSILL
LKKDHAKGWLRLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSPGVAVALCSEWLQDGVSGPGAHP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 453-473

**N-glycosylation sites:**Amino acids 118-122;186-190;198-202;211-215;238-242;  
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 552-556

**N-myristoylation sites:**Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;  
692-698;696-702;700-706

**FIGURE 599**

GGTCCTTAATGGCCAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
 TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
 TCCCTAAGTTTCAACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
 TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCTGGGGAAGAACTAA  
 ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
 AGCAACTGCGTGACATTCACTGGAGAATTACACACCCCAAGGAACCCCTCACCTGACAGGCAA  
 GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
 GGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTTCATCCTGGAGCCA  
 GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATTACTTCTCAA  
 TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
 GTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCACTCAGGGCCACAGCCACCACC  
 TCATCCTTTGCTGCCTCCTCATCATCTCCCTGCCTTCATCCTCCCTGGCATCTGAAGGAGAGT  
 CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCACGGTCTTGATCAAACT  
 TCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
 CATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCTTTTGCCAACAATTTTA  
 CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
 CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTCTCTTTTGGTGGAAAA  
 TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAAATGATATTGTGAGTAAAAATAATCAG  
 TTAGACTTCAGACCTCTGGGATTTCTTCCGTGCTCAGAAAGAGAATTTTAAATATTATTAAT  
 AAGAAAAATTTATATTAATGATTGTTTCCCTTAGTAATTTATGTTCTGTACTGATATTTAA  
 ATAAAGAGTTCTATTTCCTCAAAAAAAAAAAAAAAAAA



605/615

## **FIGURE 600**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF  
FLHYDCGNKTVTPVSPGLGKKNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 224-246

#### **N-glycosylation site.**

amino acids 68-72, 82-86

#### **N-myristoylation site.**

amino acids 200-206, 210-216

#### **Amidation site.**

amino acids 77-81

2025 RELEASE UNDER E.O. 14176

**FIGURE 601**

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTGTGCCTT  
 GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA  
 CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG  
 GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC  
 GCACAGAGCAGAGGCTCCCTCTTCAACGTGGCGACCACTGAGCCCTGACCCCTGCTGACTTTGT  
 GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTTCAGTACTACCAGCTCT  
 CCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT  
 TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC  
 TCTGTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA  
 AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGCAGCAAAAGTTGGGAGGACTGTAAT  
 ATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAGAAGACCTGGAATTTG  
 CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTTCGCCCTGACA  
 GTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA  
 TAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA  
 AGGACTGCAAAGAAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA  
 GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAT  
 AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA  
 TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCGTGTTTCCGTTCAGGATCAC  
 CAGCATTCTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCAACAAGAAGCTTTATTTACATGC  
 CACCAACCAACCTCAGAAACCCATAATGTCTATCTGCCCTCTTGGCTTAGAGATAACTTTTAGC  
 TCTCTTCTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCCTTACACTTGGTGGA  
 ATAAGAAAATTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCCTTTCTCTGACAGTCAAG  
 TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATCTTTT  
 TTGTTTTGTTTCAGTTCTACTAGTCCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGT  
 CCATGCCGTTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
 GCATTCTTCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA  
 GGAAAGAAATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGGATATTCCTTCAG  
 AGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCACTCTGCACCTGTAATAGTTTTCAGTTCCCTA  
 TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA  
 AATACTGTGAAAAA

**THE UNIVERSITY OF CHICAGO**

MQAKYSSTRDMLDDGGDTTMSLHSQASATTRPEPRRTEHRAPSSWTRPVALTLLTCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNKLAGSLQHVAEKLCRBLY  
NKAGAHRCSPCTBQWKHGDNCQYFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPDGSKAWLWMDGTPFTSELFHIIIDVTSRSPSRDCVAILNGMIFSKDKCEL  
KRCVCERRAGMVKPESLHVPPETLGGD

**FIGURE 603**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
 CAGCAAT**ATGC**ATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
 GTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
 GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC  
 CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
 GTTGGACAAAGGCGTCCAGGGGCTCAACCAAGGATGGACAAGGTTGCCCATGAGATCAACCA  
 TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
 ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
 GAAGGAAGCAGAGAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
 GGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
 TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
 CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
 CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG  
 CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG  
 TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTA**CTGGG**ATTGTGAATAAA  
 CTTGATACACCA

609/615

## FIGURE 604

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

2025-10-08 09:00:00

610/615

**FIGURE 605**

GCACGCGCGCGGGCGGCGAGAGGAAACGCGCGCCGGGCCCGGCCCTGGAGATGG  
TCCCCGGGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG  
GCTTCCGTATCCATGATTATTGTACTTTCAAGTGCTGAGTCTGGGGACATTCGATACATCT  
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCAAC  
TTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC  
AGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCAAAGACTCGGGTGGTCCAGGAGC  
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA  
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGGCCGAGACG  
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG  
TCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCTGGACCTTCTGGTAGAAGA  
GTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC  
TACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGAGGCCAGGTAGAGGAAAAGGGTTTGGG  
CGTTGCTAGGCTGAAAAGGGAAGCCACACCCTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG  
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA  
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACTACCTGGCTCCAGCC  
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTTGTGGAGTGGTTTAAAGAGCT  
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAAGCTTCTCATCAGGGTTG  
CAAAAAAAAAAAAAAAAAAAAAAAAAA

1055555-011502

611/615

## FIGURE 606

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISTPVNVTSIPTFELLQPPWTFW
```

**Signal peptide:**

amino acids 1-20

202110.011500

**FIGURE 607**

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATGT**GGCTGC  
 CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA  
 GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA  
 TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT  
 CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCAGCTTCA  
 CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTACTGGTGTGGGATTGAAAGAA  
 GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA  
 CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCAAGAGGAACCACT  
 ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT  
 TGAAGGGGTCTCAGAGGTCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACCTCTCCG  
 AACCTCTGACTAAAGACATGGCCACT**T**AGAGAGATGGATCTGCAGAGCCTTCTGCCCTGGCC  
 ACGTTTCCAGAAGAGACTCGGGCTGTGGAGGAACATCTACGAGTCTCTCGGATGCAGTGACT  
 GAGATAGGGGCCCTGGGCCCTCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC  
 AGCTCAGGGACTTAGCCAGGTCTCTCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG  
 TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG  
 GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTGGGGGAGACCCCCCAG  
 CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGGCCTGAGAACCTGATATATCC  
 GTGTTTTTAAATTTTTTTTTTTTCTAGCAAAAGTGGGTTTTAATGACTTATGTTCATAGGAAAC  
 CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCTGGTTCTAGGGCATGAGG  
 GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT  
 GGGAACTCCTTGGCCCGGCCCGGTGCTTGTCTCTCCCTCCCACCTCTTCTCTCTCTAGCT  
 CCCCAGCTCCTGCTATTTCCCCACCTCCGAGGGGTGACAGCTTGGGAGCCTCCTCAGCAT  
 GACAGCTTGGGTCTCTCCCCAAAGAGCCTGTGAGGCTCAAGAACACCTCCAGGTGGGGA  
 GGGCAGTAACGAAAACCATGCGAGGAATGGCACCTCCTTTTTCGGTGATGTTGAAATCATG  
 TTACTAATGAAAACGTGCTTAGGGAAGTGGTCTGTCTCTCACAGGCTTCAACCACGGCGAT  
 GAGGCCCTTGAATGTGCTACTTTGTGCTGATGGTTGAGGGACCTCACACCAAAGGGACCT  
 TCCCATGTGAGATGTGCTCCCGCCCCACCTGCCCAAGCAACACACACATGTTCCGGC  
 ATGTTGCCCTTTGAACACCATGAGGACGCTCCCAACCTGCTCTGGTTCTAATAGGGAGTAC  
 TGACTGTGACGAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT  
 CCCCCTCTTCTGTCTCTCAGCCAAAGAGAACTTCTCTGACTTTGAACTGAATTTAGGTCTC  
 TGGCCAATGATGGGCTGAAAAATTCATAATGGCCAGAGGAGAGTTTCGAGCCCGGCTAAGA  
 TCCCTTGAGTCATCTGTGAGGGACCAAGACCCACAGTCCACAGCCCGAGGGCCCTACTCTC  
 TGGAAATGCTTTCTGGATGCTTCCCGAAGATCCGACCAAGCCAGGGAGGACGGCACCGC  
 TCCGCGGGAGGGAAAGCCAAAGCATGGTGTTCACAGCTGGAGCTCAGGGGCGAGGGACATG  
 GCGCTTGTCAACGTGATGTCTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC  
 CGTCAATCTCTCGGAAAAA



613/615

## **FIGURE 608**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETIYIKWWCRGVWRDTCIKI
LIETRGSEQGEKSDRSIKDNQKDRFTFTVTMEGLRRDDADVWCGIERRGPDLTGTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFSLEPLTKDMAT
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-17

#### **Transmembrane domain:**

Amino acids 151-170

#### **N-glycosylation site:**

Amino acids 190-194

#### **Tyrosine kinase phosphorylation site:**

Amino acids 95-103

#### **N-myristoylation sites:**

Amino acids 66-72;125-131

#### **Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 5-16

2025.04.25 10:01:50

**FIGURE 609**

GATGGCGCAGCCAAGCTTCTGTGAGATTTCGATTTCTCCCAAGTTCCTGTGGGTCTGAGGG  
 GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCAAA  
 ACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
 CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
 ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTACGGGAG  
 GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGGCTAAGATGAAAGCCTCTAGT  
 CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
 ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
 GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACT  
 GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTGCTAAGACTC  
 TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
 AGCCTCGCCAATTCCTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
 TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTACAGATTTCTTCTGCAATGGATGGAG  
 GAGACAGAA**TAGG**AGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
 TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACTGTACTAGTCTTGTGCT  
 GGTACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGATGATTGTCTTTATGCATCCCC  
 AATCTTAATTGAGACCATACTTGATAAGATTTTGTAAATATCTTTCTGCTATTGGATATATT  
 TATTAGTTAATATATTATTTATTTTTTGCTATTTAATGATTATTTTTTTACTTGGACATG  
 AAACCTTTAAAAAAATTACAGATTATATTTATAACCTGACTAGAGCAGGTGATGATTTTTTAT  
 ACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTTATTCAATTGTAT  
 TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
 TACTTAGGATGGGTTGTGGAATAAGTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
 ACCATCCCAGTAGACTCCCAGTCCCATAATTGTGTATCTTCAGCCAGGAATCCTACACGG  
 CCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

615/615

**FIGURE 610**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL  
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVI  
ATNLQEI R N G F S E I R G S V Q A K D G N I D I R I L R R T E S L Q D T K P A N R C C L L R H L L R L Y L D R V F  
K N Y Q T P D H Y T L R K I S S L A N S F L T I K K D L R L S H A H M T C H C G E E A M K K Y S Q I L S H F E K L E P Q  
A A V V K A L G E L D I L L Q W M E E T E

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 192-196;225-229

**N-myristoylation sites:**

Amino acids 42-48;46-52;136-142

10052585.011502